Abstract

Title of Thesis: IDENTIFICATION OF PUTATIVE O-REPEAT POLYSACCHARIDE BIOSYNTHETIC GENES IN *NEISSERIA SICCA* 4320

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Lipopolysaccharide (LPS) and lipooligosaccharide (LOS) are important virulence determinants found in gram-negative bacteria. LOS differs from LPS in that it lacks the O-repeat characteristic of LPS. While the genetic basis of LOS production in the pathogenic Neisseria has been extensively studied, little research has focused on the genetics underlying LOS production and resulting diversity in commensal *Neisseria*. A commensal strain that caused a fatal case of bacterial endocarditis, *Neisseria sicca* 4320, was found to produce a unique polysaccharide similar to the O-repeat of LPS in addition to typical *Neisseria* LOS. *N. sicca* 4320 was analyzed by bioinformatic and molecular biological gene-finding screens to identify putative O-repeat biosynthesis genes. Twenty-one open reading frames (ORFs) with similarity to other polysaccharide biosynthesis genes were located in the screens of *N. sicca* 4320. Two open reading frames with similarity to glycosyltransferases were found to be unique to *N. sicca* 4320.

IDENTIFICATION OF PUTATIVE O-REPEAT BIOSYNTHETIC GENES IN *NEISSERIA SICCA* 4320

by

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List of Abbreviations

GCK	Gonococcal media
HRP	Horseradish peroxidase
LOS	Lipooligosaccharide
LPS	Lipopolysaccharide
ORF	Open reading frame
ROI	Region of interest

Chapter 1: Introduction

Background

Members of the genus *Neisseria*, nonmotile gram-negative diplococci, contain both commensal strains (bacteria that do not cause disease in the host) and pathogenic strains (bacteria that cause a disease state in the host) which coexist on mucosal surfaces [1]. *N. gonorrhoeae* is an obligate human pathogen that colonizes urogenital mucosal surfaces and causes the sexually transmitted disease gonorrhea. Infection can be symptomatic or asymptomatic and can lead to epididymitis in men and pelvic inflammatory disease in women. *N. gonorrhoeae* is responsible for more than 350,000 new infections every year in the United States. *N. meningitidis* inhabits mucosal surfaces of the nasopharynx and can cause septicemia and meningitis. It has been estimated that up to ten percent of individuals are carriers of *N. meningitidis*. Unlike their pathogenic cousins, commensal *Neisseria* rarely cause disease in humans. In certain circumstances, such as IV drug use or poor oral hygiene, commensal *Neisseria* gain access to the blood stream and can encounter areas not normally associated with Neisserial colonization. This can result in infection and disease [2, 3]. Similar phenomena can be seen with immunocompromised individuals [3]. In all other cases the commensal strains coexist with other resident flora and do not perturb the host.

Both commensal and pathogenic *Neisseria* interact with their environment through their surface molecules. The surface of gram-negative bacteria is termed the outer membrane and composed of a lipid bilayer containing lipidated sugar molecules and proteins which mediate the interaction of the bacteria with the environment and the

uptake of exogenous molecules [4]. Surface structures important for *Neisseria* include pili (important for attachment to host cells), *Por* proteins (form the porin channel for nutrient flow), and *Opa* proteins (mediate attachment and microcolony formation) [4]. *N. meningitidis*, unlike *N. gonorrhoeae,* also possess a capsule which can help to mediate host cell attachment and immune evasion [4].

Another important surface molecule is lipooligosaccharide (LOS). LOS lacks the O-repeat unit found in the more typical lipopolysaccharide (LPS). LOS biosynthesis in *N. meningitidis* and *N. gonorrhoeae* has been extensively studied and can serve as a model for LPS/LOS biosynthesis despite the variation found among the LOS of *Neisseria* [5-8]. LOS in *Neisseria* is composed of lipid A, which anchors the oligosaccharide chains to the membrane, an inner core composed of two KDO and two heptose residues, and an oligosaccharide extension from the inner core. Inner core residues connect the outer core to the lipid A anchor (Figure 1) [9]. In the case of LPS, *Escherichia coli* attachment of the inner core to lipid A occurs in the cytoplasm [10]. The *E. coli* structure is then transported to the periplasm through the action of MsbA. Some LPS producing *E. coli* strains add O-antigen to the structure in the periplasm. The resulting molecule is transported across the outer-membrane by an unknown mechanism [11]. A strain must possess all the genes necessary for the synthesis of precursors, assembly of the inner and outer core, and transport mechanisms to successfully produce LOS.

The genes responsible for the production of LOS in *Neisseria* are found at five genomic locations [9, 12-16]. One location contains the *lgtABCDE* cluster, which encodes genes responsible for the extension of the α chain [13]. Another location contains *lgtF* and *rfaK*, which encode for genes responsible for the initiation of the α

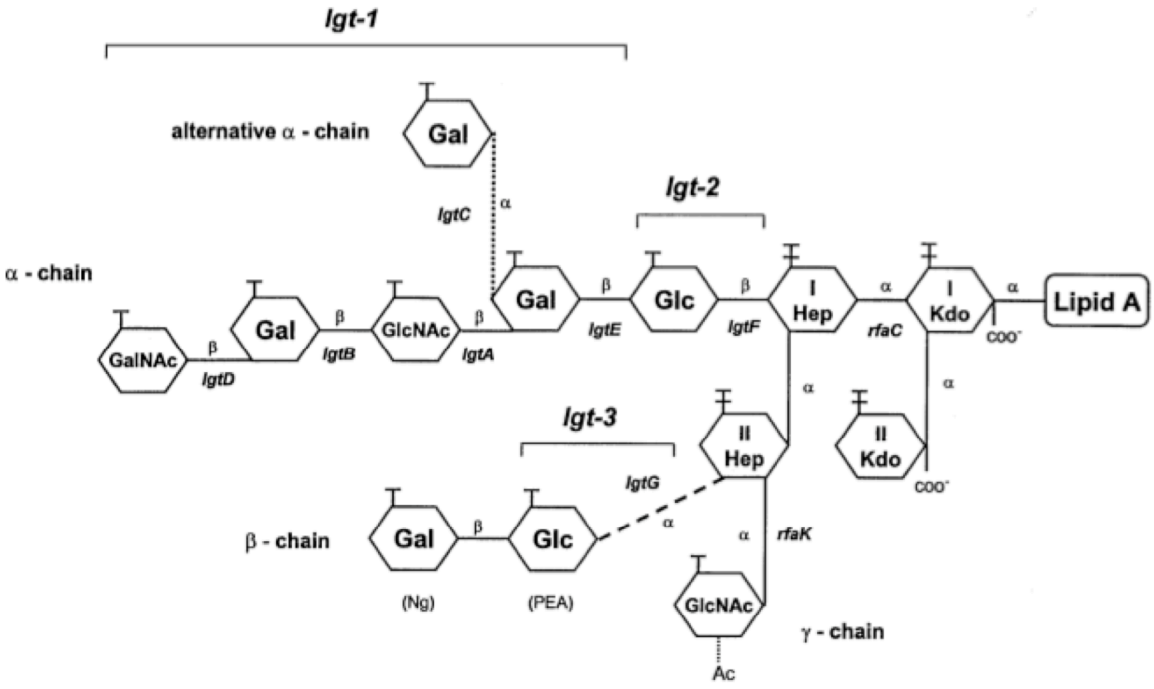

Figure 1. Schematic representation of Neisserial LOS and genes responsible for its biosynthesis. From [2]

chain and synthesis of the γ chain [15]. A third location contains *lgtG*, which encodes the gene responsible for the synthesis of the β chain [12]. The fourth location contains *rfaC* whose product adds a heptose residue to KDO [17]. The product of *rfaF,* contained in the fifth location, adds a second heptose residue to the first heptose [13, 18, 19]. LgtF can now add a glucose residue to the first heptose. The α chain can now be synthesized by the sequential addition of monosaccharides by the products of the *lgtABCDE* cluster in the order shown in Figure 1 [13]. β chain synthesis is initiated by the addition of a glucose residue to the second heptose. This process is mediated by the product of *lgtG* [12]. γ chain synthesis is mediated by the product of *rfaK* that attaches a *N*-acetylglucosamine to the second heptose residue [20]. This organization, along with examples from other organisms, indicates that LPS/LOS biosynthesis genes are maintained as clusters occurring at a few discrete loci within the chromosome [21, 22].

Comparison of pathogenic and commensal *Neisseria* has shown that some LOS producing commensal *Neisseria* lack all the genes found in the first three locations. *N. sicca*, for example, was found to have no hybridizable sequence with the genes of the first three locations [21, 23]. This indicates that, at least within some commensal species, there are glycosyltransferase genes found in other locations that are responsible for LOS production [21, 23].

Considerable heterogeneity exists in the LOS structures produced by *Neisseria* both within a species and across species [24]. Alterations in LOS structure are based on modifications of core oligosaccharides or variations in the composition of chain extensions from the heptose residues [25, 26]. Variations in LOS production between strains result from the absence of all or part of a LOS locus, rearrangements within the

locus, or because of the presence of additional genes in the locus. For example, it was shown that *N. gonorrhoeae* PID2 was able to express six different LOS structures and had undergone recombination in the *lgtABCDE* cluster [25]. Another example can be found in *N. meningitidis* strains. These strains have been found to have deletions of genes in the *lgtABCDE* cluster resulting in alternative LOS molecules [14]. Heterogeneity within a strain is seen in variations of type and amount of LOS produced [3]. The length of the chain extensions can be changed through phase variation [13, 18, 19]. Poly-guanine tracts found within some genes, such as *lgtA, lgtC, and lgtD*, can lead to variation in the number of guanines present. This can in turn result in genes that shift in and out of frame, affecting expression levels of functional protein [14, 27, 28]. These types of expression systems are useful because they could allow a member of a population to acquire an advantageous phenotype. For example, acquisition of a structure that mimics one found on host tissue would allow the pathogen to evade host defenses while acquisition of a phenotype that is associated with invasion could aid in dissemination of the bacteria [29-33].

A strain of *N. sicca, N. sicca* 4320, was isolated from a patient who died of infective endocarditis and can illustrate the variation of LOS. *N. sicca* is a commensal *Neisseria* species. *N. sicca* has been shown to cause pneumonia, osteomyelitis, infective endocarditis, and meningitidis [43-46]. Other commensal *Neisseria* have been shown to cause similar disease [46]. This strain was analyzed by SDS-PAGE/silver staining and found to produce two structurally distinct classes of surface liposaccharides. One class was characterized by a fast migrating band on the SDS-PAGE gel of similar molecular weight as LOS found in other *Neisseria* species. The other class of molecule contained

repeating units that gave a ladder-banding pattern on the SDS-PAGE gel characteristic of the O-repeat found in lipopolysaccharide (LPS) [34]. The synthesis of this molecule did not correlate with the presence of plasmid within the bacteria [47]. Structural studies were carried out to determine the linkage and composition of the novel LPS molecule. Monosaccharide composition studies, glycosidase digestion, lectin binding, gas chromatography, and mass spectrometry determined that the O-repeat was a disaccharide composed of repeating units of *N*-acetylglucosamine and rhamnose, with *N*-acetylglucosamine as the terminal sugar. The rhamnose was found to link with the preceding *N*-acetylglucosamine through a β (1-3) bond. The *N*-acetylglucosamine was linked to the preceding rhamnose through a β (1-4) bond. The linkage of the O-repeat to the membrane, while not characterized, appeared to involve a novel chemistry or linkage molecule [48]. This is similar to *Haemophilus ducreyi,* which can synthesis an LPS containing only a disaccharide [49, 50]. The same study also compared *N. sicca* 4320 genomic DNA contained in shotgun clones to neisserial genomic data contained in online databases. It was found that most of the *N. sicca* 4320 clones showed significant similarity to the *N. meningitidis* genome. This allowed the mapping of the shotgun clones to the MC58 chromosome [48].

As stated earlier, *N. gonorrhoeae* PID2 was found to simultaneously produce six different LOS structures. Note that while there were multiple molecules produced, they were all variations of LOS. While some species, such as *Campylobacter jejuni,* can produce both LOS and LPS, an organism producing both has not been seen in *Neisseria*. It is also worth noting that the LPS produced by *N. sicca* 4320 contains rhamnose [34]. Rhamnose was also found in *N. sicca* strains, and also *N. canis* and *N. subflava* (39).

Recent research has not found the presence of rhamnose in any pathogenic LOS structures despite the presence of cryptic rhamnose biosynthesis genes in *N. gonorrhoeae*. Deletion of the genes did not alter LOS production or structure. This novel molecule was associated with an organism showing increased virulence. The potential for the transfer of these biosynthetic genes to another *Neisseria* exists [35-37]. *Neisseria* are competent for the uptake of exogenous DNA throughout their lifecycle [38]. Commensal *Neisseria* have been shown to act as a source of genetic diversity by transferring genes responsible for penicillin and erythromycin resistance [39-41]. Genomic studies on *N. lactamica* have found regions of horizontally acquired DNA and the presence of many *N. meningitidis* associated genes [42]. Sequence analysis of *lgt* loci in *N. meningitidis* revealed exchange between MC58 and *N. subflava* 44 [9].

Scope of Project

As stated previously *N. sicca* 4320 was found to produce a polysaccharide structure similar to lipopolysaccharide (LPS) on a SDS-PAGE gel [51]. Structural analysis of the polysaccharide indicated that the repeat was composed of a disaccharide with a novel linkage [34]. This project was undertaken to identify putative polysaccharide biosynthesis genes since the genetics underlying the production of this structure are unknown. The hypothesis guiding this research was that the genetic elements responsible for the production of the polysaccharide were acquired as a group by horizontal gene transfer. This was hypothesized for three reasons. The initial analysis of *N. sicca* 4320 failed to find any isolatable plasmids which indicates that the LPS biosynthesis genes are found on the chromosome [47]. *Neisseria* species and many other organisms arrange their LPS/LOS biosynthesis genes into clusters [9]. This structure was novel and has never been seen in any other *Neisseria*. The novelty of the linkage and structure of the polysaccharide produced by *N. sicca* 4320, as compared to other neisserial LOS, indicates that the genes for this structure were acquired horizontally.

The project can be separated into two phases. Phase 1 consisted of a bioinformatic gene-hunting screen. The genome of *N. sicca* 4320 was sequenced, the species designation was confirmed by phylogenetic comparison, the five LOS biosynthetic loci identified and compared to other *Neisseria*, and the sequences searched for open reading frames (ORF) with similarity to polysaccharide biosynthesis genes. Phase 2 involved cloning a subset of the identified putative polysaccharide biosynthesis genes and randomly screening the *N. sicca* 4320 genome in an attempt to locate other putative genes not found in the bioinformatic screen.

This project, and studies of *Neisseria* in general, are of interest because two of the species, *N. meningitidis* and *N. gonorrhoeae* are important human pathogens. *N. meningitidis* can cause septicemia and meningitis, resulting in a mortality rate of 10-14% [3]. *N. gonorrhoeae* infects approximately 360,000 people every year causing gonorrhea [2]. The incidence of gonococcal infection, spread by sexual contact, decreased from 1975 to 2004, but recent data show an increasing gonococcal infection rate [2]. The other *Neisseria* species, while commensal, can cause infection and disease in rare cases. *N. sicca* has been shown to cause pneumonia, osteomyelitis, and infective endocarditis [44-46]. *N. sicca* 4320, the strain under study, was isolated from a patient who died due to infective endocarditis. Every year some 3 billion dollars are spent on containing and treating neisserial infections [2]. Study of virulence determinants of *Neisseria* will aid in the design of better treatment methods.

LPS and LOS are phase variable surface structures in the *Neisseria* [28, 52]. LOS structures, lacking a LPS-like polysaccharide, are found in both pathogenic and commensal species [9, 47, 53]. Studies on alternative LPS/LOS structures, especially those found on an organism with increased virulence like the strain under study in this project, will lead to a greater understanding of the potential repertoire of surface structures available to *Neisseria* and their underlying synthesis mechanisms. This in turn could help overcome some of the difficulties associated with neisserial vaccines and aid in the assessment of novel glycosyltransferases found in other *Neisseria* species.

This project is also important because the genetic potential of commensal species is an understudied area within the field. Recent research has compared the genomic organization of commensals and pathogens, but little has focused on the genetic basis of

commensal LPS/LOS biosynthesis [21, 54, 55]. It has been shown that some LOS producing commensal species lack some of the LOS biosynthetic genes found in the pathogenic *Neisseria*, suggesting commensal species have alternative LOS genes. This research will increase the available knowledge concerning commensal species and their LPS/LOS genetic potential and organization. An understanding of this potential is important because pathogenic and commensal species share the same mucosal surfaces. Commensal species can act as a source of genetic diversity for neighboring *Neisseria* because *Neisseria* species are competent throughout their life cycle and readily take up exogenous DNA [38]. *Neisseria* have been found to acquire antibiotic resistance and *lgt* genes through horizontal gene transfer [40, 57]. Commensal strains have in some cases aided in the transfer of genetic information from unrelated species to pathogens [56]. Given that alteration of LOS plays an important role in disease potential and *N. sicca* 4320 shows an increased virulence, strains like *N. sicca* 4320 provide the potential for the acquisition of a more virulent phenotype by other, neighboring *Neisseria*.

Chapter 2: Materials and Methods

Chemicals, reagents, and enzymes. All chemicals were reagent grade or better and were purchased from Sigma (St. Louis, MO) unless otherwise noted. Tris/Tricine SDS-PAGE running buffer was purchased from Biorad (Hercules, CA). The lectin GS-II was purchased from EY Laboratories (San Mateo, CA). Restriction enzymes, T4 DNA ligase, and hexosaminidase were purchased from New England Biolabs (Ipswich, MA).

Bacterial strains and growth conditions. Bacterial strains used in this study are listed in table MM-1. *Escherichia coli* (E. coli) strains were grown at 37^{o} C in LB Agar Miller or LB Broth Miller (USBiological; Swampscott, MA). Additions to the media included ampicillin (60 μg/ml), kanamycin (50 μg/ml), spectinomycin (50 μg/ml, 30 μg/ml), and X-gal. All *Neisseria* strains were grown at 37^{o} C in GCK agar or GCP broth (BD; Sparks, MD) supplemented with Kellogg's (1X). Strains grown on agar were incubated in a 10% CO_2 incubator while strains grown in broth were further supplemented with $NACOO_3$ (0.042%) and incubated in a rotary shaker. Additions to the media included kanamycin (25 μg/ml), spectinomycin (25 μg/ml), and polymyxin B (2 μg/ml).

Bacterial transformation. *E. coli* DH5α and *Neisseria sicca* 4320 were made competent by the Inoue method and transformed using the heat-shock method [57].

Bacterial chromosomal DNA isolation. *N. sicca* 4320 chromosomal DNA was isolated by two different methods. One method was the Wizard Genomic DNA Purification Kit

(Promega; Madison, WI). The other was the DNA-spooling method. A pelleted 100 ml overnight culture was resuspended in 4 ml GTE. Lysozyme (1mg/ml) and SDS (1%) were added to the resuspended pellet and the solution was incubated at room temperature with gentle rocking. The sample was then incubated at 37^{o} C for 2 hours with added RNase (0.25 mg/ml) and Proteinase K (50 μg/ml). The sample was extracted with Tris-saturated phenol for 10 minutes, followed by multiple phenol:chloroform extractions to generate a phase clear of cellular residue. One-tenth volume 5M NaCl and 2 volumes 95% EtOH were added to the sample. The precipitated DNA was spooled using a bent glass rod, washed with 75% EtOH, 95% EtOH, dried, and resuspended in 1 ml H_2O.

Plasmid isolation. Plasmid DNA was isolated by the alkaline-lysis method [57].

Restriction digestion. Plasmid and PCR purified DNA (0.5 μg) were incubated with 1 μl of the restriction enzyme and 2 μl of the appropriate buffer in a total reaction volume of 20 μl for 2 hours. Chromosomal DNA (1 μg) was incubated with 1 μl of the restriction enzyme and 2 μl of the appropriate buffer in a total reaction volume of 20 μl overnight. Where appropriate, BSA (1X) was added to the mix.

<KAN-2> insertion. The transposon <KAN-2> was inserted into target DNA using the EZ-Tn5 kit from Epicentre Biotechnologies (Madison, WI) [58].

PCR and purification. Primers used for PCR were ordered from Integrated DNA Technologies (North Liberty, IA) and arrived as lyophilized powder. Primers were resuspend to a stock concentration of 100 μM. PCR was carried out using a PTC-100 thermocycler produced by MJ Research, Inc (Waltham, MA). Promega (Madison, WI) GoTaq was used in the reaction. PCR amplicons were purified using the Qiagen (Valencia, CA) PCR purification kit.

Inverse PCR. Isolated *N. sicca* 4320 chromosomal DNA was isolated and digested with XhoI. XhoI was chosen because it cuts outside of the region cut by EcoRI producing a fragment containing the known sequence of the shotgun clone and flanking sequence. A series of ligation reactions were carried out with decreasing DNA concentrations conditions which favor self-ligation of the product. The ligation mixes were used as template DNA in a PCR using the primers 187F-Inverse and 467R-Inverse. These primers were designed to amplify out from the know regions [57].

DNA sequencing. Regions to be sequenced using the appropriate primers. Amplified DNA was sent to Macrogen (Seoul, Korea) along with the amplification primer for sequencing.

Agarose gel electrophoresis. DNA was run on 1% agarose gel at a constant 100V in a Bio-Rad (Hercules, CA) gel tray using a Hoefer Scientific Instruments (San Francisco, CA).

LPS/LOS isolation. *N. sicca* 4320 was swabbed from a plate and resuspended to a Klett of 100 in GCP. A 1 ml aliquot of the resuspended *N. sicca* 4320 was pelleted and resuspended in 50 µl lysing buffer. Proteinase K was added to the sample and it was incubated at 60 ^{o}C. Samples were diluted 1:25 in lysing buffer while still hot [59].

SDS-PAGE of LPS/LOS. Isolated LPS/LOS was boiled for 10 minutes and loaded onto a 16.5% Tris-Tricine gel from Bio-Rad (Hercules, CA). The gel was run at a constant current of 0.03 mA until the dye front reached the bottom of the gel.

Silver-staining of LPS/LOS gel. After SDS-PAGE, the gel was placed in fixing solution overnight. The following morning the gel was washed for 1 hr with four changes of HPLC H_2O. The gel was oxidized in 0.833% periodic acid for 5 minutes and washed with four changes of HPLC H_2O over 1.5 hours. The gel was then stained with silver staining solution for 15 minutes. The gel was washed with four changes of HPLC H_2O over 1.5 hours. Developing solution (0.42% NH_4OH, 0.047M $AgNO_3$, 0.0225M NaOH) was added to the gel and it was placed on a shaking incubator. Development was stopped when LPS/LOS bands became apparent by immersion of the gel in HPLC H_2O. The gel was transferred to a Ziploc bag and scanned into a computer.

Lectin GS-II western blot. *N. sicca* 4320 LPS/LOS was transferred onto an Immobilon-P PVDF membranes (0.45µm, Millipore) using a Criterion Blotter at a constant 100V for 20 min. The PVDF membrane was dried for 1 hr and blocked in 5% dry milk for 90 minutes. The membrane was incubated overnight at 4 ^{o}C with lectin GS-II (EY

Laboratories) at a concentration of 10 μg/mL. The membrane was washed 3X with GS-II buffer and incubated with HRP-developing solution (0.006% H_2O_2, 0.08% 4-chloro-1-napthol, 50mM Tris).

α-4320 western blot. *N. sicca* 4320 LPS/LOS was transferred onto an Immobilon-P PVDF membranes (0.45μm, Millipore) using a Criterion Blotter at a constant 100V for 20 min. The PVDF membrane was dried for 1 hr and blocked in PBS buffer containing 1% gelatin (Sigma) and 0.1% Tween 20 (Fisher Scientific). The membrane was incubated with α-4320 for 90 minutes and washed 3 times with PBS containing 0.1% Tween 20. The membrane was incubated with HRP-conjugated goat α-rabbit IgG (Upstate) for 1 hr. Membranes were washed 3 times with PBS containing 0.1% Tween-20 and incubated with HRP-developing solution (0.006% H_2O_2, 0.08% 4-chloro-1-napthol, 50mM Tris).

Lectin GS-II colony blot. Colonies were blotted onto a circular nitrocellulose membrane. The membrane was dried and blocked for 1 hr using 5% dry milk. Excess colony was rubbed off of the blocked membrane. The membrane was washed 3X with GS-II buffer. The membrane was incubated for 90 minutes with lectin GS-II (EY Laboratories) at a concentration of 10 μg/mL.. The membrane was washed 3X with GS-II buffer and incubated with HRP-developing solution (0.006% H_2O_2, 0.08% 4-chloro-1-napthol, 50mM Tris).

Polymyxin B screen. Polymyxin B resistant colonies were generated using two methods. 500 µl of an overnight *N. sicca* 4320 were swabbed onto the surface of a GCK plate. After the plate dried 5 µl spots of polymyxin B were arrayed onto the plate. The plate was incubated overnight at 37 ^{o}C and polymyxin B resistant colonies selected from the zones of inhibition. The selected colonies were analyzed by GS-II colony blot and LPS/LOS western blot. In the second method, *N. sicca* 4320 colonies were swabbed across the surface of a GCK plate containing polymyxin B. The plate was incubated overnight at 37 ^{o}C and polymyxin B resistant colonies were selected. The selected colonies were analyzed by GS-II colony blot and LPS/LOS western blot [60].

Commensal *Neisseria* sequencing. Chromosomal DNA for *N. sicca* 4320, *N. sicca* DS1, *N. sicca* 342, *N. sicca* NS19, and *N. subflava* 44 was isolated. The DNA was sent for 454 pyrosequencing. The sequence reads were assembled using Newbler and the sequence was returned as a set on contigs for each commensal [61].

Mummer alignments. The contig sequences of *N. sicca* 4320 were aligned with the contig sequences of the other identified commensals using Nucmer, a component of the Mummer software package [62]. The alignments were filtered to remove repeat alignments leaving a 1-to-1 alignment between *N. sicca* 4320 and the sequenced commensal. The alignment data was exported into an Excel spreadsheet for analysis.

Geneious. The contig sequences of the commensals were loaded into the program Geneious. Custom BLAST databases of each sequenced commensal were compiled to

use for further analysis. Geneious was used to manage all sequences and to construct the sequence figures found throughout [63].

Phylogenetic analysis. 16S rRNA sequences for each sequenced commensal were identified by BLAST using the sequence of *N. sicca* Q29 (AJ239294) as a query [64]. A phylogenetic tree was constructed from the sequenced commensals along with other sequences found in the Ribosomal Database Project's database using the Ribosomal Database Project's tree builder application. The tree was exported as a .pdf document. The genes for sucrose and lactose metabolism were identified in the commensals by BLAST searches. The contig sequences of *N. meningitidis* NS44 were aligned with the genome of *N. meningitidis* MC58 using the contig mover application found within the program Mauve [65].

ORF annotation. The contig sequences of *N. sicca* 4320 were analyzed by the program Glimmer3 and putative ORFs predicted [66]. The amino acid sequences of the predicted ORFs were extracted and used as queries in BLAST searches of the DanAnn database and nr database. The annotation of the ORFs were exported to an Excel spreadsheet for further analysis. The functional annotation was determined by searching the UniProt database with the annotation of the ORFs. The Pfam annotation of each ORF was determined by searching the Pfam-A database with the ORF sequence.

Bioinformatic BLAST screen of *N. sicca* 4320. The custom *N. sicca* 4320 BLAST database was searched using the sequences with similarity to glycosyltransferases. ORFs

showing similarity to the sequences were used as a query in a BLAST search of the nr database to confirm similarity to putative O-repeat biosynthesis genes.

Chapter 3: Bioinformatic screen of *N. sicca* 4320

Introduction

It is possible to make predictions about the types of genes involved in the biosynthesis of *N. sicca* 4320 LOS and the LPS-like polysaccharide given the available structural data. The LOS of *N. sicca* 4320 is predicted to be composed of a three-heptose residue core with a two-hexose residue extension and the polysaccharide is predicted to be composed of a rhamnose--*N*-acetylglucosamine disaccharide [34]. The LOS structure would therefore require the action of three heptosyltransferase enzymes and two glycosyltransferase enzymes to synthesize the structure while the polysaccharide would require the activity of a glycosyltransferase to synthesize the disaccharide, an O-antigen polymerase to polymerize the O-repeat, and a ligase enzyme to ligate the O-repeat to its anchor [10]. The biosynthesis of these structures would also require the action of the appropriate transporters to move the structures to the periplasm and finally to the outer membrane [10].

A bioinformatic gene-finding screen was utilized to identify putative LOS and LPS-like polysaccharide biosynthesis genes. The gene-finding screen had four goals: confirmation of the species classification of *N. sicca* 4320, determining the open reading frames found in the genomic data, annotation of the ORFs, and identification of putative LOS and polysaccharide biosynthesis genes. Genomic DNA sequences of *N. sicca* 4320 were obtained from 454 sequencing of chromosomal DNA. The 16S rRNA region from *N. sicca* 4320 was used to confirm that the initial species classification was correct; genes corresponding to species-specific phenotypic characteristics were used as a second

method of confirming classification [64, 67, 68]. One of the advantages of using sequence data is the ability to compare the data with other neisserial genomic data. It will be possible to determine if the putative genes are common to all *Neisseria,* common to all commensals, common to all *N. sicca* strains, or unique to *N. sicca* 4320. The ORFs found in the genomic data were determined using the Glimmer3 program and annotated by BLAST comparison [66]. The annotated ORFs were searched to identify any putative genes that had similarity to known LOS, LPS, or capsule biosynthetic enzymes. A subset of the putative genes identified in the bioinformatic gene-finding screen was further analyzed in the following chapter.

Results

Genomic sequencing and assembly

Whole genome sequencing was undertaken to generate sequence data for use in identification of polysaccharide biosynthetic genes. Chromosomal DNA from *N. sicca* 4320 along with four other organisms previously classified as commensals, *N. sicca* DS1, *N. sicca* NS19, *N. sicca* 342, and *N. subflava* 44, was isolated and sent to a 454 pyrosequencing facility. The sequencing reads were assembled using the Newbler assembler providing a series of contigs. *N. sicca* 4320 genomic sequence was contained in 169 contigs representing 2.5 Mb of sequence (Table 1), *N. sicca* DS1 was contained in 455 contigs, *N. sicca* NS19 was contained in 132 contigs, *N. sicca* 342 was contained in 288 contigs, and *N. subflava* 44 was contained in 365 contigs. All five organisms averaged 25-30X coverage. Sequence data for two other commensal *Neisseria* sequenced at Washington University*, N. sicca* ATCC 29256 and *N. mucosa* ATCC 25996, was also obtained to use for comparison to *N. sicca* 4320. Custom BLAST databases containing the contig sequences for each organism were constructed to allow comparison and analysis of each organism.

Whole genome alignments

A software program called Nucmer, which finds regions of similarity in the two sets of genomic DNA and uses these regions to perform genome wide alignments, was used to compare the genomic sequence of *N. sicca* 4320 to each other sequenced commensal (Table 2). It was found that *N. sicca* 4320 is 95.0% identical to *N. sicca* DS1

Table 1. Sequencing statistics for *N. sicca* 4320.

Name	Description		Sequence Length
contig00001	length=12945	numreads=806	12945
contig00002	length=2736	numreads=164	2736
contig00003	length=1431	numreads=97	1431
contig00004	length=5582	numreads=347	5582
contig00005	length=5564	numreads=386	5564
contig00006	length=8788	numreads=581	8788
contig00007	length=1792	numreads=144	1792
contig00008	length=52197	numreads=3567	52197
contig00009	length=7063	numreads=532	7063
contig00010	length=80744	numreads=5133	80744
contig00011	length=56348	numreads=3896	56348
contig00012	length=14674	numreads=1016	14674
contig00013	length=8929	numreads=552	8929
contig00014	length=2310	numreads=359	2310
contig00015	length=762	numreads=65	762
contig00016	length=18465	numreads=1241	18465
contig00017	length=11661	numreads=753	11661
contig00018	length=7954	numreads=558	7954
contig00019	length=942	numreads=65	942
contig00020	length=5328	numreads=357	5328
contig00021	length=25273	numreads=1638	25273
contig00022	length=18083	numreads=1260	18083
contig00023	length=24638	numreads=1634	24638
contig00024	length=28823	numreads=1709	28823
contig00025	length=2393	numreads=165	2393
contig00026	length=21342	numreads=1423	21342
contig00027	length=25066	numreads=1615	25066
contig00028	length=55076	numreads=3567	55076
contig00029	length=15598	numreads=1124	15598
contig00030	length=4870	numreads=363	4870
contig00031	length=10520	numreads=668	10520
contig00032	length=11775	numreads=844	11775
contig00033	length=10295	numreads=680	10295
contig00034	length=147	numreads=19	147
contig00035	length=150	numreads=7	150
contig00036	length=16103	numreads=1053	16103
contig00037	length=9733	numreads=566	9733
contig00038	length=741	numreads=52	741
contig00039	length=28503	numreads=2111	28503
contig00040	length=11528	numreads=717	11528
contig00041	length=6719	numreads=513	6719
contig00042	length=10191	numreads=634	10191
contig00043	length=153	numreads=28	153
contig00044	length=23496	numreads=1551	23496

contig00045	length=103655	numreads=6477	103655
contig00046	length=35130	numreads=2305	35130
contig00047	length=25956	numreads=1674	25956
contig00048	length=15642	numreads=1082	15642
contig00049	length=27384	numreads=1724	27384
contig00050	length=28578	numreads=1786	28578
contig00051	length=65411	numreads=4139	65411
contig00052	length=41808	numreads=2774	41808
contig00053	length=17839	numreads=1027	17839
contig00054	length=194	numreads=25	194
contig00055	length=37513	numreads=2339	37513
contig00056	length=62281	numreads=4212	62281
contig00057	length=25490	numreads=1591	25490
contig00058	length=177725	numreads=11110	177725
contig00059	length=8883	numreads=643	8883
contig00060	length=29244	numreads=1780	29244
contig00061	length=11320	numreads=699	11320
contig00062	length=25889	numreads=1538	25889
contig00063	length=23947	numreads=1486	23947
contig00064	length=178	numreads=17	178
contig00065	length=109	numreads=19	109
contig00066	length=400	numreads=2	400
contig00067	length=375	numreads=2	375
contig00068	length=160	numreads=77	160
contig00069	length=2248	numreads=402	2248
contig00070	length=12365	numreads=853	12365
contig00071	length=6250	numreads=1663	6250
contig00072	length=2153	numreads=139	2153
contig00073	length=2813	numreads=216	2813
contig00074	length=1177	numreads=193	1177
contig00075	length=43995	numreads=2785	43995
contig00076	length=41072	numreads=2604	41072
contig00077	length=2793	numreads=332	2793
contig00078	length=30850	numreads=2041	30850
contig00079	length=9213	numreads=583	9213
contig00080	length=110180	numreads=7281	110180
contig00081	length=12419	numreads=724	12419
contig00082	length=925	numreads=145	925
contig00083	length=134	numreads=13	134
contig00084	length=291	numreads=8	291
contig00085	length=2591	numreads=387	2591
contig00086	length=940	numreads=518	940
contig00087	length=462	numreads=81	462
contig00088	length=16545	numreads=1166	16545
contig00089	length=14811	numreads=934	14811
contig00090	length=159	numreads=22	159
contig00091	length=159	numreads=22	159

contig00092	length=46059	numreads=2849	46059
contig00093	length=113	numreads=33	113
contig00094	length=14154	numreads=986	14154
contig00095	length=7393	numreads=572	7393
contig00096	length=4969	numreads=660	4969
contig00097	length=128	numreads=324	128
contig00098	length=271	numreads=138	271
contig00099	length=17265	numreads=1083	17265
contig00100	length=404	numreads=35	404
contig00101	length=9220	numreads=622	9220
contig00102	length=2211	numreads=365	2211
contig00103	length=304	numreads=377	304
contig00104	length=272	numreads=97	272
contig00105	length=223	numreads=29	223
contig00106	length=17583	numreads=1175	17583
contig00107	length=13492	numreads=817	13492
contig00108	length=72149	numreads=4421	72149
contig00109	length=1616	numreads=108	1616
contig00110	length=297	numreads=419	297
contig00111	length=204	numreads=616	204
contig00112	length=123	numreads=140	123
contig00113	length=98754	numreads=6062	98754
contig00114	length=157	numreads=36	157
contig00115	length=18427	numreads=1309	18427
contig00116	length=41233	numreads=2527	41233
contig00117	length=28545	numreads=1858	28545
contig00118	length=974	numreads=105	974
contig00119	length=6098	numreads=458	6098
contig00120	length=813	numreads=144	813
contig00121	length=743	numreads=163	743
contig00122	length=11448	numreads=686	11448
contig00123	length=4195	numreads=283	4195
contig00124	length=27813	numreads=1844	27813
contig00125	length=781	numreads=133	781
contig00126	length=424	numreads=46	424
contig00127	length=591	numreads=136	591
contig00128	length=206	numreads=325	206
contig00129	length=335	numreads=68	335
contig00130	length=235	numreads=575	235
contig00131	length=18145	numreads=1131	18145
contig00132	length=4582	numreads=372	4582
contig00133	length=151	numreads=185	151
contig00134	length=11655	numreads=708	11655
contig00135	length=6367	numreads=391	6367
contig00136	length=19317	numreads=1251	19317
contig00137	length=195	numreads=35	195
contig00138	length=16660	numreads=1086	16660

contig00139	length=2873	numreads=207	2873
contig00140	length=364	numreads=33	364
contig00141	length=27662	numreads=1946	27662
contig00142	length=4768	numreads=385	4768
contig00143	length=633	numreads=61	633
contig00144	length=287	numreads=111	287
contig00145	length=2893	numreads=208	2893
contig00146	length=245	numreads=83	245
contig00147	length=260	numreads=35	260
contig00148	length=43377	numreads=2645	43377
contig00149	length=39237	numreads=2530	39237
contig00150	length=2214	numreads=201	2214
contig00151	length=38640	numreads=2532	38640
contig00152	length=10463	numreads=658	10463
contig00153	length=325	numreads=24	325
contig00154	length=772	numreads=94	772
contig00155	length=1537	numreads=123	1537
contig00156	length=470	numreads=147	470
contig00157	length=1420	numreads=81	1420
contig00158	length=555	numreads=54	555
contig00159	length=158	numreads=27	158
contig00160	length=154	numreads=385	154
contig00161	length=6775	numreads=466	6775
contig00162	length=35013	numreads=2135	35013
contig00163	length=350	numreads=30	350
contig00164	length=105	numreads=33	105
contig00165	length=135	numreads=39	135
contig00166	length=138	numreads=29	138
contig00167	length=22359	numreads=1427	22359
contig00168	length=459	numreads=537	459
contig00169	length=379	numreads=33	379

50.8% GC

Table 2. Alignment of *N. sicca* 4320 to *N. sicca* DS1 by Nucmer. The contig sequences of *N. sicca* 4320 were aligned to the contig sequences of *N. sicca* DS1 by the program Nucmer to determine conservation between these two *sicca* strains. Query: *N. sicca* 4320 contigs. Q Start: Hit start in query. Q End: Hit end in query. Reference: *N. sicca* DS1 contig. R Start: Hit start in reference. R End: Hit end in reference. %ID: Percent identity of alignment.

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00001	1	12402	contig00031	15046	2571	95.68
contig00001	12446	12942	contig00362	75663	76160	94.78
contig00003	78	1429	contig00425	27322	25970	95.64
contig00004	4	5582	contig00364	11	5592	92.66
contig00005	1	5562	contig00031	15066	20619	95.53
contig00006	45	5924	contig00025	27421	33302	95.7
contig00006	6052	6955	contig00025	33429	34333	92.83
contig00006	7666	8737	contig00025	34352	35421	93.29
contig00007	607	1612	contig00049	42554	41553	93.84
contig00008	2	2389	contig00372	1	2386	95.4
contig00008	2491	9063	contig00372	2341	8937	96.24
contig00008	9150	14304	contig00372	8826	13970	95.12
contig00008	14305	34443	contig00372	14179	34306	96.22
contig00008	36641	36908	contig00372	34353	34620	95.52
contig00008	37061	40860	contig00039	16993	13192	94.72
contig00008	41627	43618	contig00039	10514	8517	94.31
contig00008	43616	52053	contig00039	8414	5	95.12
contig00009	1	402	contig00012	190	591	92.59
contig00009	468	2228	contig00449	13196	11422	94.37
contig00009	2209	2494	contig00069	283	1	98.95
contig00009	5429	6959	contig00449	9231	7700	96.41
contig00010	267	4896	contig00420	4824	92	93.22
contig00010	4898	7486	contig00049	50360	47780	94.44
contig00010	7485	18214	contig00027	14285	25037	95.04

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00010	18455	20425	contig00441	12218	10250	96.4
contig00010	28591	28881	contig00127	1	291	100
contig00010	47136	47489	contig00053	354	1	100
contig00010	56010	56410	contig00121	400	1	99.5
contig00010	61865	65748	contig00441	10269	6389	95.52
contig00010	65754	69985	contig00441	6278	2021	92.84
contig00010	70104	70948	contig00441	1905	1062	91.03
contig00010	71156	71824	contig00441	884	211	95.99
contig00010	71827	71927	contig00441	102	1	96.08
contig00010	71933	73983	contig00450	15605	13549	95.09
contig00010	73908	76931	contig00450	13512	10489	95.84
contig00011	1	4988	contig00008	9232	4232	94.73
contig00011	5168	7759	contig00008	2583	1	93.87
contig00011	7758	9559	contig00024	63	1861	93.9
contig00011	9670	11194	contig00024	1869	3393	95.61
contig00011	11195	13543	contig00024	3500	5851	95.45
contig00011	13645	16382	contig00024	5848	8621	95.36
contig00011	16487	24343	contig00024	8621	16439	93.23
contig00011	24343	24501	contig00024	16560	16722	92.07
contig00011	24498	24605	contig00019	5672	5779	99.07
contig00011	24606	27557	contig00024	16722	19684	96.32
contig00011	27557	35298	contig00024	19788	27547	96.01
contig00011	35299	35411	contig00437	13936	14048	96.46
contig00011	35406	38763	contig00051	1	3348	95.16
contig00011	38760	38920	contig00360	30035	30195	95.06
contig00011	38918	40316	contig00051	3348	4747	97.43
contig00011	40477	42256	contig00051	4747	6526	97.25
contig00011	42390	43224	contig00051	6669	7503	97.49
contig00011	43242	43351	contig00360	6094	5985	99.09
contig00011	44131	46733	contig00051	8229	10842	95.18

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00011	46741	56348	contig00051	10934	20509	94.73
contig00012	79	4130	contig00394	50547	54601	95.83
contig00012	4158	4314	contig00007	80145	79988	99.37
contig00012	4311	11793	contig00394	54631	62119	96.52
contig00012	11795	12148	contig00394	62308	62661	96.61
contig00012	12144	14674	contig00010	2638	105	94.87
contig00013	728	2119	contig00030	61491	62885	96.49
contig00013	2112	8929	contig00028	1	6815	94.35
contig00015	134	760	contig00011	5761	5135	93.3
contig00016	2	3484	contig00007	42121	38639	97.59
contig00016	3577	11461	contig00007	38453	30640	94.06
contig00016	11615	11729	contig00007	30640	30526	96.52
contig00016	11732	13229	contig00007	30419	28932	94.01
contig00016	13223	13339	contig00037	25733	25848	94.87
contig00016	13334	18465	contig00007	28932	23784	95.15
contig00017	1	1531	contig00442	8823	7294	97.58
contig00017	2021	4510	contig00442	6828	4338	96.67
contig00017	4508	4615	contig00049	42660	42553	100
contig00017	4615	8773	contig00442	4338	183	94.79
contig00017	8868	11661	contig00413	254	3050	96.1
contig00018	331	1540	contig00435	14544	13328	89.67
contig00018	2457	5421	contig00435	12468	9494	86.66
contig00019	292	939	contig00380	21568	22213	93.98
contig00020	35	5203	contig00049	47777	42658	95.81
contig00020	5208	5319	contig00412	1	112	99.11
contig00021	20	126	contig00437	2	108	98.13
contig00021	126	1710	contig00014	10344	8760	98.04
contig00021	1844	3734	contig00014	8631	6742	94.5
contig00021	3736	3849	contig00030	15333	15441	93.86
contig00021	3916	9906	contig00014	6688	715	96.08

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00021	9912	10496	contig00014	608	24	96.07
contig00021	10494	22006	contig00433	1	11492	94.57
contig00021	22048	22198	contig00361	77320	77171	94.7
contig00021	22242	23979	contig00433	11492	13228	95.4
contig00021	23925	24086	contig00433	13282	13444	87.12
contig00021	24009	25273	contig00440	36660	35343	88.42
contig00022	2	10066	contig00394	50512	40335	94.35
contig00022	13261	18083	contig00394	39988	35191	93.17
contig00023	58	3282	contig00004	34746	31522	95.17
contig00023	3696	3802	contig00367	25352	25458	99.07
contig00023	3801	4741	contig00004	31345	30396	95.16
contig00023	4745	5034	contig00004	30296	30008	95.17
contig00023	5063	6300	contig00004	29841	28607	94.43
contig00023	6258	18073	contig00004	29153	17342	95.48
contig00023	18076	18231	contig00360	10945	11100	100
contig00023	18229	24638	contig00004	17343	10903	94.29
contig00024	1	13487	contig00370	8448	22016	95.88
contig00024	13643	18656	contig00370	22016	27028	96.41
contig00024	18652	28823	contig00047	10314	112	94.76
contig00025	4	93	contig00033	90	1	98.89
contig00025	111	2393	contig00403	99263	101544	95.18
contig00026	36	879	contig00371	2279	1436	96.33
contig00026	922	2081	contig00371	1163	4	97.67
contig00026	6928	8796	contig00426	1725	3589	95.24
contig00026	8815	13043	contig00419	5112	888	95.34
contig00026	13043	13777	contig00419	733	1	94.01
contig00026	13902	18178	contig00030	1	4294	95.51
contig00027	2053	8272	contig00007	74757	68532	95.25
contig00027	8782	13262	contig00007	68020	63539	94.23
contig00027	13428	14488	contig00007	63528	62468	95.66

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00027	14479	14642	contig00403	118121	117960	96.36
contig00027	14640	23959	contig00007	62470	53147	96.54
contig00027	24068	24442	contig00415	375	1	93.07
contig00027	24444	25041	contig00362	2	599	95.66
contig00028	197	408	contig00399	11737	11526	94.34
contig00028	287	429	contig00437	105	244	96.5
contig00028	414	3261	contig00026	27670	30508	96.1
contig00028	3416	8744	contig00026	30508	35831	95.48
contig00028	10873	12908	contig00026	39772	41807	93.91
contig00028	12911	15406	contig00026	41915	44409	93.83
contig00028	15571	18379	contig00428	6	2813	96.3
contig00028	20471	24226	contig00428	3305	7059	96.46
contig00028	24226	24333	contig00362	34873	34766	95.37
contig00028	24333	25677	contig00428	7061	8404	96.06
contig00028	25710	30330	contig00428	9077	13696	96.47
contig00028	30340	30445	contig00035	9989	9884	98.11
contig00028	30444	31781	contig00428	13715	15048	95.81
contig00028	31765	41442	contig00374	5458	15112	94.91
contig00028	42499	50885	contig00374	15114	23448	93.09
contig00028	51161	54701	contig00374	23646	27188	94.84
contig00028	54697	55075	contig00018	523	146	96.83
contig00029	1498	2576	contig00423	1078	1	92.8
contig00029	2809	5010	contig00360	6954	9156	96.46
contig00029	4996	5117	contig00228	9996	9874	97.56
contig00029	5694	7496	contig00360	9144	10945	96.73
contig00029	7494	9156	contig00360	11098	12760	95.07
contig00029	9765	11576	contig00360	12716	14525	94.71
contig00029	11765	15598	contig00360	14542	18372	96.25
contig00030	154	2546	contig00362	51891	49501	95.86
contig00030	2834	2936	contig00361	83458	83560	85.58

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00030	3851	4870	contig00362	48533	47520	88.75
contig00031	1	1141	contig00382	6450	7588	95.71
contig00031	1295	5034	contig00382	7588	11328	95.51
contig00031	5043	5150	contig00049	33006	32899	100
contig00031	5262	6789	contig00382	11328	12856	93.59
contig00032	219	1617	contig00380	252	1650	96.07
contig00032	1619	1735	contig00380	1763	1879	95.73
contig00032	2534	3551	contig00380	1867	2884	95.97
contig00032	3551	4262	contig00380	2989	3703	93.71
contig00032	9560	10997	contig00380	6752	8198	92.75
contig00032	10695	11532	contig00380	10051	10873	93.08
contig00033	1	6789	contig00425	7224	438	94.98
contig00033	8059	10293	contig00425	11380	13615	96.16
contig00036	236	899	contig00425	9650	8987	89.16
contig00036	1634	13478	contig00403	97097	85184	93.94
contig00036	13697	14824	contig00403	85146	84019	85.55
contig00036	14948	16103	contig00403	83924	82767	94.91
contig00037	1243	1545	contig00017	3592	3290	92.76
contig00037	1556	1811	contig00227	261	1	97.32
contig00037	1969	2101	contig00017	333	201	93.23
contig00038	3	338	contig00046	1938	1598	90.96
contig00039	265	8449	contig00040	832	9011	95.95
contig00039	8451	17202	contig00040	9760	18513	96.42
contig00039	17195	19707	contig00381	2517	1	98.29
contig00039	19733	26901	contig00422	7166	2	97.1
contig00039	26983	27163	contig00019	14442	14623	96.7
contig00039	27337	28501	contig00413	4237	3073	96.48
contig00040	3	10459	contig00364	5585	16054	93.65
contig00040	10488	11454	contig00367	15196	16161	97.1
contig00041	2240	2721	contig00288	1	484	99.59

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00041	4141	5394	contig00425	7944	6691	93.86
contig00041	5222	5559	contig00425	11073	10736	93.2
contig00042	2234	4450	contig00360	35668	33451	96.71
contig00042	4529	6692	contig00360	29989	27826	96.44
contig00042	6707	10010	contig00360	25782	22460	95.94
contig00043	53	153	contig00010	4	104	100
contig00044	5	784	contig00404	118	891	95.9
contig00044	794	3865	contig00015	1	3073	97.04
contig00044	3866	4045	contig00399	235	414	94.44
contig00044	4150	4319	contig00399	414	585	94.77
contig00044	4424	6790	contig00399	585	2948	96.28
contig00044	6825	7019	contig00444	28468	28276	82.65
contig00044	7027	7350	contig00361	13271	12935	89.32
contig00044	7504	8513	contig00361	12935	11930	95.64
contig00044	8512	8665	contig00437	3511	3358	91.61
contig00044	8620	9721	contig00361	11927	10814	95.96
contig00044	9870	20367	contig00361	10660	180	95.4
contig00044	20355	21509	contig00440	611	1754	94.12
contig00044	21800	21973	contig00440	2080	2252	89.14
contig00045	434	8054	contig00032	13738	6109	94.07
contig00045	8055	8161	contig00401	31294	31188	97.2
contig00045	8162	11480	contig00032	6106	2791	95.15
contig00045	12195	18617	contig00361	70749	77171	96.26
contig00045	18617	21555	contig00361	77293	80236	94.5
contig00045	21566	24523	contig00361	80402	83362	96.49
contig00045	26413	30827	contig00361	83647	88030	94.59
contig00045	30826	33465	contig00032	118	2772	95.26
contig00045	33512	36362	contig00361	70656	67800	95.38
contig00045	36418	36600	contig00017	183	1	89.62
contig00045	36462	36612	contig00041	6016	5864	78.71

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00045	36605	39169	contig00361	67352	64807	95.36
contig00045	39449	43374	contig00361	62832	58908	95.57
contig00045	43408	44215	contig00361	58481	57677	93.22
contig00045	44370	49566	contig00361	57675	52545	89.53
contig00045	49796	53069	contig00361	52328	49056	96.4
contig00045	53347	54682	contig00361	48439	47104	96.33
contig00045	55884	59258	contig00361	46564	43190	96.48
contig00045	59338	60802	contig00361	42238	40774	95.5
contig00045	61668	63768	contig00361	40074	37974	95.95
contig00045	64633	67942	contig00361	37990	34683	96.56
contig00045	68147	68480	contig00361	34677	34345	94.61
contig00045	68526	70061	contig00361	32290	30752	96.69
contig00045	70164	76825	contig00361	30754	24091	96.08
contig00045	76825	84599	contig00361	23988	16214	96.61
contig00045	85484	86300	contig00361	16173	15360	97.56
contig00045	86388	87644	contig00361	14520	13265	96.66
contig00045	87644	94042	contig00399	3210	9633	96.33
contig00045	95164	96680	contig00399	11273	9751	94.55
contig00045	96795	97657	contig00360	6937	6092	89.36
contig00045	97657	103642	contig00360	5987	1	95.77
contig00046	1133	9375	contig00440	2302	10543	96.46
contig00046	9568	13880	contig00440	10582	14888	95.85
contig00046	14017	16871	contig00440	15028	17868	90.49
contig00046	17413	17660	contig00440	18407	18656	95.2
contig00046	18270	19931	contig00440	19293	20926	86.97
contig00046	20838	32438	contig00440	20967	32581	96.13
contig00046	32688	35130	contig00440	32896	35340	95.62
contig00047	1	8135	contig00394	9805	17890	95.64
contig00047	8113	8335	contig00371	1058	1283	79.04
contig00047	8281	12880	contig00394	17807	22406	96.11

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00047	12879	12985	contig00031	2457	2351	99.07
contig00047	12983	13726	contig00394	22404	23146	96.64
contig00047	13707	13831	contig00026	25002	24876	92.13
contig00047	13819	19118	contig00394	23134	28442	93.92
contig00047	19115	19223	contig00048	37124	37016	100
contig00047	19221	25956	contig00394	28440	35174	95.64
contig00048	1	3344	contig00436	219	3562	97.28
contig00048	3376	15642	contig00052	12313	44	96.44
contig00049	2	9263	contig00048	54544	45319	94.85
contig00049	10513	18850	contig00048	45351	37121	94.01
contig00049	18848	27384	contig00048	37018	28424	93.87
contig00050	1323	7199	contig00427	5555	11426	95.08
contig00050	7310	8334	contig00427	11537	12561	96
contig00050	8578	16409	contig00427	12601	20436	96.65
contig00050	17673	18949	contig00427	20440	21711	95.07
contig00050	19766	20884	contig00427	21698	22817	94.82
contig00050	20887	22452	contig00001	31975	30409	93.75
contig00050	22691	22928	contig00001	30206	29971	93.28
contig00050	23238	28578	contig00001	29660	24328	94.12
contig00051	69	2838	contig00048	83698	80930	94.84
contig00051	3722	5691	contig00048	76474	74505	96.09
contig00051	5728	7098	contig00048	74243	72873	95.4
contig00051	7245	8171	contig00048	69096	68170	89.86
contig00051	8290	9715	contig00048	68051	66629	91.8
contig00051	11093	17089	contig00048	65440	59459	95.39
contig00051	17332	21896	contig00048	59205	54641	95.2
contig00051	22474	22627	contig00048	54617	54465	94.81
contig00051	22627	22782	contig00030	14630	14785	87.82
contig00051	23004	30692	contig00030	15953	23636	96.06
contig00051	32017	37402	contig00030	24445	29863	96.11

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00051	38107	49829	contig00030	30571	42143	94.68
contig00051	50382	50492	contig00441	213	103	99.1
contig00051	50769	51811	contig00030	42148	43191	95.02
contig00051	55832	58074	contig00030	43239	45480	94.66
contig00051	58073	58180	contig00038	15631	15524	100
contig00051	58181	60253	contig00030	45482	47554	95.51
contig00051	60255	64292	contig00030	47708	51734	94.8
contig00052	185	2790	contig00430	4709	2105	95.17
contig00052	2789	2970	contig00399	7	188	98.9
contig00052	2971	5016	contig00430	2048	1	95.66
contig00052	5020	7046	contig00005	4	2031	95.51
contig00052	7080	8144	contig00003	1	1067	96.81
contig00052	8325	9602	contig00003	1082	2366	94.5
contig00052	17154	18456	contig00003	2322	3624	97.7
contig00052	18457	18718	contig00019	1	267	96.63
contig00052	18716	18820	contig00024	19683	19786	99.05
contig00052	18821	22119	contig00019	265	3561	96.82
contig00052	22116	22274	contig00228	9037	8879	99.37
contig00052	22276	24384	contig00019	3563	5672	96.59
contig00052	24384	28882	contig00019	5777	10271	93.93
contig00052	29052	33217	contig00019	10269	14441	94.89
contig00052	33222	34009	contig00019	14630	15414	95.44
contig00052	34334	39972	contig00029	19	5659	95.67
contig00052	40226	41794	contig00029	5676	7232	95.99
contig00053	19	5807	contig00038	83763	77992	94.57
contig00053	6080	7846	contig00038	77541	75775	94.69
contig00053	8169	17628	contig00038	75413	65952	96.4
contig00055	3833	12732	contig00362	52113	61013	95.35
contig00055	14612	18768	contig00362	63046	67206	96.56
contig00055	18831	20658	contig00362	73613	75442	91.38

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00055	21143	23116	contig00009	32720	30747	96.1
contig00055	23247	33255	contig00009	30615	20772	94.22
contig00055	33359	33852	contig00009	20773	20280	97.37
contig00055	33856	36879	contig00009	3095	84	88.78
contig00055	37021	37195	contig00361	175	5	91.43
contig00056	3	550	contig00435	7890	8437	95.44
contig00056	1032	1142	contig00036	807	917	95.5
contig00056	1143	1491	contig00034	432	84	87.14
contig00056	2578	3528	contig00395	5670	4723	83.87
contig00056	4609	5664	contig00395	4356	3302	88.03
contig00056	5983	6937	contig00395	3025	2069	84.46
contig00056	8059	8765	contig00395	893	187	87.75
contig00056	8950	12015	contig00397	1	3128	90.78
contig00056	12631	31234	contig00397	3152	21779	95.12
contig00056	31344	31613	contig00397	21976	22245	94.81
contig00056	31609	32064	contig00397	22442	22900	95.87
contig00056	32048	45880	contig00397	23296	37096	93.69
contig00056	45904	50164	contig00397	38000	42249	98.22
contig00056	50275	51753	contig00397	42205	43618	89.22
contig00056	51768	52551	contig00397	44930	45713	97.32
contig00056	52594	54220	contig00397	46916	48542	95.33
contig00056	54220	55360	contig00397	48647	49788	93.88
contig00056	55516	59434	contig00397	49788	53701	96.46
contig00056	59463	62281	contig00008	12076	9260	96.49
contig00057	1	471	contig00007	99265	98791	88.68
contig00057	1109	6176	contig00007	98077	93010	95.82
contig00057	6178	7300	contig00007	92865	91743	94.21
contig00057	7993	12159	contig00007	91652	87490	93.93
contig00057	12119	15345	contig00007	86561	83325	94.97
contig00057	15355	18360	contig00007	83222	80160	94.09

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00057	18575	23664	contig00007	79958	74870	96.61
contig00058	27	6886	contig00359	9	6866	96.78
contig00058	6773	7216	contig00153	1	444	100
contig00058	6892	12403	contig00035	1	5511	95.18
contig00058	26810	31193	contig00035	5508	9885	96.01
contig00058	31193	31440	contig00035	9989	10236	96.37
contig00058	31443	38842	contig00035	10370	17773	96.5
contig00058	41594	59416	contig00035	19592	37465	96.07
contig00058	60319	63269	contig00035	38221	41170	95.87
contig00058	63369	64451	contig00035	42012	43093	94.74
contig00058	64544	66662	contig00035	43664	45781	96.13
contig00058	67014	70002	contig00437	21415	18429	94.26
contig00058	70607	72633	contig00437	16102	14077	96.05
contig00058	72821	75934	contig00437	13939	10815	96.03
contig00058	76426	83662	contig00437	10711	3509	96.19
contig00058	96066	96277	contig00224	311	97	91.67
contig00058	122084	123874	contig00437	3360	1570	95.93
contig00058	131167	135186	contig00038	4	4023	96.37
contig00058	135935	137047	contig00038	4023	5138	95.25
contig00058	137292	138866	contig00038	5369	6943	96.63
contig00058	138977	140692	contig00038	8653	10369	96.8
contig00058	140848	146019	contig00038	10371	15526	93.78
contig00058	146019	148513	contig00038	15631	18123	92.55
contig00058	148686	155286	contig00038	18289	24888	96.06
contig00058	155290	177725	contig00038	24997	47406	94.33
contig00059	8620	8883	contig00425	13357	13617	95.83
contig00060	1	14495	contig00403	101441	115956	94.72
contig00060	15056	16961	contig00403	116056	117969	95.19
contig00060	16961	24286	contig00403	118120	125437	95.8
contig00060	24209	24407	contig00038	65581	65783	81.73

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00060	24415	25662	contig00403	125453	126700	97.2
contig00060	25773	27518	contig00403	126706	128441	94.33
contig00060	27539	27646	contig00007	30527	30420	99.07
contig00060	27646	29229	contig00403	128469	130052	95.52
contig00061	297	2154	contig00394	9142	7285	96.88
contig00061	3087	5868	contig00394	7136	4360	91.11
contig00061	7773	11079	contig00394	4225	921	96.1
contig00061	11124	11245	contig00052	12313	12435	97.56
contig00062	158	11836	contig00363	11709	1	95.54
contig00062	11914	18040	contig00044	1	6119	96.23
contig00062	18465	19494	contig00044	6512	7542	94.68
contig00062	19651	23645	contig00044	7545	11539	96.95
contig00062	23750	24965	contig00044	11539	12754	96.55
contig00062	25058	25829	contig00382	5631	6402	94.05
contig00063	1	2430	contig00454	5840	8265	95.19
contig00063	2490	4774	contig00454	8472	10757	94.14
contig00063	5314	5990	contig00454	12893	13571	96.04
contig00063	6450	7470	contig00454	13569	14622	92.99
contig00063	7466	8573	contig00428	46485	45379	96.75
contig00063	8571	9197	contig00428	45226	44594	92.42
contig00063	10065	15707	contig00428	43625	37982	96.25
contig00063	16183	23916	contig00428	37535	29808	95.54
contig00069	1	2245	contig00425	23077	25323	93.51
contig00070	4	1563	contig00380	11476	13035	93.27
contig00070	1587	1712	contig00455	126	1	98.41
contig00070	1713	2127	contig00446	836	422	94.94
contig00070	2267	2988	contig00380	13050	13768	88.78
contig00070	10883	11529	contig00380	20046	20692	91.65
contig00071	1	6250	contig00365	7	6257	98.18
contig00072	1	2153	contig00001	22163	24310	93.04

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00073	1681	2643	contig00360	35666	36628	97.72
contig00074	47	959	contig00386	913	1	97.37
contig00074	960	1177	contig00436	1	218	99.08
contig00075	3985	14663	contig00403	48858	38226	93.91
contig00075	16096	20056	contig00403	37332	33381	94.73
contig00075	20090	23617	contig00403	33249	29722	96.46
contig00075	23617	25929	contig00403	29617	27304	92.52
contig00075	25923	27645	contig00403	27098	25376	95.3
contig00075	28798	33013	contig00403	24853	20640	94.47
contig00075	32999	43926	contig00403	20834	9925	93.42
contig00076	40	4073	contig00403	48876	52912	95.64
contig00076	4072	8140	contig00403	53016	57084	97.45
contig00076	8178	12341	contig00403	57508	61680	94.07
contig00076	12959	16770	contig00403	61677	65496	94.82
contig00076	17217	19090	contig00403	65898	67771	91.09
contig00076	24211	24368	contig00389	1	158	98.1
contig00076	24594	24765	contig00361	2	173	95.35
contig00076	26980	35857	contig00403	68613	77485	96.29
contig00076	35851	41072	contig00403	77588	82753	94.91
contig00077	2	2793	contig00425	16423	13618	93.91
contig00078	69	795	contig00013	75	801	95.05
contig00078	1199	5181	contig00013	1156	5128	94.93
contig00078	6402	14128	contig00043	28	7798	94.92
contig00078	14168	19376	contig00043	7948	13158	96.05
contig00078	19560	24888	contig00043	14253	19593	95.31
contig00078	24918	25301	contig00271	1	384	99.74
contig00078	28036	30594	contig00043	22672	25165	92.24
contig00079	1	9208	contig00367	25382	16175	97.12
contig00080	3190	3496	contig00182	310	1	98.71
contig00080	5148	6174	contig00425	27450	28483	92.65

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00080	6288	8174	contig00425	28594	30480	91.59
contig00080	8537	29366	contig00425	30829	51707	94.61
contig00080	29368	31724	contig00425	51814	54140	93.62
contig00080	31725	31831	contig00007	42402	42296	98.13
contig00080	31834	33431	contig00425	54145	55741	95.75
contig00080	33436	37994	contig00425	55853	60410	96.62
contig00080	37994	49852	contig00425	60565	72463	95.38
contig00080	49834	55963	contig00425	74011	80145	94.38
contig00080	64576	68602	contig00362	595	4670	94.48
contig00080	68803	69601	contig00362	4814	5612	93.63
contig00080	69709	76129	contig00362	5615	12031	92.78
contig00080	76104	85064	contig00362	12114	21066	94.86
contig00080	85184	98283	contig00362	21184	34278	95.02
contig00080	98762	100901	contig00362	35013	37150	95.98
contig00080	102159	109495	contig00362	36657	44034	93.19
contig00081	187	3285	contig00434	3145	46	95.32
contig00081	3428	6773	contig00023	3347	1	95.52
contig00081	6775	7597	contig00403	136503	135681	96.6
contig00081	7692	7913	contig00403	135681	135465	89.19
contig00081	8727	8842	contig00004	3339	3224	96.55
contig00081	8966	10220	contig00403	134414	133156	94.84
contig00081	10408	11966	contig00403	132887	131329	95.32
contig00086	1	940	contig00033	180	1119	96.17
contig00088	1	239	contig00041	12022	11783	96.67
contig00088	347	4256	contig00041	11780	7869	95.91
contig00088	5500	7206	contig00041	7896	6190	97.19
contig00088	7501	11580	contig00392	319	4399	96.59
contig00088	11647	16545	contig00041	1	4900	95.13
contig00089	44	2762	contig00027	14192	11477	93.32
contig00089	2858	2921	contig00007	38539	38478	96.88

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00089	2922	8938	contig00027	11474	5462	94.75
contig00089	8948	9055	contig00038	77684	77577	96.3
contig00089	9058	14422	contig00027	5449	84	95.45
contig00089	14408	14711	contig00015	3061	3363	93.75
contig00089	14549	14714	contig00011	5769	5604	95.18
contig00089	14715	14808	contig00006	666	759	96.81
contig00092	248	700	contig00046	837	385	89.23
contig00092	538	1017	contig00045	481	1	97.94
contig00092	1034	2519	contig00405	4741	3256	96.64
contig00092	3872	6075	contig00405	2206	3	96.55
contig00092	6081	10002	contig00371	42195	38278	95.64
contig00092	10068	13049	contig00371	37801	34821	95.44
contig00092	13154	17547	contig00371	34821	30431	95.43
contig00092	17660	29608	contig00371	30426	18434	94.57
contig00092	29602	29712	contig00028	6851	6961	96.4
contig00092	29716	34999	contig00371	18434	13166	93.44
contig00092	34996	35104	contig00037	25841	25733	99.08
contig00092	35104	35654	contig00371	13166	12616	95.64
contig00092	36124	46049	contig00371	12144	2284	93.85
contig00093	1	113	contig00006	628	740	96.46
contig00094	9	5578	contig00454	5843	271	96.43
contig00094	5576	11607	contig00442	17868	11841	95.09
contig00094	11607	11929	contig00442	11743	11425	90.12
contig00094	12058	14152	contig00442	10924	8828	93.47
contig00095	35	1482	contig00425	16418	17865	95.58
contig00095	5588	6337	contig00425	22319	23073	95.9
contig00098	1	269	contig00394	63379	63111	97.03
contig00099	507	4614	contig00042	404	4511	95.62
contig00099	11717	13460	contig00042	4903	6613	93.98
contig00099	13978	14133	contig00228	12169	12014	95.51

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00099	14378	16396	contig00228	12014	9997	96.09
contig00099	16439	16545	contig00362	49534	49428	85.32
contig00101	301	4311	contig00435	4357	349	96.98
contig00101	4577	4700	contig00425	27454	27331	93.6
contig00101	4596	4705	contig00425	55741	55850	98.18
contig00101	4703	5046	contig00435	345	1	97.1
contig00101	5049	8453	contig00423	3945	546	96.48
contig00102	1	1450	contig00435	7887	6438	92.69
contig00102	2014	2211	contig00133	342	145	100
contig00103	58	229	contig00391	1	172	100
contig00104	1	246	contig00412	23	268	95.93
contig00106	1307	6305	contig00428	25925	20927	96.38
contig00106	6410	12324	contig00428	20927	15010	96.67
contig00106	12337	12967	contig00374	5141	4514	97.15
contig00106	13081	17583	contig00374	4504	1	97.29
contig00107	1	246	contig00394	63252	63497	94.72
contig00107	4	628	contig00006	624	1	95.04
contig00107	635	1619	contig00380	22217	23201	94.62
contig00107	1656	4979	contig00403	374	3690	95.56
contig00107	5249	6299	contig00403	3751	4800	92.22
contig00107	8415	13492	contig00403	4837	9925	95.42
contig00108	12	2488	contig00369	27381	29857	97.25
contig00108	2486	8337	contig00401	1	5853	97.03
contig00108	8323	8789	contig00401	9790	9324	96.57
contig00108	10171	12862	contig00401	9051	6357	94.45
contig00108	13009	14374	contig00401	9776	11140	95.61
contig00108	14636	27657	contig00369	27314	14295	97.22
contig00108	27762	41788	contig00369	14295	272	95.91
contig00108	42018	42192	contig00019	14455	14627	91.48
contig00108	42195	44639	contig00368	67	2514	96.61

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00108	44656	44870	contig00023	14850	14635	90.32
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contig00108	50589	50740	contig00025	20997	20846	88.82
contig00108	50964	51662	contig00025	20633	19937	92.59
contig00108	52432	53618	contig00025	17686	16500	90.31
contig00108	53623	55301	contig00025	16390	14711	95.18
contig00108	55349	55460	contig00007	53027	53138	99.11
contig00108	55404	55504	contig00429	5555	5451	89.72
contig00108	55611	61765	contig00025	14725	8576	94.79
contig00108	62124	62640	contig00025	7272	6756	94.59
contig00108	62726	72105	contig00401	17835	27221	95.7
contig00109	1	324	contig00425	25968	26291	96.3
contig00109	1204	1593	contig00030	14697	14319	95.91
contig00110	51	176	contig00453	127	1	96.85
contig00110	53	297	contig00030	63141	62896	96.75
contig00111	1	203	contig00392	84	286	95.1
contig00111	131	204	contig00014	10467	10394	100
contig00113	921	2621	contig00363	12688	14390	94.89
contig00113	2623	13831	contig00037	53793	42585	95.8
contig00113	14127	14684	contig00037	42442	41891	80.88
contig00113	15980	18655	contig00037	40714	38039	95.96
contig00113	18665	30637	contig00037	37913	25964	94.07
contig00113	30789	31451	contig00037	25711	25048	87.84
contig00113	31582	35513	contig00037	24869	20932	94.98
contig00113	35619	37325	contig00037	20930	19224	96.13
contig00113	38202	42993	contig00037	17401	12592	95.24
contig00113	43517	44562	contig00037	12099	11052	96.28
contig00113	44661	44968	contig00037	11063	10756	91.91
contig00113	45073	50974	contig00037	10654	4750	94.5
contig00113	50976	55565	contig00037	4643	54	95.06

Query	Q Start	Q End	Reference	R Start	R End	%ID
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contig00113	57119	58378	contig00429	1543	2801	95.95
contig00113	58485	61178	contig00429	2804	5488	94.88
contig00113	61689	68251	contig00429	5648	12190	95.02
contig00113	68402	69660	contig00429	12187	13445	95
contig00113	69689	78603	contig00429	13807	22733	95.21
contig00113	78693	78877	contig00440	503	318	98.39
contig00113	78696	78877	contig00361	14672	14854	96.72
contig00113	78923	79033	contig00017	24424	24314	100
contig00113	79244	80456	contig00012	662	1878	95.89
contig00113	80456	81285	contig00012	1965	2794	95.66
contig00113	81283	81389	contig00361	23988	24092	96.26
contig00113	81390	83657	contig00012	2794	5066	95.16
contig00113	83680	85693	contig00012	7183	9197	94.74
contig00113	85957	88460	contig00012	9287	11791	97.21
contig00113	88460	91611	contig00004	1	3151	95.18
contig00113	91581	95179	contig00004	3344	6966	95.25
contig00113	95179	98420	contig00004	7070	10311	98.03
contig00113	98414	98751	contig00004	10548	10885	99.11
contig00115	1	823	contig00038	47408	48217	94.54
contig00115	771	15070	contig00038	65625	51459	94.41
contig00115	15404	18426	contig00038	51252	48194	94.97
contig00116	2649	4042	contig00017	6022	7415	93.9
contig00116	4098	9925	contig00017	7762	13591	94.8
contig00116	9926	10034	contig00024	3390	3498	99.08
contig00116	10036	20834	contig00017	13595	24314	93.94
contig00116	20840	22558	contig00017	24432	26150	94.76
contig00116	22558	25355	contig00017	26253	29050	95.68
contig00116	27037	31369	contig00017	30732	35057	94.21

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00116	39565	41186	contig00450	9141	10763	91.52
contig00116	40910	41232	contig00410	1	323	95.67
contig00117	1	205	contig00001	22162	21958	92.2
contig00117	818	9309	contig00001	8488	1	96.03
contig00117	9327	10683	contig00028	26726	25357	94.68
contig00117	10685	11542	contig00028	25250	24377	87.99
contig00117	12245	14599	contig00028	24374	22017	95.38
contig00117	14594	14751	contig00012	7181	7028	92.41
contig00117	14704	17374	contig00028	22016	19340	93.25
contig00117	17453	18323	contig00028	18656	17786	93.34
contig00117	18477	22424	contig00028	17656	13708	94.66
contig00117	22968	23532	contig00028	13692	13128	95.75
contig00117	23717	28509	contig00028	11753	6961	96.06
contig00119	609	4998	contig00425	17869	22262	94.36
contig00121	1	736	contig00396	1	737	93.36
contig00122	1875	6166	contig00049	16934	21222	94.42
contig00122	6454	8973	contig00030	55611	58130	94.85
contig00122	8988	9320	contig00030	58291	58623	92.49
contig00122	9398	10561	contig00030	59286	60451	93.91
contig00122	10564	11448	contig00030	60593	61477	94.24
contig00123	1	4039	contig00360	18373	22411	96.41
contig00124	5	8319	contig00022	8298	2	96.21
contig00124	8321	9069	contig00393	940	192	94.39
contig00124	9759	19136	contig00021	5	9373	94.4
contig00124	19154	27526	contig00421	8318	6	94.24
contig00127	1	590	contig00425	25967	25378	98.14
contig00129	1	335	contig00012	427	93	94.63
contig00131	1	1906	contig00401	14976	16882	95.6
contig00131	1928	4054	contig00025	6731	4613	94.89
contig00131	4052	4158	contig00429	5554	5660	100

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00131	4159	8764	contig00025	4613	11	96.29
contig00131	8794	9916	contig00407	1	1125	93.33
contig00131	10068	11891	contig00407	1128	2948	94.68
contig00131	12757	13138	contig00148	1	383	99.74
contig00131	13277	18145	contig00367	30257	25400	95.79
contig00134	86	184	contig00007	42200	42298	97.98
contig00134	184	4011	contig00007	42403	46228	94.8
contig00134	4165	8843	contig00007	46228	50949	93.65
contig00134	8837	8946	contig00425	27327	27435	98.18
contig00134	8948	11010	contig00007	50949	53011	97.58
contig00135	1	5679	contig00370	8430	2754	96.74
contig00136	46	6033	contig00007	5177	11157	92.86
contig00136	6480	12925	contig00007	11599	18066	94.5
contig00136	13073	13772	contig00007	18226	18930	91.4
contig00136	14864	19317	contig00007	19328	23782	95.07
contig00138	1	461	contig00382	13559	14019	93.71
contig00138	1264	5382	contig00049	173	4317	93.22
contig00138	6083	16660	contig00049	4373	14923	95.3
contig00139	166	2102	contig00370	3	1909	94.63
contig00140	189	364	contig00435	4355	4529	94.35
contig00141	12	2668	contig00026	27657	25004	95.53
contig00141	2703	27493	contig00026	24865	102	94.95
contig00142	320	501	contig00402	182	1	93.41
contig00142	500	2218	contig00022	8294	10012	95.41
contig00142	2215	2555	contig00002	17	356	96.19
contig00142	2812	4768	contig00002	427	2383	96.01
contig00145	1	96	contig00429	22835	22740	96.88
contig00146	1	243	contig00374	27485	27727	94.24
contig00147	3	109	contig00012	109	3	99.07
contig00147	3	117	contig00015	3558	3672	94.78

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00148	1	3820	contig00401	14973	11155	96.07
contig00148	3826	14858	contig00023	3343	14378	94.01
contig00148	14976	17069	contig00420	4822	6911	93.6
contig00148	17131	17240	contig00048	2355	2464	100
contig00148	17238	21726	contig00367	68	4557	94.6
contig00148	21721	21883	contig00429	1386	1546	96.93
contig00148	21879	29006	contig00367	4557	11671	94.75
contig00148	30682	32729	contig00367	13124	15172	96.34
contig00148	32803	36060	contig00401	38034	34784	93.99
contig00148	36164	39640	contig00401	34784	31291	93.49
contig00148	39640	41639	contig00401	31186	29186	95.8
contig00148	41642	43359	contig00401	28939	27223	97.26
contig00149	1	12617	contig00444	219	12773	95.14
contig00149	12617	18318	contig00444	12878	18519	92.99
contig00149	18688	21871	contig00444	18651	21816	94.45
contig00149	21886	21992	contig00004	7070	6964	99.07
contig00149	22009	26604	contig00444	23279	27873	93.41
contig00149	26878	28755	contig00444	28636	30513	95.37
contig00149	28756	33075	contig00408	6970	2654	95.88
contig00149	33229	35830	contig00408	2654	52	96.35
contig00149	36030	37763	contig00449	2	1728	95.56
contig00149	37781	38876	contig00449	5694	6789	95.53
contig00150	1	1289	contig00049	14666	15964	87.1
contig00150	1154	1553	contig00175	409	10	97.76
contig00151	7	2968	contig00048	28413	25454	93.06
contig00151	2966	3124	contig00443	5398	5240	100
contig00151	3123	9601	contig00048	25454	18973	96.32
contig00151	9726	20327	contig00048	13194	2595	93.98
contig00151	20980	23029	contig00048	2050	1	96.59
contig00151	23030	23264	contig00411	1	235	100

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00151	23265	35703	contig00452	14736	2348	95.27
contig00151	36337	38123	contig00452	1778	1	95.69
contig00151	38256	38628	contig00031	1	373	93.83
contig00152	1	10156	contig00030	14393	4295	93.59
contig00152	10168	10438	contig00440	271	1	97.42
contig00153	13	321	contig00394	9802	9500	89.64
contig00153	63	325	contig00444	28466	28211	86.36
contig00154	250	690	contig00435	6015	6455	95.92
contig00154	629	772	contig00133	1	144	100
contig00155	31	561	contig00060	530	1	99.25
contig00155	562	1537	contig00428	28722	29702	92.58
contig00156	32	256	contig00016	225	1	99.56
contig00156	258	407	contig00431	156	7	99.33
contig00158	17	555	contig00049	40962	41499	96.48
contig00161	185	4780	contig00031	25193	20595	95.01
contig00161	4680	6705	contig00031	329	2352	94.97
contig00162	6	10326	contig00031	25303	35653	94.36
contig00162	10331	13322	contig00443	11627	8635	95
contig00162	13442	18655	contig00443	5214	1	94.07
contig00162	18652	25311	contig00050	1	6670	93.73
contig00162	25316	34175	contig00228	3	8882	95.87
contig00162	34175	35011	contig00228	9037	9872	96.65
contig00163	1	212	contig00425	202	413	91.98
contig00167	143	1036	contig00049	40926	40031	94.98
contig00167	1036	3196	contig00049	39876	37707	95.58
contig00167	3331	7995	contig00049	37678	33004	94.78
contig00167	7994	19015	contig00049	32900	21865	94.11
contig00167	19936	20872	contig00049	22111	21178	93.81
contig00167	20984	21476	contig00030	55060	54567	95.76
contig00167	21777	22288	contig00030	54566	54033	90.26

Query	Q Start	Q End	Reference	R Start	R End	%ID
contig00168	5	459	contig00446	674	220	95.16

at the nucleotide level, 74.6% identical to *N. sicca* NS19, 74.5% identical to *N. sicca* 342, and 73.0% identical to *N. subflava* 44 (Table 3).

16S rRNA phylogenetic analysis of sequenced commensals

The sequenced commensals were originally classified based on physical properties such as colony characteristics and sugar utilization (Table 4) [69]. A phylogenetic analysis of each sequenced commensal was undertaken to determine if the original classification of the organism was correct. The region encoding 16S rRNA sequence from each commensal was identified by BLAST using the 16S rRNA sequence of *N. sicca* Q29 from the rRNA Database as the query sequence [70]. The identified 16S rRNA sequence was used, along with sequences deposited in the rRNA Database, to generate a phylogenetic tree (Figure 2). This data indicates that *N. sicca* 4320, *N. sicca* DS1, and *N. sicca* ATCC 29256 all cluster with the other *N. sicca* sequences, supporting the original classification of these commensals. *N. sicca* 342 clusters with the *N. polysaccharea*, *N. sicca* NS19 clusters with the *N. lactamica*, and *N. subflava* 44 clusters with the *N. meningitidis* sequences. This indicates that these three commensals were originally misidentified.

Genotypic phylogenetic analysis of sequenced commensals

As further confirmation of the identity of the sequenced commensals, a set of genes were identified in each commensal. Only *N. lactamica* strains have the ability to metabolize lactose. A search of the sequenced genomes for the presence of the β-galactosidase gene, a requirement for lactose metabolism, indicated that only *N. sicca*

Sequenced Commensal	%ID
N. sicca DS1	95.0
N. lactamica NS19	74.6
N. polysaccharea NS342	74.5
N. meningitidis NS44	73.0

Table 3. Percent identity between *N. sicca* 4320 and the sequenced commensals. *N. sicca* 4320 was aligned with each of the other sequenced commensals using Nucmer. The percent identity of the alignment was averaged over the entire genome to determine the percent identity between the sequenced organisms.

Characteristic	*N. gonorrhoeae*	*N. meningitidis*	*N. lactamica*	*N. sicca*	*N. subflava*	*N. mucosa*	*N. cinerea*
Cocci	+	+	+	+	+	+	+
Rods	-	-	-	-	-	-	-
Pairs	+	+	+	+	+	+	+
Tetrads	-	-	-	+	+	-	-
Yellow Pigment	-	-	+	+	+	+	+
Glucose Metabolism	+	+	+	+	+	+	-
Maltose Metabolism	-	+	+	+	+	+	-
Fructose Metabolism	-	-	-	+	+	+	-
Sucrose Metabolism	-	-	-	+	+	+	-
Mannose Metabolism	-	-	-	-	-	-	-
Lactose Metabolism	-	-	+	-	-	-	-
Nitrate Reduction	-	-	-	-	-	+	-
Nitrite Reduction	-	-	+	+	+	+	+
Gas from nitrite	-	-	+	+	+	+	+

Table 4. Physical characteristics of *Neisseria* species. Physical characteristics used to identify different *Neisseria* species. +: Species possess characteristic. -: Species lack characteristic.

Figure 2. 16S rRNA Tree. A 16S rRNA phylogenetic tree was constructed to determine the phylogenetic relationships between the sequenced commensals. Arrows: Sequenced commensals.

NS19 contained the gene, consistent with misidentification of the strain. *N. meningitidis* strains are unable to metabolize sucrose. It is therefore expected that *N. subflava* 44 would lack the genes required for sucrose metabolism. A search of the commensal genomes revealed that only *N. sicca* 4320, *N. sicca* DS1, and *N. sicca* 342 had the sucrose metabolism gene consistent with misidentification of *N. subflava* 44 and consistent with the correct identification of *N. sicca* 4320 given the utilization patterns given in the phenotypic table (Table 5).

Reference genome alignment for phylogenic determination

The contig sequence for *N. subflava* 44 was aligned to the genomic sequence of *N. meningitidis* MC58 using a program called Mauve (Figure 3). Mauve reorders contigs and aligns them with a reference genome. A series of aligned contigs with no rearrangement between the sequenced organism and the reference are represented as a colored "block" with the shading in the block representing percent identity between the sequenced organism and the reference. A rearrangement between the sequenced organism and the reference (identified by a contig whose beginning sequence matches one location and the ending sequence matches a second location) results in a new "block" and alignment of contig sequences at the new location. If the query contigs and reference genome have very high similarity there will be a small number of blocks with a high percent identity.

As can be seen in the figure, the contig sequence closely aligns with the reference genome in few blocks, giving further proof that this is indeed a *N. meningitidis* strain. As a counter example, *N. sicca* 4320 contig sequences were aligned with the *N. meningitidis*

Sequenced Commensals	Lactose Metabolism Gene	Sucrose Metabolism Gene
N. sicca 4320	-	+
N. sicca DS1	-	+
N. lactamica NS19	+	-
N. polysaccharea NS342	-	+
N. meningitidis NS44	-	-

Table 5. Specific gene content of sequenced commensals. The sequenced commensals were searched for the presence of genes responsible for lactose and sucrose metabolism. +: Gene present. -: Gene absent.

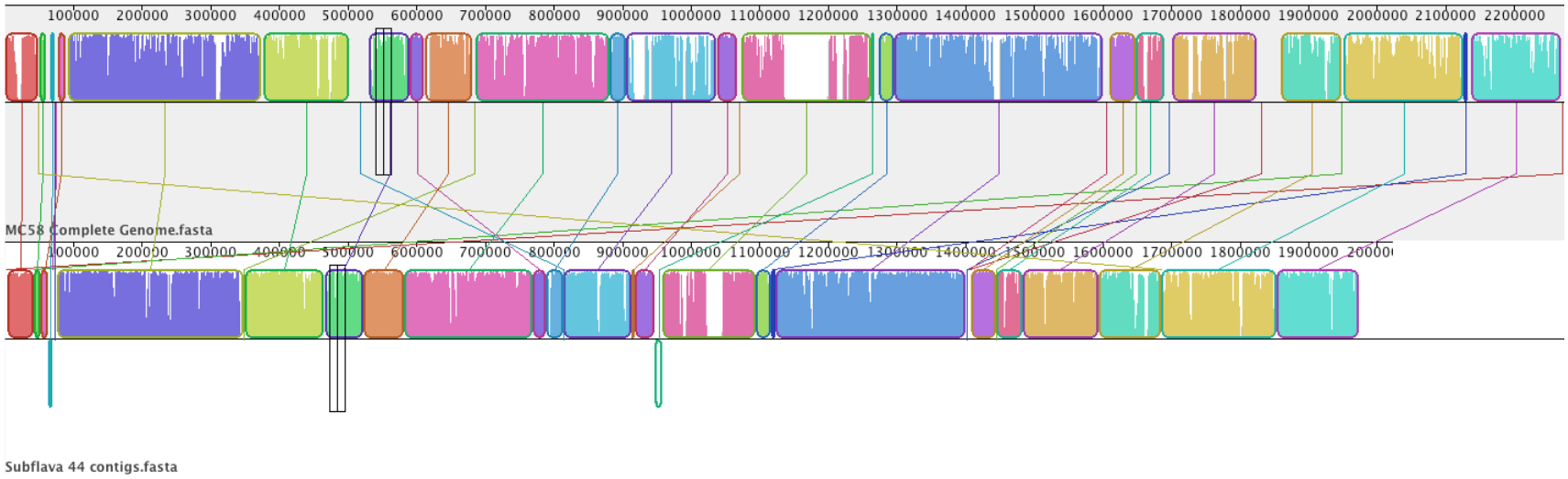


Figure 3. Mauve alignment of *N. subflava* 44 and *N. meningitidis* MC58. The program Mauve was used to align the contig sequence of *N. subflava* 44 to the genomic sequence of *N. meningitidis* MC58. The colored blocks represent homologous sequence in a contiguous block. The lines between *N. meningitidis* MC58 blocks and *N. subflava* 44 indicate the location of the contiguous block in each genome. As can be seen, there were rearrangements between the two genomes.

MC58 reference genome (Figure 4). As can be seen in the figure, the contig sequence fails to align with the reference genome in a few sets of contiguous sequence. This indicates further divergence between the reference genome and the contig sequence, giving further evidence of differing species.

Given the phylogenetic evidence for the misidentification of the three commensal strains, *N. sicca* 342 was renamed *N. polysaccharea* NS342, *N. sicca* NS19 was renamed *N. lactamica* NS19, and *N. subflava* 44 was renamed *N. meningitidis* NS44.

ORF identification and annotation

The ORFs in the *N. sicca* 4320 contigs were identified using the Glimmer3 program. The program identified 2690 ORFs across the contigs (Appendix A). The ORFs were labeled by their contig number and ORF number (Example: contig00028-orf00017; for the remainder of the thesis this will be shortened as contig28-17). The predicted amino acid sequences of the ORFs were used as a query in a BLAST search of two databases, one specially constructed at the University of Maryland Center for Bioinformatics and Computational Biology of manually curated sequences (DanAnn) and the other the NCBI non-redundant database (nr). The annotation according the DanAnn database contained 842 hypothetical proteins and 155 ORFs with no similarity to any known protein (Appendix B). The annotation according to the nr database contained 687 hypothetical proteins and 464 ORFs with no similarity to any known protein (Appendix C). The DanAnn database annotation set was chosen for further analysis. The functional category of each annotated ORF was determined from the Uniprot database (Appendix

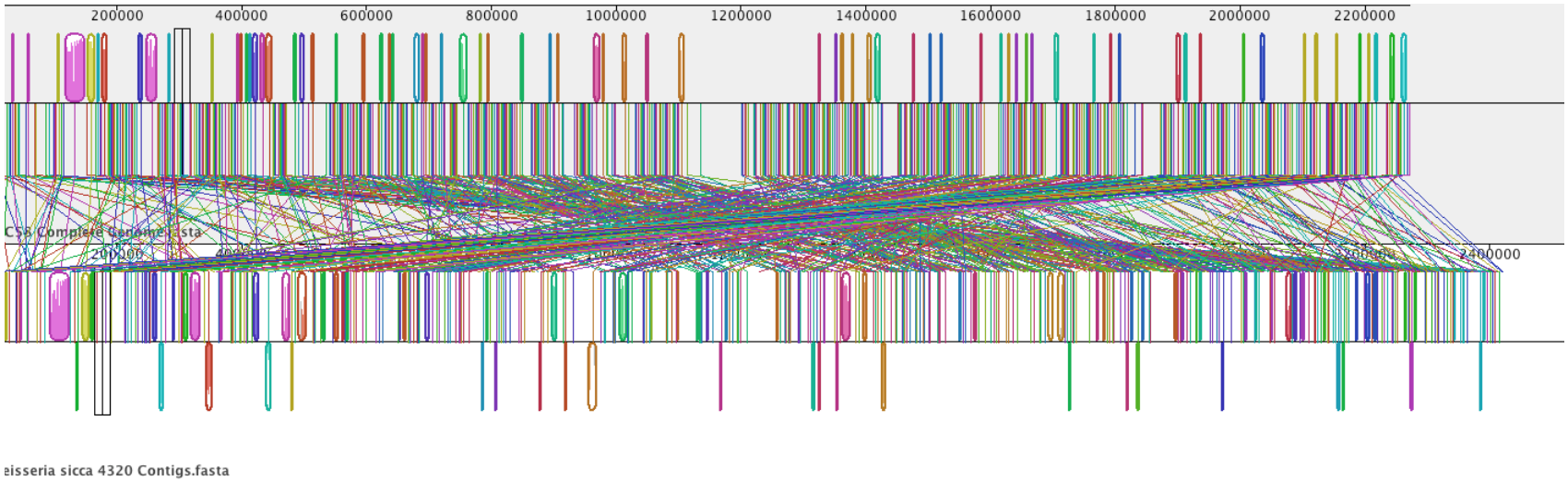


Figure 4. Mauve alignment of *N. sicca* 4320 and *N. meningitidis* MC58. The program Mauve was used to align the contig sequence of *N. sicca* 4320 to the genomic sequence of *N. meningitidis* MC58. The colored blocks represent homologous sequence in a contiguous block. The lines between *N. meningitidis* MC58 blocks and *N. sicca* 4320 indicate the location of the contiguous block in each genome. As can be seen, the two genomes have little continuity and are more divergent than the previous alignment.

D). The Pfam domains found within each annotated ORF were also determined (Appendix E).

Identification of putative LOS and LPS-like polysaccharide biosynthesis genes

Open reading frames that show similarity to genes that could be involved in O-repeat biosynthesis were termed regions of interest (ROI) in this study. Identification of these ROIs is the primary goal of the project. A gene-finding bioinformatic screen was undertaken to identify possible ROIs in *N. sicca* 4320.

Identification of regions unique to N. sicca *4320*

It is possible that the O-repeat biosynthetic genes are only found in *N. sicca* 4320 since the polysaccharide structure is not found in any other *Neisseria*. ORFs unique to *N. sicca* 4320 were identified by comparing *N. sicca* 4320 genomic DNA with *N. meningitidis* MC58 genomic sequence, the other sequenced commensals, *N. sicca* ATCC 29265, and *N. mucosa* ATCC 25996 using Nucmer to determine which ORFs had homologs in the other *Neisseria*. This alignment indicated that 244 ORFs were unique to *N. sicca* 4320 (Table 6). Analysis of the 244 ORFs showed that two ORFs, contig28-17 and contig28-18, had similarity to known glycosyltransferases.

Mapping of LOS biosynthesis locations in N. sicca *4320*

The synthesis of LOS in the pathogenic strains is controlled by the action of glycosyltransferase genes found in 5 locations on the bacterial chromosome. The genomic sequence of *N. sicca* 4320 was searched for the presence of these genes. The

Table 6. ORFs unique to *N. sicca* 4320. The ORFs predicted in the contigs of *N. sicca* 4320 were compared to *N. gonorrhoeae* FA1090, *N. meningitidis* MC58, and the sequenced commensals to determine which ORFs had no homologs in the other *Neisseria.*

Query	Subject	%ID
contig00002-orf00001	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	44.93
contig00006-orf00011	#N/A	#N/A
contig00006-orf00012	#N/A	#N/A
contig00008-orf00079	cysteinyl-tRNA synthetase [Mesoplasma florum L1]	31.09
contig00008-orf00107	#N/A	#N/A
contig00010-orf00008	#N/A	#N/A
contig00010-orf00030	prophage CP4-57 regulatory [Ralstonia eutropha JMP134]	40.32
contig00010-orf00032	hypothetical protein SAR11 0011 [Candidatus Pelagibacter ubique HTCC1062]	38.53
contig00010-orf00033	#N/A	#N/A
contig00010-orf00036	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	84.92
contig00010-orf00038	imidazoleglycerol-phosphate dehydratase [Sulfolobus acidocaldarius DSM 639]	32.84
contig00010-orf00040	TonB-dependent receptor [Xanthomonas campestris pv. campestris str. ATCC 33913]	33.96
contig00010-orf00041	hypothetical protein BURPS1710b A1695 [Burkholderia pseudomallei 1710b]	28.22
contig00010-orf00042	exonuclease VIII [Escherichia coli APEC O1]	37.64
contig00010-orf00043	putative periplasmic protein [Dehalococcoides sp. CBDB1]	30.16
contig00010-orf00045	putative lipoprotein [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]	32.43
contig00010-orf00047	hypothetical protein pNG6182 [Haloarcula marismortui ATCC 43049]	40.43
contig00010-orf00049	#N/A	#N/A
contig00010-orf00050	type III restriction enzyme, res subunit [Silicibacter sp. TM1040]	28.79
contig00010-orf00051	hypothetical protein BLi02293 [Bacillus licheniformis ATCC 14580]	44.83
contig00010-orf00053	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	90.91
contig00010-orf00056	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	97.22
contig00010-orf00057	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	79.03

Query	Subject	%ID
contig00010-orf00058	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	77.33
contig00010-orf00059	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	65.28
contig00010-orf00061	putative DNA replication protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	80.98
contig00010-orf00062	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	56.52
contig00010-orf00063	#N/A	#N/A
contig00010-orf00065	hypothetical protein lmo2268 [Listeria monocytogenes EGD-e]	58.33
contig00010-orf00067	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	63.11
contig00010-orf00068	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	41.98
contig00010-orf00069	hypothetical protein Nmul A1530 [Nitrosospira multiformis ATCC 25196]	32.73
contig00010-orf00071	hypothetical protein UTI89 C2655 [Escherichia coli UTI89]	63.08
contig00010-orf00072	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	90.49
contig00010-orf00074	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	83.96
contig00010-orf00075	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	91.32
contig00010-orf00076	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	82.54
contig00010-orf00077	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	72.73
contig00010-orf00078	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	70
contig00010-orf00079	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	89.44
contig00010-orf00081	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	82.88
contig00010-orf00082	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	85.26
contig00010-orf00084	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	92.05
contig00010-orf00085	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	92.96
contig00010-orf00086	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	89.53
contig00010-orf00087	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	71.11
contig00010-orf00088	DNA topoisomerase IV subunit A [Geobacillus kaustophilus HTA426]	30.3
contig00010-orf00090	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	85.11
contig00010-orf00091	hypothetical protein NGO0511 [Neisseria gonorrhoeae FA 1090]	36.17
contig00010-orf00092	putative tail length tape measure protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	73.79
contig00010-orf00093	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	53.49
contig00010-orf00095	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	52.13

Query	Subject	%ID
contig00010-orf00100	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	39.68
contig00010-orf00101	AbpK sensory transduction histidine kinase [Lactobacillus salivarius UCC118]	31.25
contig00010-orf00102	hypothetical protein PCP51 [Clostridium perfringens str. 13]	32.63
contig00010-orf00103	prophage PSPPH01, site-specific recombinase phage integrase family protein [Pseudomonas syringae pv. phaseolicola 1448A]	42.34
contig00010-orf00112	#N/A	#N/A
contig00010-orf00131	#N/A	#N/A
contig00010-orf00133	hypothetical protein Sden 1113 [Shewanella denitrificans OS217]	35.44
contig00010-orf00134	hypothetical protein SCO7003 [Streptomyces coelicolor A3(2)]	41.67
contig00010-orf00135	#N/A	#N/A
contig00010-orf00136	galactose mutarotase-like protein [Lactobacillus brevis ATCC 367]	31.91
contig00011-orf00082	putative modification methylase [Neisseria gonorrhoeae FA 1090]	88.07
contig00017-orf00003	#N/A	#N/A
contig00020-orf00004	#N/A	#N/A
contig00022-orf00020	cephalosporin hydroxylase [Rickettsia bellii RML369-C]	25.83
contig00023-orf00007	integral membrane sulfate transportor [Haemophilus ducreyi 35000HP]	53.83
contig00024-orf00038	#N/A	#N/A
contig00026-orf00010	#N/A	#N/A
contig00026-orf00020	sugar transporter [Chromohalobacter salexigens DSM 3043]	49.06
contig00027-orf00018	hypothetical protein Pcryo 1832 [Psychrobacter cryohalolentis K5]	30.38
contig00028-orf00017	glycosyl transferase [Pyrococcus abyssi GE5]	28.7
contig00028-orf00018	putative glycosyl transferase [Burkholderia thailandensis E264]	30.86
contig00028-orf00032	#N/A	#N/A
contig00028-orf00081	#N/A	#N/A
contig00029-orf00002	#N/A	#N/A
contig00029-orf00003	hypothetical protein NGO1387 [Neisseria gonorrhoeae FA 1090]	97.22
contig00029-orf00023	#N/A	#N/A
contig00030-orf00008	hypothetical protein tll0709 [Thermosynechococcus elongatus BP-1]	46.15
contig00031-orf00016	urea transporter or sodium transporter [Rhodopirellula baltica SH 1]	75
contig00031-orf00017	#N/A	#N/A

Query	Subject	%ID
contig00031-orf00018	#N/A	#N/A
contig00031-orf00021	#N/A	#N/A
contig00031-orf00022	#N/A	#N/A
contig00032-orf00009	LysR protein [Mannheimia succiniciproducens MBEL55E]	67.68
contig00041-orf00007	hypothetical protein NMA0482 [Neisseria meningitidis Z2491]	100
contig00042-orf00006	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	81.08
contig00044-orf00024	TonB1 protein [Shewanella oneidensis MR-1]	30.61
contig00044-orf00053	excisionase/Xis, DNA-binding [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	45.83
contig00044-orf00054	hypothetical protein Cag 1180 [Chlorobium chlorochromatii CaD3]	35.14
contig00045-orf00132	#N/A	#N/A
contig00045-orf00164	hypothetical protein NMA0089 [Neisseria meningitidis Z2491]	94.69
contig00045-orf00191	#N/A	#N/A
contig00045-orf00205	#N/A	#N/A
contig00046-orf00005	#N/A	#N/A
contig00046-orf00045	#N/A	#N/A
contig00046-orf00047	#N/A	#N/A
contig00046-orf00048	#N/A	#N/A
contig00049-orf00016	hypothetical protein PSEEN3677 [Pseudomonas entomophila L48]	27.8
contig00049-orf00032	#N/A	#N/A
contig00050-orf00009	#N/A	#N/A
contig00050-orf00037	hypothetical protein MGA 1222 [Mycoplasma gallisepticum R]	26.87
contig00050-orf00043	#N/A	#N/A
contig00051-orf00008	inner membrane protein [Burkholderia pseudomallei 1710b]	36.96
contig00051-orf00009	protein VirD4 [Vibrio fischeri ES114]	38.29
contig00051-orf00011	hypothetical protein Mhun 1899 [Methanospirillum hungatei JF-1]	32.35
contig00051-orf00012	#N/A	#N/A
contig00051-orf00013	#N/A	#N/A
contig00051-orf00023	putative metalloproteinase [Candidatus Protochlamydia amoebophila UWE25]	43.33
contig00051-orf00032	#N/A	#N/A

Query	Subject	%ID
contig00051-orf00046	LacI family sugar-binding transcriptional regulator [Streptococcus pneumoniae TIGR4]	28.12
contig00051-orf00080	OsmC family protein [Burkholderia ambifaria AMMD]	34.26
contig00051-orf00081	YdfQ [Bacillus licheniformis ATCC 14580]	50
contig00051-orf00083	ArsR family transcriptional regulator [Neisseria gonorrhoeae FA 1090]	96.12
contig00051-orf00084	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	92.65
contig00051-orf00085	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	92.41
contig00051-orf00086	#N/A	#N/A
contig00051-orf00089	#N/A	#N/A
contig00051-orf00090	ARA1 protein [Mannheimia succiniciproducens MBEL55E]	71.59
contig00051-orf00091	aldo/keto reductase family oxidoreductase [Listeria welshimeri serovar 6b str. SLCC5334]	61.83
contig00051-orf00107	SMC family chromosome segregation protein [Candidatus Pelagibacter ubique HTCC1062]	27.27
contig00052-orf00026	SLT domain-containing protein [Lactococcus lactis subsp. cremoris SK11]	33.33
contig00052-orf00027	hypothetical protein all5192 [Nostoc sp. PCC 7120]	22.73
contig00052-orf00028	protein AraJ [Escherichia coli UTI89]	31.91
contig00052-orf00029	#N/A	#N/A
contig00052-orf00030	hypothetical protein CPS 4814 [Colwellia psychrerythraea 34H]	35.29
contig00052-orf00031	VirB6 family type IV secretion system protein [Ehrlichia chaffeensis str. Arkansas]	30.36
contig00052-orf00033	#N/A	#N/A
contig00052-orf00034	#N/A	#N/A
contig00052-orf00037	hypothetical protein plu0852 [Photorhabdus luminescens subsp. laumondii TTO1]	54.63
contig00053-orf00018	#N/A	#N/A
contig00055-orf00003	hypothetical protein NMA0029 [Neisseria meningitidis Z2491]	98.71
contig00055-orf00065	respiratory nitrate reductase alpha chain [Chromobacterium violaceum ATCC 12472]	78.15
contig00056-orf00013	hypothetical protein MS2001 [Mannheimia succiniciproducens MBEL55E]	57.14

Query	Subject	%ID
contig00056-orf00094	hypothetical protein Mbar A1323 [Methanosarcina barkeri str. Fusaro]	27.27
contig00057-orf00004	unknown transmembrane protein [Mesoplasma florum L1]	35
contig00057-orf00013	#N/A	#N/A
contig00057-orf00047	#N/A	#N/A
contig00058-orf00027	#N/A	#N/A
contig00058-orf00028	phenol hydroxylase P1 protein [Ralstonia eutropha H16]	50.15
contig00058-orf00029	monooxygenase component MmoB/DmpM [Ralstonia eutropha JMP134]	49.43
contig00058-orf00031	phenol hydroxylase P3 protein [Ralstonia eutropha H16]	66.33
contig00058-orf00032	phenol hydroxylase region [Ralstonia eutropha JMP134]	48.31
contig00058-orf00034	acetaldehyde dehydrogenase [Dechloromonas aromatica RCB]	78.26
contig00058-orf00036	hydratase/decarboxylase [Dechloromonas aromatica RCB]	65.64
contig00058-orf00039	ferredoxin [Ralstonia metallidurans CH34]	50.7
contig00058-orf00040	catechol 2,3-dioxygenase [Ralstonia eutropha H16]	58.16
contig00058-orf00042	hydratase/decarboxylase [Ralstonia metallidurans CH34]	63.46
contig00058-orf00059	type II restriction enzyme HpaII (endonuclease HpaII) [Bacillus thuringiensis serovar konkukian str. 97-27]	32.59
contig00058-orf00096	CsbD-like [Mesorhizobium sp. BNC1]	63.08
contig00058-orf00158	hypothetical protein amb2120 [Magnetospirillum magneticum AMB-1]	45.16
contig00058-orf00208	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative [Treponema denticola ATCC 35405]	29.17
contig00058-orf00209	hypothetical protein Sfri 1687 [Shewanella frigidimarina NCIMB 400]	33.33
contig00058-orf00210	hypothetical protein RSc0877 [Ralstonia solanacearum GMI1000]	40.28
contig00058-orf00233	type I restriction-modification system specificity determinant [Geobacillus kaustophilus HTA426]	62.07
contig00058-orf00244	putative Rhs family protein [Pseudomonas aeruginosa UCBPP-PA14]	51.61
contig00058-orf00245	hypothetical protein Acid 1654 [Solibacter usitatus Ellin6076]	38.64
contig00059-orf00008	putative sensor histidine kinase [Myxococcus xanthus DK 1622]	28.88
contig00059-orf00009	DNA helicase/exodeoxyribonuclease V, gamma subunit [Prochlorococcus marinus str. MIT 9312]	19.47
contig00059-orf00011	DNA repair protein [Azoarcus sp. EbN1]	44.08

Query	Subject	%ID
contig00061-orf00005	#N/A	#N/A
contig00061-orf00010	putative clavaminate synthase-like (oxidase) [Frankia alni ACN14a]	31.8
contig00062-orf00032	#N/A	#N/A
contig00063-orf00008	sugar permease [Thermoplasma volcanium GSS1]	32.26
contig00063-orf00013	TonB-dependent receptor [Myxococcus xanthus DK 1622]	33.33
contig00063-orf00025	#N/A	#N/A
contig00063-orf00033	gamma-glutamyltransferase [Burkholderia cenocepacia HI2424]	32.08
contig00067-orf00001	carboxy-terminal protease [Shigella sonnei Ss046]	98.55
contig00070-orf00010	CRISPR-associated helicase Cas3 [Methylococcus capsulatus str. Bath]	46.04
contig00070-orf00011	hypothetical protein LA0688 [Leptospira interrogans serovar Lai str. 56601]	46.09
contig00070-orf00013	CRISPR-associated Csd1 family protein [Methylococcus capsulatus str. Bath]	46.59
contig00070-orf00014	hypothetical protein CT1132 [Chlorobium tepidum TLS]	60.19
contig00071-orf00003	glucan phosphorylase [Clostridium acetobutylicum ATCC 824]	47.06
contig00073-orf00001	#N/A	#N/A
contig00075-orf00003	#N/A	#N/A
contig00075-orf00048	abortive infection bacteriophage resistance protein [Nitrosococcus oceani ATCC 19707]	46.86
contig00076-orf00037	hypothetical protein Pcar 0125 [Pelobacter carbinolicus DSM 2380]	48.65
contig00076-orf00038	putative NTP-binding protein TniB [Pelobacter carbinolicus DSM 2380]	60.43
contig00076-orf00039	hypothetical protein Tcr 1645 [Thiomicrospira crunogena XCL-2]	43.58
contig00076-orf00042	hypothetical protein Tcr 1640 [Thiomicrospira crunogena XCL-2]	33.22
contig00078-orf00011	flagellar protein, putative [Borrelia garinii PBi]	44.44
contig00080-orf00002	hypothetical protein CRP 180 [Candidatus Carsonella ruddii PV]	32.81
contig00080-orf00105	transporter [Salmonella typhimurium LT2]	51.78
contig00080-orf00110	#N/A	#N/A
contig00080-orf00113	hypothetical protein plu3515 [Photorhabdus luminescens subsp. laumondii TTO1]	45.88
contig00080-orf00118	#N/A	#N/A
contig00080-orf00197	nuclear export factor GLE1 [Deinococcus geothermalis DSM 11300]	31.25

Query	Subject	%ID
contig00081-orf00017	putative outer membrane lipoprotein (lipocalin) [Acinetobacter sp. ADP1]	48.77
contig00088-orf00008	putative flippase [Bacteroides thetaiotaomicron VPI-5482]	28.79
contig00088-orf00010	#N/A	#N/A
contig00088-orf00011	#N/A	#N/A
contig00092-orf00005	amino acid transporter LysE [Colwellia psychrerythraea 34H]	51.53
contig00092-orf00007	GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961]	43.59
contig00092-orf00008	#N/A	#N/A
contig00092-orf00064	hypothetical protein PBPRB0577 [Photobacterium profundum SS9]	32.46
contig00095-orf00010	#N/A	#N/A
contig00095-orf00014	#N/A	#N/A
contig00096-orf00002	cyclic nucleotide-binding protein [Brucella suis 1330]	30.19
contig00096-orf00010	RNA polymerase sigma factor [Candidatus Protochlamydia amoebophila UWE25]	44.9
contig00096-orf00011	#N/A	#N/A
contig00099-orf00009	prophage CP4-like integrase [Chromobacterium violaceum ATCC 12472]	47.18
contig00099-orf00010	hypothetical protein c2416 [Escherichia coli CFT073]	23.23
contig00099-orf00016	hypothetical protein SAV 4435 [Streptomyces avermitilis MA-4680]	42.86
contig00099-orf00018	#N/A	#N/A
contig00099-orf00023	putative prophage primase [Pectobacterium atrosepticum SCRI1043]	35.71
contig00105-orf00001	#N/A	#N/A
contig00106-orf00002	methylation [Polaromonas sp. JS666]	32.39
contig00106-orf00006	cobalamin biosynthesis protein N [Methanothermobacter thermautotrophicus str. Delta H]	30.19
contig00106-orf00011	hypothetical protein NTHI0694 [Haemophilus influenzae 86-028NP]	52.05
contig00106-orf00012	hypothetical protein NTHI0694 [Haemophilus influenzae 86-028NP]	71.82
contig00107-orf00014	urease accessory protein UreF [Mesorhizobium loti MAFF303099]	41.38
contig00108-orf00101	#N/A	#N/A
contig00113-orf00001	hypothetical protein NMB1870 [Neisseria meningitidis MC58]	28.57
contig00113-orf00026	hypothetical protein BH1415 [Bacillus halodurans C-125]	45.71

Query	Subject	%ID
contig00113-orf00120	#N/A	#N/A
contig00113-orf00126	#N/A	#N/A
contig00115-orf00017	hypothetical protein TK0088 [Thermococcus kodakarensis KOD1]	30.34
contig00116-orf00002	hypothetical protein MCA1617 [Methylococcus capsulatus str. Bath]	46.15
contig00116-orf00003	hypothetical protein MCA1617 [Methylococcus capsulatus str. Bath]	60.71
contig00116-orf00022	#N/A	#N/A
contig00117-orf00033	hypothetical protein BT9727 1913 [Bacillus thuringiensis serovar konkukian str. 97-27]	40
contig00118-orf00001	DNA-binding protein [Neisseria meningitidis Z2491]	96.55
contig00119-orf00002	hypothetical protein Gmet A3576 [Geobacter metallireducens GS-15]	29.03
contig00119-orf00003	#N/A	#N/A
contig00119-orf00004	hypothetical protein Swol 0432 [Syntrophomonas wolfei subsp. wolfei str. Goettingen]	48.81
contig00119-orf00005	hypothetical protein SAR2498 [Staphylococcus aureus subsp. aureus MRSA252]	57.14
contig00119-orf00009	#N/A	#N/A
contig00119-orf00014	#N/A	#N/A
contig00122-orf00002	#N/A	#N/A
contig00125-orf00001	inorganic phosphate transporter [Chlamydia trachomatis D/UW-3/CX]	30.77
contig00125-orf00003	acyltransferase 3 [Pseudomonas syringae pv. syringae B728a]	38.3
contig00126-orf00001	#N/A	#N/A
contig00132-orf00002	hypothetical protein Tery 3131 [Trichodesmium erythraeum IMS101]	19.73
contig00132-orf00004	Smc-like [Mycoplasma gallisepticum R]	28.32
contig00132-orf00005	#N/A	#N/A
contig00136-orf00024	hypothetical protein all4935 [Nostoc sp. PCC 7120]	21.21
contig00138-orf00016	NADH dehydrogenase [Shewanella denitrificans OS217]	38.1
contig00139-orf00004	#N/A	#N/A
contig00145-orf00004	AspS [Buchnera aphidicola str. Cc (Cinara cedri)]	46.15
contig00145-orf00007	filamentous haemagglutinin [Xanthomonas axonopodis pv. citri str. 306]	53.39
contig00148-orf00057	methyl-accepting chemotaxis protein [Vibrio fischeri ES114]	29.03

Query	Subject	%ID
contig00148-orf00058	#N/A	#N/A
contig00151-orf00014	#N/A	#N/A
contig00154-orf00001	#N/A	#N/A
contig00162-orf00026	#N/A	#N/A

first location, the *lgtABCDE* cluster, was not found in *N. sicca* 4320. The cluster is preceded by the *glyS* gene in the pathogenic *Neisseria.* The *glyS* gene was found in *N. sicca* 4320 and the sequence following it determined (Figure 5). As can be seen in the figure, *N. sicca* 4320 has the organization *glyS*-*plsX*-phosphoribosyltransferase-hypothetical-*maf*-tetrapyyrole methylase-*uddP* instead of the *lgtABCDE* gene cluster found in the pathogenic strains, *N. lactamica* NS19, and *N. polysaccharea* NS342. The second and third location, the *lgtF-rfaK* cluster (Figure 6) and the *lgtG* gene (Figure 7) are not found in *N. sicca* 4320. *N. sicca* 4320 does however have the gene immediately upstream of *lgtG*. The fourth location and fifth location, the *rfaC* (Figure 8) and *rfaF* (Figure 9) genes, are found in all sequenced *Neisseria*. This was expected because they are responsible for the addition of the two heptose residues to the LOS core.

BLAST-based gene finding

Sequences of genes known to be involved in rhamnose biosynthesis, LOS biosynthesis, LPS biosynthesis, or capsule biosynthesis were used to search the *N. sicca* 4320 BLAST database to identify similar sequences. The sequences used for the search can be found in Table 7. The search yielded a further 17 ROIs (Table 8; Appendix F). The identified ROIs were then used to search the nr database to confirm similarity to polysaccharide biosynthesis genes.

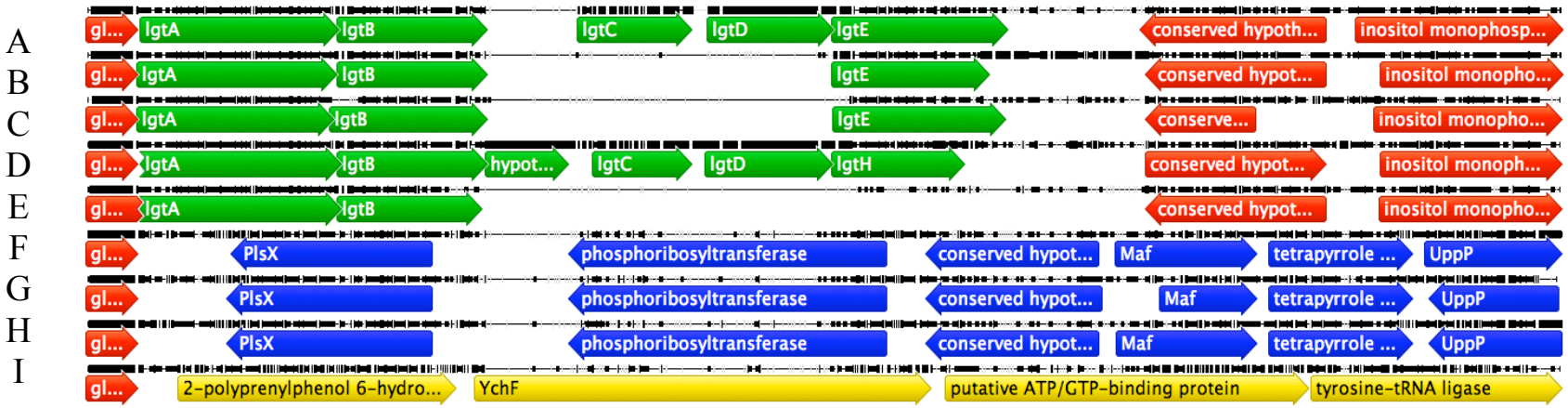


Figure 5. Alignment of *lgtABCDE* region in various *Neisseria.* The *lgtABCDE* region in the *Neisseria* was determined by locating the sequences downstream of the glycyl-tRNA synthetase, beta chain (shown in red). The green regions show the individual *lgt* genes found in each strain. Genes labeled in red downstream of the glycyl-tRNA synthetase, beta chain are conserved in five of the strains. *N. sicca* 4320, *N. sicca* DS1, and *N. mucosa* ATCC 25996 have a different organization downstream of the glycyl-tRNA synthetase, beta chain gene (shown in blue). A subsequent BLAST search determined that *N. sicca* 4320 lacked all five *lgt* genes found in this region. *N. sicca* ATCC 29256 contained an organization differing from the other sequenced *Neisseria* (shown in yellow). A: *gonorrhoeae* FA1090. B: *meningitidis* MC58. C: *meningitidis* NS44. D: *lactamica* NS19. E: *polysaccharea* 342. F: *sicca* 4320. G: *sicca* DS1. H: *mucosa* ATCC 25996. I: *sicca* ATCC 29256.

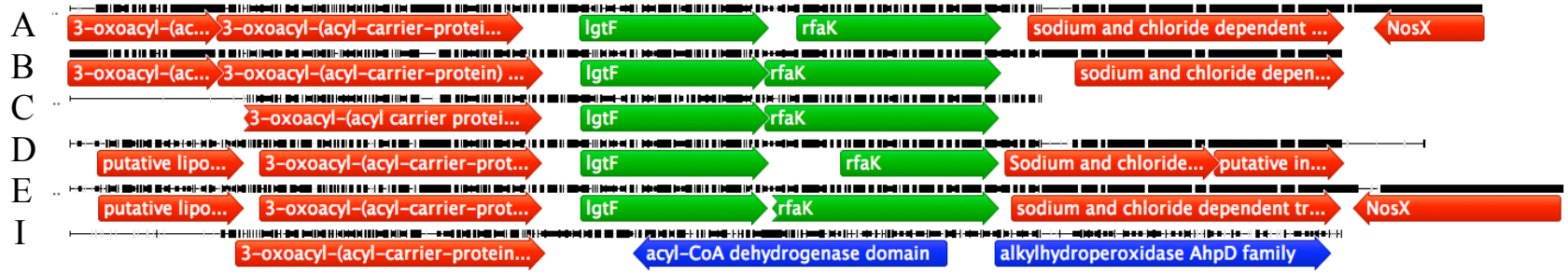


Figure 6. Alignment of *lgtF - rfaK* region in various *Neisseria*. The *lgtF - rfaK* region in the *Neisseria* was determined by locating the 3-oxoacyl-(acyl-carrier-protein) synthase II. The region downstream of the gene was determined. The *lgtF* and *rfaK* genes are shown in green. *N. sicca* 4320, *N. sicca* DS1, and *N. mucosa* ATCC 25996 lacked the 3-oxoacyl-(acyl-carrier-protein) synthase II gene and the *lgtF* and *rfaK* genes. A: *gonorrhoeae* FA1090. B: *meningitidis* MC58. C: *meningitidis* NS44. D: *lactamica* NS19. E: *polysaccharea* 342. F: *sicca* 4320. G: *sicca* DS1. H: *mucosa* ATCC 25996. I: *sicca* ATCC 29256.

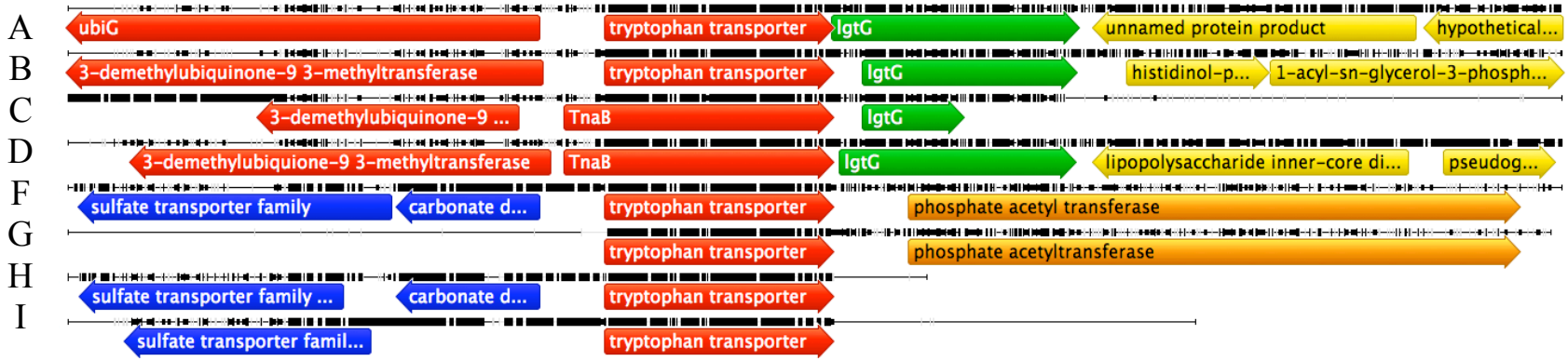


Figure 7. Alignment of the *lgtG* region in various *Neisseria.* The *lgtG* region in the *Neisseria* was determined by locating the *tnaB* gene. The region downstream of the gene was determined. The *lgtG* gene is shown in green. *N. sicca* 4320, *N. sicca* DS1, *N. mucosa* ATCC 25996, and *N. sicca* ATCC 29256 lacked the *lgtG* gene. A: *gonorrhoeae* FA1090. B: *meningitidis* MC58. C: *meningitidis* NS44. D: *lactamica* NS19. E: *polysaccharea* 342. F: *sicca* 4320. G: *sicca* DS1. H: *mucosa* ATCC 25996. I: *sicca* ATCC 29256.

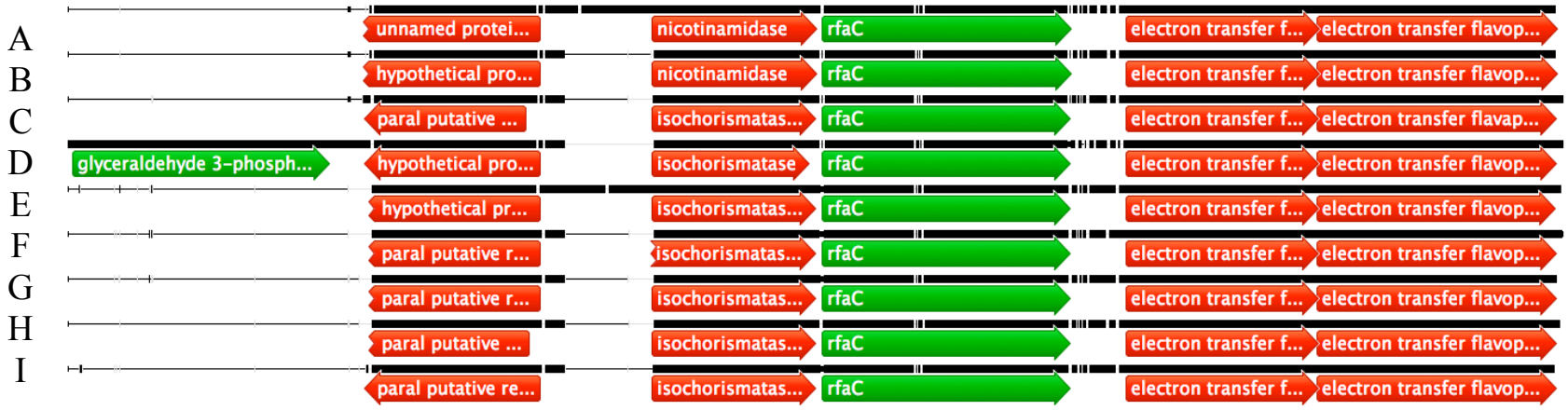


Figure 8. Alignment of the *rfaC* region in various *Neisseria.* The *rfaC* region in the *Neisseria* was determined by locating the nicotinamidase gene. The region downstream of the gene was determined. The *rfaC* gene is shown in green. It is conserved in all sequenced *Neisseria*. A: *gonorrhoeae* FA1090. B: *meningitidis* MC58. C: *meningitidis* NS44. D: *lactamica* NS19. E: *polysaccharea* 342. F: *sicca* 4320. G: *sicca* DS1. H: *mucosa* ATCC 25996. I: *sicca* ATCC 29256.

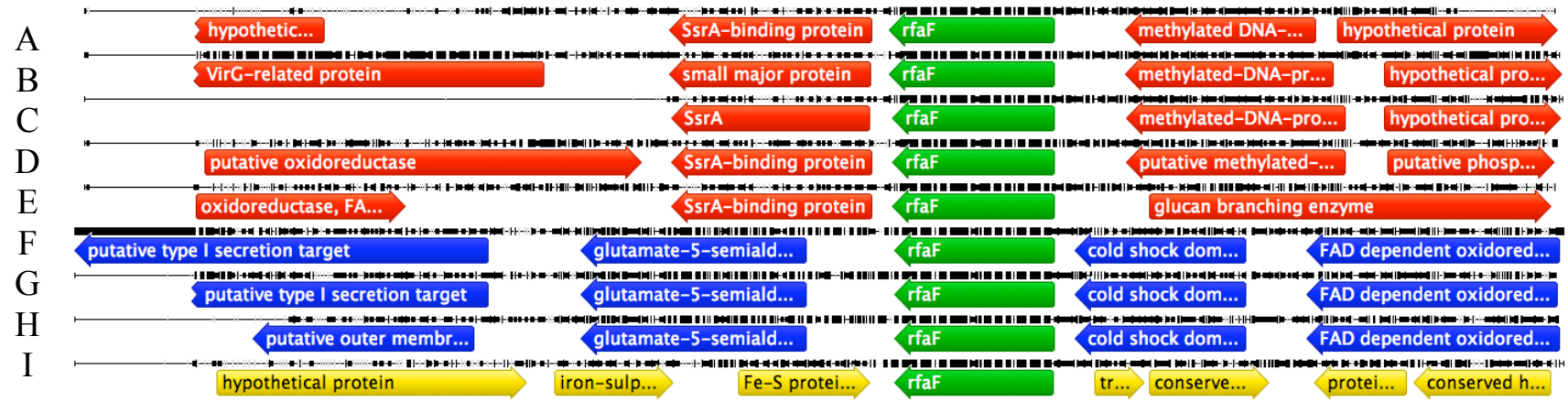


Figure 9. Alignment of the *rfaF* region in various *Neisseria.* The *rfaF* region in the *Neisseria* was determined by locating the *rfaF* gene and sequencing the surrounding region. The *rfaF* gene is shown in green. It is conserved in all sequenced *Neisseria*. A: *gonorrhoeae* FA1090. B: *meningitidis* MC58. C: *meningitidis* NS44. D: *lactamica* NS19. E: *polysaccharea* 342. F: *sicca* 4320. G: *sicca* DS1. H: *mucosa* ATCC 25996. I: *sicca* ATCC 29256.

Table 7. Sequences used for BLAST screen. Sequences used as BLAST queries to search the contig sequences of *N. sicca* 4320.

Sequence Query	Query Organ.	Program
Lgt A	MC58	Blastn
Lgt 2-1	4320	Blastn
E467	4320	Blastn
Lgt A	MC58	Blastx
Lgt 2-1	4320	Blastx
Lgt F AA	MC58	t Blastp
Lgt A AA	MC58	t Blastp
glycosyl + RNA		
synthase	MC58	Megablast
NMB-1933	MC58	Megablast
NMB-1924	MC58	Megablast
Lgt B	MC58	Megablast
Lgt B AA	MC58	t Blastp
NMB-1927	MC58	Megablast
NMB-1927 AA	MC58	t Blastp
Lgt E	MC58	Megablast
Lgt E AA	MC58	t Blastp
Gal E	MC58	Megablast
Gal E AA	MC58	t Blastp
Lgt C	FA1090	Megablast
		Blastn
		t Blastx
Lgt C AA	FA1090	t Blastp
Lgt D	FA1090	Megablast
		Blastn
		t Blastx

Sequence Query	Query Organ.	Program
Lgt D AA	FA1090	t Blastn
Lgt G	MC58	Megablast
		Blastn
		t Blastx
rfak	MC58	Mega
		Blastn
		t Blastx
rfak AA	MC58	t Blastn
rtaF	MC58	Mega
		Blastn
rfaF AA	MC58	t Blastn
rfaC	MC58	Mega
		Blastn
		t Blastx
rfaC AA	MC58	t Blastn
SiaC	MC58	Mega
		Blastn
		t Blastx
SiaC AA	MC58	t Blastp
CtrA	MC58	Mega

Sequence Query	Query Organ.	Program
		Blastn
		t Blastx
CtrA AA	MC58	t Blastp
LipA	MC58	Mega
		Blastn
		t Blastx
LipA AA	MC58	t Blastn
LpxB	MC58	Mega
		Blastn
		t Blastx
LpxB AA	MC58	t Blastn
PlsX	MC58	Mega
		t Blastx
PlsX AA	MC58	t Blastn
msb B	FA1090	Mega
		Blastn
msbB AA	FA1090	t Blast p
kpsM	E. coli APEC	Mega
		Blastn
		t Blastx
kpsM AA	E. coli APEC	t Blastn
kpsT AA	C. jejuni NTCC	t Blastn
kpsT	C. jejuni NTCC	Mega
		Blastn
		t Blastn
kpsC	C. jejuni	Mega
		Blastn
		t Blastx
kpsC AA	C. jejuni	t Blastn

ROI	ROI Annotation	%ID
contig 94-21	rmlA	88
contig 94-20	rmlB	89
contig 23-13	rmlC	93
contig 20-7	rmlD	71
contig 45-6	rfaC	92
contig 162-37	rfaF	78
contig 124-31	hep3	40
contig 50-49A	4-α-glucanotransferase	75
contig 50-49B	1,4-α-glucan-branching enzyme	86
contig 56-25	hypothetical glycosyltransferase	92
contig 28-18	glycosyltransferase	40
contig 28-17	glucosyltransferase	35
contig 106-30	LPS biosynthesis related glycosyltransferase	68
contig 131-13	LOS biosynthesis glycosyltransferase	44
contig 56-23	putative glycosyltransferase	81
contig 56-20	O-antigen ligase/polymerase	33
contig 56-40	chain length determinant protein	42
contig 56-37	Polysaccharide export protein	47
contig 56-18	LPS biosynthesis translocase	48
contig 11-2	capsular polysaccharide protein	31
contig 56-45	LPS oxidoreducatase	61

Table 8. ROI identified in bioinformatic screen.

Discussion

Genomic sequencing of the commensals

The selected commensal *Neisseria* were sequenced primarily to provide the sequence of *N. sicca* 4320. Having the genomic sequence allowed a bioinformatic analysis of *N. sicca* 4320 to identify those genes with a possible role in LOS or LPS-like polysaccharide biosynthesis. Nucleotide comparison of *N. sicca* 4320 to the other sequenced commensals was undertaken to determine the similarity of the *N. sicca* 4320 genomic sequence to the other sequenced commensals. It showed that *N. sicca* DS1 was the most similar, at 95.0%. This is as expected given that the other commensals were misidentified and would therefore be expected to be more divergent.

A benefit of the sequencing secondary to this project was an increase in the amount of sequence data available concerning commensal *Neisseria*. All of the previously sequenced *Neisseria* were either strains of *N. gonorrhoeae* or *N. meningitidis* with the exception of one *N. lactamica* strain. This sequence data can now be used to compare the commensals to the pathogenic strains and determine what genetic characteristics make a pathogen and what make a particular type of commensal.

Phylogenetic analysis

The phylogenetic analysis was undertaken to confirm that *N. sicca* 4320 had correctly been identified as a *N. sicca* strain. The sequenced commensals were identified before the benefit of 16S rRNA analysis or genotypic content analysis and it was possible that ambiguous sugar utilization or other physical property results could have resulted in a misidentification. According to Bergey's Manual of Systematic Bacteriology there are

no differences in sugar utilization or reduction potential between *N. sicca* and *N. subflava*, and the only difference between these two and *N. mucosa* is *N. mucosa*'s ability to reduce nitrate. The close similarity between the commensals makes correct identification in the absence of genomic data quite difficult.

Most importantly, the data showed that *N. sicca* 4320 was in fact a *N. sicca*. Comparing *N. sicca* 4320 with the other two *N. sicca* strains which have been sequenced, *N. sicca* DS1 and *N. sicca* ATCC 29265, will identify what is different between *N. sicca* 4320 and other *N. sicca* species. Comparison of *N. sicca* 4320 with other species wouldn't determine what was unique to *N. sicca* 4320, because differences between *N. sicca* strains and other commensal species would also be identified. Differences between *N. sicca* 4320 and *N. sicca* strains are of interest because of the novel nature of the O-repeat produced by *N. sicca* 4320. The O-repeat is predicted to be synthesized by enzymes unique to *N. sicca* 4320.

Secondarily to this, the analysis showed that three of the commensals were misidentified at the species level. Their true species identity was confirmed by a combination of 16S rRNA and gene content analysis. The gene content analysis was carried out to identify genes that would have to be present based on the physical properties chart found in the Bergey's Manual. For example, *N. meningitidis* is not able to metabolize lactose while *N. lactamica* is able to metabolize lactose. Therefore any *N. lactamica* would have lactose metabolic genes while and *N. meningitidis* would lack lactose metabolic genes. The correct identification of the three species was important because when they were used for comparative purposes it was essential to know that they were not actually *N. sicca* strains and therefore would be expected to be more divergent.

ORF Annotation

Identification of the open reading frames found within the contigs of *N. sicca* 4320 was undertaken so that the ORFs could be searched for similarity to genes hypothesized to be involved in polysaccharide biosynthesis. The ORFs were identified using a program called Glimmer3. Glimmer3 uses a probability model to determine what characteristics an ORF in the particular organism possesses. The program then takes the model and applies it to the entire genomic sequence (in this case the contig sequences) and identifies the ORFs found within the sequence. The model for this particular ORF identification used a companion program called longorf. Longorf assumes that the longest ORFs in a sequence are genes and uses their characteristics to build the probability model. Glimmer3 identified 2690 ORFs in *N. sicca* 4320. The sequencing of *N. sicca* ATCC 29256 at Washington University identified 2660 ORFs, which is comparable to the number of ORFs identified in *N. sicca* 4320. The amino acid sequences of the identified ORFs were extracted to use for further analysis because homologous sequences are less divergent at the amino acid level than the nucleotide level.

The identified ORFs were annotated by BLAST to determine the putative function of each ORF and to determine if this putative function was related to polysaccharide biosynthesis. The amino acid sequence of each ORF was used as a query to search two different BLAST databases. One database, DanAnn, was developed at CBCB and consisted of manually curated protein sequences. Manually curated sequence data is useful for annotation because the curated sequence has been expertly reviewed

and a higher confidence of correct annotation can be assumed. The second BLAST database used for the ORF annotation was the NCBI non-redundant sequence database. This database is composed of all sequence deposited with NCBI, both manually curated and sequence automatically annotated by gene finding algorithms. The annotation generated by BLAST using the DanAnn database was used for the remainder of the project because it was composed of sequences with a higher degree of confidence in the annotation. The functional category of each identified ORF and the Pfam domains found within each ORF was determined to gain further insight into the function of the identified ORFs.

Identification of regions of interest

The identification of ORFs that could possibly be involved in polysaccharide biosynthesis (termed regions of interest (ROI)) is the central focus of this project. A bioinformatic screen was used to identify the ROIs. The first part of the screen involved identifying ORFs that were unique to *N. sicca* 4320. Unique regions are of interest because of the novel nature of the LPS-like polysaccharide structure found in *N. sicca* 4320. The hypothesis guiding the research states that the polysaccharide biosynthetic genes were acquired by horizontal gene transfer and would therefore be unique to *N. sicca* 4320. The contig sequences from *N. sicca* 4320 were compared to the genomic sequences of *N. gonorrhoeae* FA1090, *N. meningitidis* MC58, *N. polysaccharea* NS342, *N. mucosa* ATCC 25996, *N. sicca* DS1, and *N. sicca* ATCC 29256 using the alignment program Nucmer. *N. sicca* 4320 was compared with these six organisms because they represent a broad *Neisseria* set and will identify ORFs that *N. sicca* 4320 has in common

with the pathogens, other commensals, and ORFs common to *N. sicca* strains. It was found that 244 *N. sicca* 4320 ORFs had no similarity to any ORFs in the organisms used for comparison and of these unique ORFs, two were annotated as glycosyltransferases, and were therefore ROIs.

The second step in the bioinformatic screen involved searching the *N. sicca* 4320 contig sequences for the presence of LOS biosynthetic genes found in the pathogenic *Neisseria*. The synthesis of LOS in the pathogenic strains is controlled by the action of glycosyltransferase genes found in 5 locations on the bacterial chromosome. Three of the locations in *N. sicca* 4320 contained a different genomic organization than that found in the pathogens and did not contain ORFs with similarity to glycosyltransferase genes. The other two regions contained the genes responsible for the addition of the two heptose residues found in the LOS of all *Neisseria*. These two regions appear to be conserved across all sequenced *Neisseria*.

The third step in the screen involved using known LPS, LOS, and capsule biosynthesis genes as query sequences in a BLAST search of the *N. sicca* 4320 contig sequences. These sequences were chosen as queries because they represent a broad class of sugar structure biosynthetic enzymes and are known to be involved in the production of LPS/LOS/capsule in other organisms. The rhamnose biosynthetic genes were also used as query sequences because the disaccharide repeat in the polysaccharide of *N. sicca* 4320 contains rhamnose.

The ORF, functional, and Pfam annotation of *N. sicca* 4320 was examined for any indication of glycosyltransferase or LPS/LOS biosynthesis as a final step in the

bioinformatic screen. All ROIs found by this examination had already been identified in the third step of the bioinformatic screen.

The bioinformatic screen identified 21 ROIs. Four of the ROIs had similarity to the four rhamnose biosynthetic genes. This was expected because *N. sicca* 4320 has rhamnose in the polysaccharide and would thus have to be able to synthesize rhamnose. Three of the ROIs showed similarity to heptosyltransferase genes. This was again expected because the LOS of *N. sicca* 4320 is predicted to have three heptose residues. Two of the ROIs were a 4-α-glucanotransferase and a 1,4-α-glucan-branching enzyme. These were labeled ROIs because they are involved in sugar structure modification. Six of the ROIs had similarity to glycosyltransferases. These are of interest because the disaccharide of the O-repeat and the LOS of *N. sicca* 4320 would be synthesized by the sequential addition of sugars by glycosyltransferases. It is predicted that there are two glycosyltransferases involved in the synthesis of the LOS because LOS is predicted to have a two-sugar extension from the heptose core and two glycosyltransferases involved in the synthesis of the polysaccharide disaccharide. One ROI had similarity to an O-antigen ligase/polymerase, one ROI had similarity to a chain length determinant protein, and two ROIs have similarity to LPS translocase/export proteins. These four ROIs are of interest because it is predicted that *N. sicca* 4320 would have an O-antigen ligase to ligate the LPS-like polysaccharide to its anchor, a chain length determinant protein to determine the range of polysaccharide lengths, and translocase proteins to export the polysaccharide structure. One ROI has similarity to a capsular polysaccharide biosynthesis protein and one ROI has similarity to a LPS biosynthesis oxidoreductase. These were chosen as ROIs because they are sugar structure modification enzymes.

Overall the bioinformatic screen was successful in several respects. It was able to identify *N. sicca* 4320 DNA sequences with similarity to genes encoding the different classes of expected biosynthetic enzymes. Two of the identified ORFs were unique to *N. sicca* 4320 and had similarity to glycosyltransferase enzymes, fitting with the hypothesis that the genes were acquired by *N. sicca* 4320.

Future Directions

The closure of the gaps between the contigs is important because it will give the complete closed sequence of *N. sicca* 4320. The annotated ORFs can be laid out based on chromosomal coordinates and the chromosome can be compared to other completed, closed *Neisseria* chromosomes to determine inversions, duplications, deletions, and rearrangements between the chromosomal sequences.

Another reason that gap closure is important is because there is sequence missing between the gaps and this sequence could be a ROI. Assembly programs like Newbler usually leave a gap in sequence that is repetitive or in repeat sequences that are located in multiple places in the chromosome. Therefore, any ORFs containing repetitive sequence or sequence that is found in multiple places would not have been identified in the ORF annotation because there is a gap in the ORF. Closing the gaps will reveal this dropped sequence and increase the confidence that all ORFs have been identified.

There are a few different ways to close the gaps found in the *N. sicca* 4320 chromosomal sequence. One way is to align the ends of the contigs with other *Neisseria* sequences, such as *N. meningitidis* MC58 and *N. sicca* ATCC 29256, to determine if any of the contig ends are found adjacent to each other after alignment. This could indicate that the two contigs should be connected. PCR can be used to confirm that the contig ends match and the gap closed. Another way to close gaps is to use a program called ABBA that identifies possible protein sequence at the ends of contigs and tries to match up the contigs based on this protein sequence [71]. The program can use a reference sequence and the unassembled single reads to assemble the gap between the contigs. A final way to close the contig gaps in *N. sicca* 4320 is to undertake a PCR strategy.

Primers can be designed for the ends of the contigs and used in different combinations to attempt to close the gaps. If two particular primers produce a band then those two contigs match together. This approach can be tedious because many different combinations have to be tried in batches to determine the correct order of the sequences. This approach might best be saved for those gaps not closed by the previous methods.

Chapter 4: Screens and cloning

Introduction

The previous chapter of the thesis focused on bioinformatic analysis of *N. sicca* 4320 as a way to identify putative LPS-like polysaccharide biosynthesis genes. This chapter focuses on the use of two screening methods to select *N. sicca* 4320 mutants with an altered polysaccharide structure, a method of generating random *N. sicca* 4320 mutants, and a method of cloning and insertionally inactivating the regions of interest located in the previous chapter.

A subset of these ROIs were selected to clone into pUC19 and be insertionally inactivated using the Ω cassette. The Ω cassette was engineered from a fragment of an *E. coli* plasmid containing the spectinomycin resistance gene *aadA* [72, 73]. The cassette has transcriptional terminators at each end. This allows the cassette to cause premature termination when inserted into a gene. The presence of the spectinomycin resistance gene allows for selection of transformants based upon the acquisition of spectinomycin resistance. Insertion of the Ω cassette into the ROIs and their subsequent transformation back into *N. sicca* 4320 would allow the specific inactivation of one region of interest at a time thus allowing the determination of the effect of the knockout on polysaccharide structure. In addition, previously generated shotgun clones of *N. sicca* 4320 were analyzed to determine if they could be used for insertional inactivation of polysaccharide biosynthesis genes.

One of the limitations of the previous bioinformatic gene-finding screen was its reliance on the sequences of polysaccharide biosynthesis genes from previously

sequenced organisms. Novel *N. sicca* 4320 genes which might be involved in polysaccharide biosynthesis would not be identified because they might not share sufficient similarity to previously identified polysaccharide modification enzymes to be picked up in the screen (>30% similarity over the length of the gene at the amino acid level). Random Tn5 transposition of *N. sicca* 4320 chromosomal DNA was one method used to overcome this limitation. The Tn5 system has been used previously to generate gene knockouts and was shown to integrate randomly into the target DNA [26, 74]. This allowed the production of chromosome wide random gene knockouts that were transformed into *N. sicca* 4320, thus removing a selection bias. The two screens were used to help analyze the large number of colonies needed to ensure complete chromosomal coverage during the random insertional mutagenesis.

This phase of the project had three main goals. The first goal was to determine if the lectin GSII and polymyxin B could be used to identify *N. sicca* 4320 mutants with altered polysaccharide structures. The second goal was to carry out a genome wide gene knockout experiment to determine if any putative polysaccharide biosynthesis genes were missed in the bioinformatic screen. The third goal was to clone the putative polysaccharide biosynthesis genes identified in the previous chapter.

Results

Lectin GS-II colony blot

Lectin GS-II was tested as a means of screening for polysaccharide biosynthesis mutants because it specifically binds terminal *N*-acetylglucosamine residues (the terminal sugar on *N. sicca* 4320 LPS-like polysaccharide) [48, 75]. Colonies of *N. sicca* 4320 and *N. polysaccharea* NS342 were transferred to a nitrocellulose membrane, blocked with 5% dry milk, and incubated with HRP-conjugated GS-II lectin. Development of the membrane showed dark blue staining in the *N. sicca* 4320 sector and no staining in the *N. polysaccharea* NS342 sector (Figure 10). This was expected because *N. polysaccharea* NS342 only makes LOS, and not the repeating polysaccharide structure.

Lectin GS-II western blot

The lectin screen will not be able to identify alterations in polysaccharide structure if the LOS molecule on *N. sicca* 4320 also contains a terminal *N*-acetylglucosamine. This was tested using a polyclonal antibody raised against *N. sicca* 4320. Whole cell preparations were treated with Proteinase K to remove protein from the samples [76]. The extracts were run on a 16.5% Tris-Tricine SDS-PAGE gel until the dye front reached the bottom. Samples were transferred to a PVDF membrane in a criterion blotter at a constant 100V for 20 minutes. The membrane was blocked, incubated with lectin, and developed. The lectin specifically bound the LPS repeat bands, showing the characteristic ladder pattern, but did not bind the lower molecular weight LOS (Figure 11A). The membrane was then stripped, blocked, and incubated with α-4320. Development of the membrane showed that α-4320 bound both LOS (lower

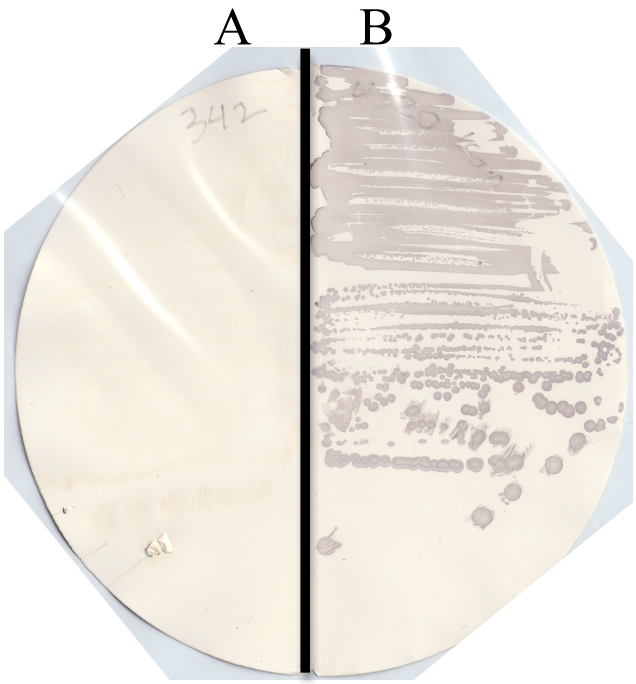


Figure 10. Colony blot of *N. sicca* 4320 and *N. polysaccharea* NS342. *N. sicca* 4320 and *N. polysaccharea* NS342 were each struck on half a plate. The plate was blotted with nitrocellulose and stained with lectin GS-II. Only the *N. sicca* 4320 sector developed. A: *N. polysaccharea* NS342. B:.*N. sicca* 4320.

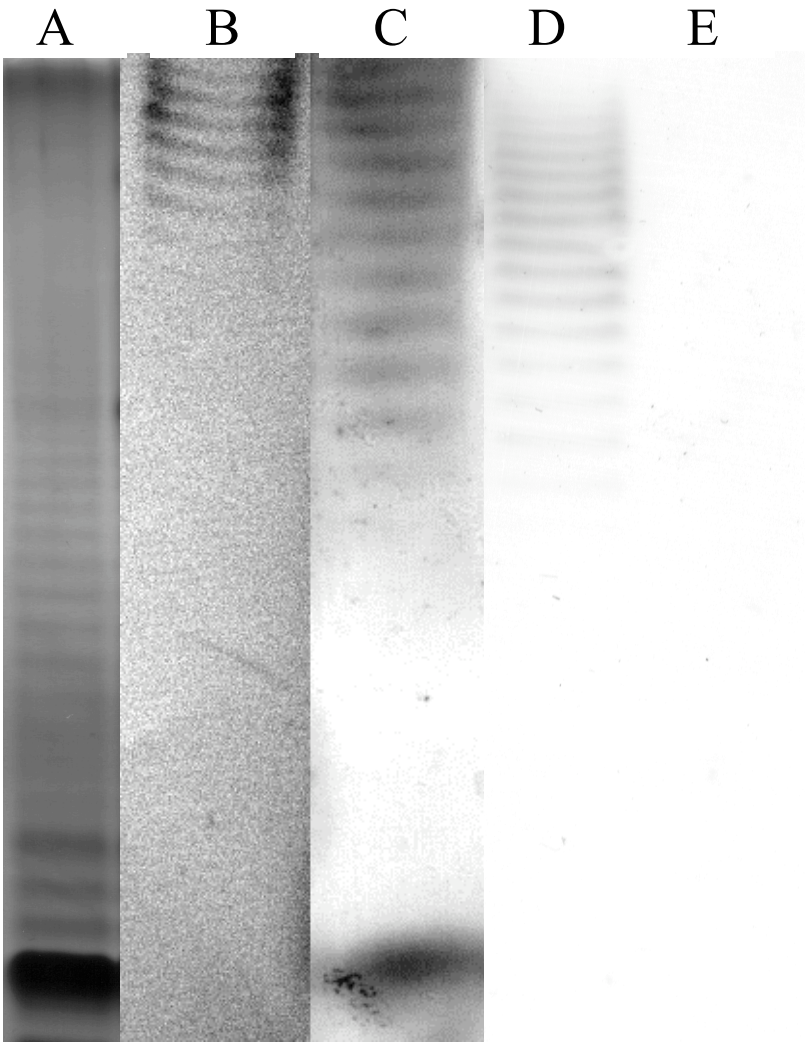


Figure 11. Western blot of *N. sicca* 4320 LPS/LOS using lectin GS-II. *N. sicca* 4320 LPS/LOS was run on a 16.5% Tris-Tricine SDS-PAGE. The LPS/LOS was transferred to a membrane and probed using lectin GS-II. The membrane was then stripped and probed using an α-4320 antibody. Lane A: Silver stained LPS/LOS. Lane B: LPS/LOS blotted with lecting GS-II. Lane C: LPS/LOS blotted with α-4320. Lane D: LPS/LOS blotted with lectin GS-II. Lane E: Hexosaminidase digestion of LPS/LOS blotted with lectin GS-II.

band) and the polysaccharide ladder (Figure 11B). This shows that both LOS and the polysaccharide repeat transferred to the membrane and lectin GS-II specifically recognizes the polysaccharide structures and not LOS. This is similar to the development seen in silver stained SDS-PAGE samples (Figure 11C) [77]. A hexosaminidase digestion of the *N. sicca* 4320 LPS/LOS failed to bind lectin, as expected (Figure 11D). Taken together, these data show that lectin GS-II can be used as a method of identifying *N. sicca* 4320 mutants that lack a terminal N-acetylglucosamine residue.

Polymyxin B screen

It has been shown that antimicrobial peptides such as polymyxin B can be used to isolate spontaneous mutants with altered LOS. Changes in the surface of the bacteria decreases the affinity of the cationic antimicrobial peptides for the bacteria thus resulting in an increase in bacterial resistance to the antimicrobial agents [78, 79]. A screen was developed to determine if polymyxin B could be used to select for *N. sicca* 4320 mutants with truncated LPS/LOS. This would indicate that polymyxin B could be used as a method of screening polysaccharide mutants generated by other methods; polysaccharide deficient mutants would be more resistant to polymyxin B than wild-type *N. sicca* 4320. *N. sicca* 4320 was resuspended to an approximate concentration of 10^9 CFU/ml. An aliquot of 500 µl was plated onto a GCK plate containing polymyxin B at a concentration of 2 µg/ml. The plate was incubated 48 hrs at 37 C. Polymyxin B resistant colonies were isolated and passaged on GCK media without polymyxin B. After passage in the absence of selection the isolated samples were returned to media containing polymyxin B at 2 µg/ml to ensure the polymyxin B resistant phenotype was stably expressed.

Colonies that were found to stably express polymyxin B resistance were patched onto a GCK plate containing 2 μg/ml polymyxin B. The plate was incubated overnight and the patches were transferred to a nitrocellulose membrane. The membrane was incubated with lectin as described above. The development on the membrane is illustrative of the types of variation seen in these lectin blots (Figure 12). As can be seen in figure 13, wild-type *N. sicca* 4320 stained a dark blue (red square) while wild-type *N. polysaccharea* NS342 failed to bind lectin (green circle). Some of the bands resulted in full blue staining, some resulted in light staining (solid arrow), and some resulted in no staining. Samples exhibiting reduced or absent staining are expected to have altered polysaccharide repeat structures and were prepped for SDS-PAGE separation followed by silver staining. One polymyxin B resistant mutant was been found exhibiting an altered polysaccharide when visualized by silver staining (Figure 13).

Random chromosomal transposon mediated gene knockout

<KAN-2> was used as a method of generating random insertional knockouts chromosome wide in an effort to generate a polysaccharide biosynthetic mutant. *N. sicca* 4320 chromosomal DNA was isolated and the Tn5 insertion kit was used to insert <KAN-2> into the chromosomal DNA. The 4320::KAN-2 DNA was used to transform chemically competent *N. sicca* 4320. The resulting kanamycin resistant colonies were blotted onto nitrocellulose and screened using lectin GS-II as previously discussed (Figure 14). The blots were examined for the presence of sectored colonies, colonies with lighter binding patterns, or colonies that failed to bind the lectin, all of which would represent possible polysaccharide repeat mutants. Over one hundred blots were screened,

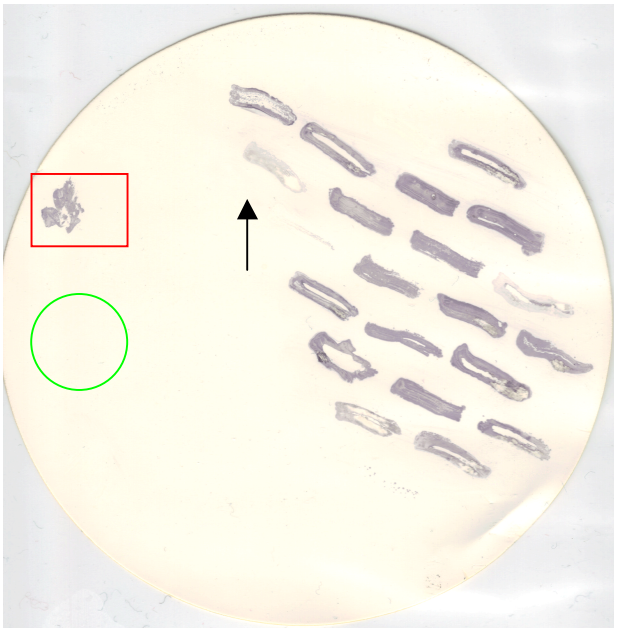


Figure 12. Polymyxin B resistant *N. sicca* 4320 mutant colony blot. Red box: Wildtype *N. sicca* 4320. Green Circle: *N. sicca* 342 (negative control). Arrow: Example of light staining patch.

1 2 3

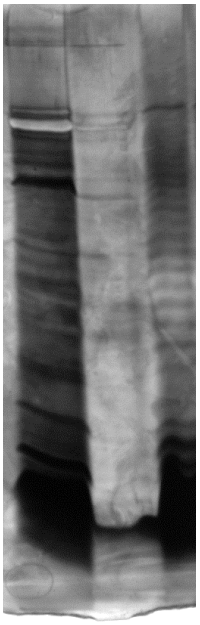


Figure 13. Polymyxin B resistant *N. sicca* 4320 mutant SDS-PAGE. LPS/LOS from two polymyxin B resistant mutants was run on a 16.5% Tris-Tricine SDS-PAGE gel and silver stained. Lane 1: Wild-type. Lane 2: PxB mutant 1. Lane 3: PxB mutant 2.

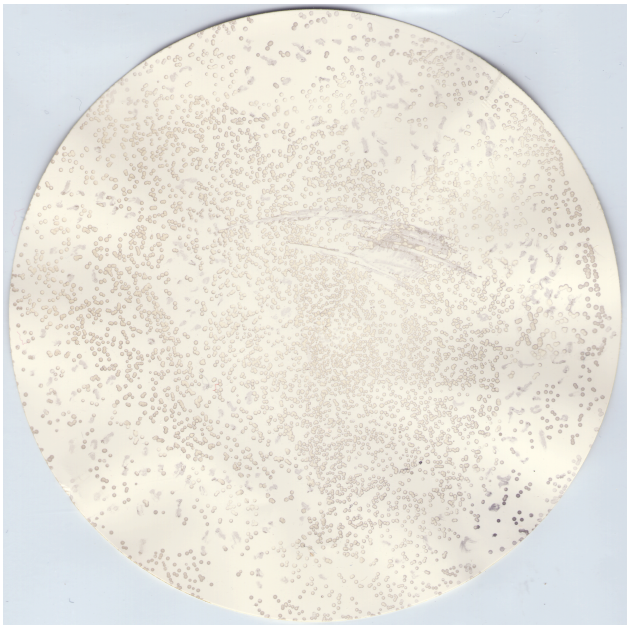


Figure 14. Random *N. sicca* 4320 Kan^R colony blot. The <KAN-2> transposon was randomly inserted into *N. sicca* 4320 chromosomal DNA. The DNA was then used to transform *N. sicca* 4320 to generate Kan^R colonies. The colonies were blotted onto nitrocellulose and probed with lectin GS-II.

representing thousands of colonies. No putative polysaccharide repeat deficient colonies were identified.

Shotgun Clone Analysis

Previously generated shotgun clones of *N. sicca* 4320 were utilized because they could potentially contain ROIs. Four shotgun clones, E187, E368, E467, and A73, were chosen for further analysis based on their sequence similarity to genes encoding known polysaccharide enzymes in an effort to determine if they play a role in the LPS-like polysaccharide biosynthesis. It is important to note that the shotgun clones were not completely sequenced; there was only one sequencing reaction in the forward direction. The plasmids containing the clones were digested with EcoRI or AccI to generate two linear DNA fragments, one representing the plasmid, pUC19, and the other representing the clone. These fragments were analyzed on a 1% agarose gel to determine the size of the clone. Two of the clones, E368 and A73, consistently showed a band representing the clone fragment that was smaller than the previously determined sequence (Data not shown). This indicated that the plasmid had undergone a deletion event and the full-length clone was lost. These two clones were not further characterized because of the deletion.

Shotgun clone insertional gene knockout

Clone E467, the larger of the two remaining clones, was chosen for an insertional inactivation experiment. The <KAN-2> transposon contains the kanamycin resistance gene whose insertion is mediated by Tn5. Insertion of <KAN-2>, which is 1221 bp in

length, into a gene should result in the inactivation of that gene. Thus, insertion of <KAN-2> into the region of clone E467 with similarity to the glucan branching enzyme should result in inactivation of the glucan branching enzyme. The insertion of <KAN-2> into E467 was carried out using conditions described by the kit supplier and resulting *E. coli* transformants were selected on both ampicillin and kanamycin plates to select insertion events that did not affect the pUC19 native selectable marker, amp^r. This insertion was conducted twenty times (2 kits) to generate a large quantity of stock plasmid. Plasmid from these transformants was isolated and used to transform chemically competent *N. sicca* 4320. Only three Kan^r *N. sicca* 4320 colonies were produced by transformation using the E467::KAN-2 plasmid DNA.

SDS-PAGE analysis of polysaccharides

To determine if insertion of <KAN-2> into E467 had affected the production of the polysaccharide, LPS/LOS from the E467::<KAN-2> *N. sicca* 4320 strains was isolated by the quick gonococcal LOS prep procedure. This LPS/LOS was run on a 16.5% Tris-Tricine SDS-PAGE gel, along with a wild-type control, to determine if the E467::KAN-2 strains showed a different gel profile. There was no difference between the wild-type control and the E467::KAN-2 strains (Data not shown).

Shotgun clone sequencing

Clone E467::KAN-2 was sequenced to determine the sequence of the whole clone and to identify the site of <KAN-2> insertion. One of the E467::KAN-2 clones was used for sequencing to take advantage of the <KAN-2> insertion. Since there is a 1221 bp

DNA fragment of known sequence in the clone, it can be used as a platform from which to sequence from the middle of the clone while also sequencing from the ends (Figure 15). The clone was amplified using pUC19 amplification primers M13F and M13R. A series of single extension sequencing reactions were carried out using M13F, M13R, KanF, and KanR to sequence four pieces of the shotgun clone. The newly acquired sequence was used to generate four new primers, 467F-extension, 467R-extension, KanF-extension, and KanR-extension. These primers were used to generate another set of single extension sequencing. These eight sequences were aligned using the NCBI Align 2 sequences web service. The alignment showed that the sequences covered the entire clone and a consensus sequence was determined from the sequences. The distance between the beginning of the two remaining E467::KAN-2 clones and the edge of the <KAN-2> insertion was determined by PCR (data not shown). This indicated that the <KAN-2> had inserted outside of the glucan branching enzyme sequence in all three transformants. Therefore, the glucan branching enzyme sequence was not disrupted in the E467::Kan-2 strains.

Clone E187 was sequenced in four single extension reactions using primers 187F, 187R, 187F-extension, 187R-extension and a consensus sequence determined. E187 appeared to be the region of the glucan branching enzyme directly upstream of E467 based on similarity comparisons to the *N. denitrificans* 1,4-α-glucan branching enzyme sequence.

Inverse PCR sequencing of flanking regions

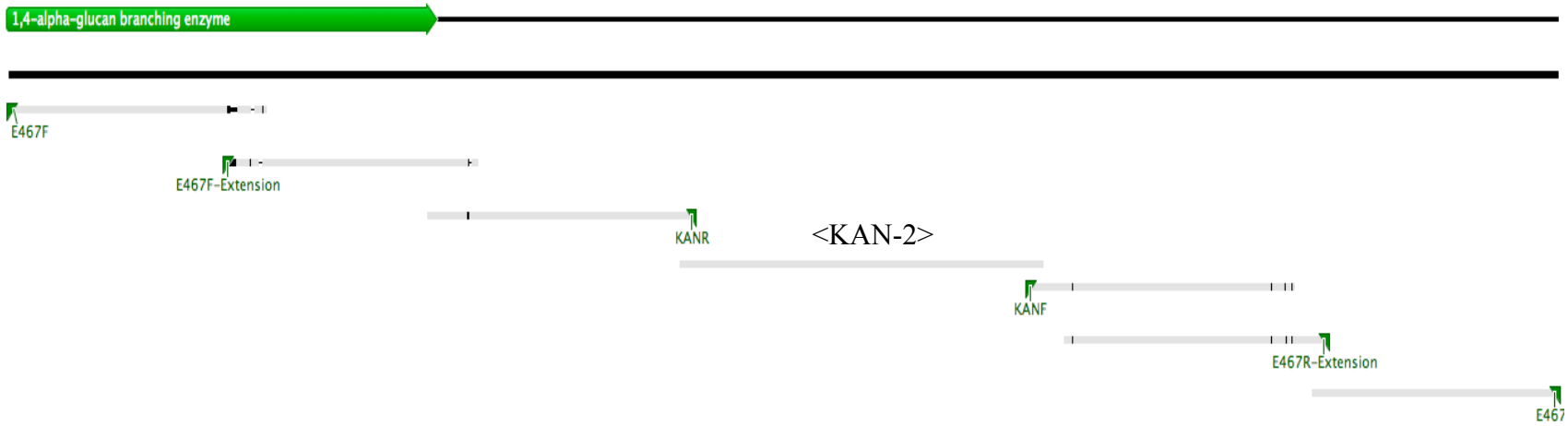


Figure 15. PCR sequencing of E467::KAN-2. The complete sequence of E467::KAN-2 was determined in six primer-walking sequencing steps. The <KAN-2> transposon sequence found in the middle of E467::KAN-2 was used as a platform to sequence out from the middle. The primers used for sequencing are shown in green. The six sequences obtained from Macrogen and the sequence of <KAN-2> are shown in their relative position along the consensus sequence. A: E467F. B: E467F-Extension. C: KANR. D: <KAN-2>. E: KANF. F: E467R-Extension. G: E467R.

Inverse PCR was undertaken to determine the sequence of the region flanking E187-E467 in the *N. sicca* 4320 chromosome (Figure 26). *N. sicca* 4320 chromosomal DNA was isolated and digested with XhoI. The fragments were ligated under conditions favoring self-ligation. The self-ligated fragments were used as template DNA in PCRs using primers 187-InverseF + 187-InverseR and E467-InverseF + E467-InverseR. These primers were chosen because they amplify outward from the known regions. Self-ligated fragments containing the complement to the inverse PCR primer sets will amplify giving a fragment that can be sequenced. The sequence of the fragment will represent the regions flanking the known region since the PCR primers were selected to go out from the known region. The sequence was combined with the previous E187-E467 sequence to generate a consensus representing the E187-E467 and flanking regions.

Cloning of selected putative polysaccharide biosynthesis genes

Nine regions of interest identified in the bioinformatic screen of *N. sicca* 4320 were also selected for a cloning experiment. The four rhamnose biosynthetic regions, *rmlA, rmlB, rmlC,* and *rmlD*, were chosen because rhamnose is found in the O-repeat. Inactivation of any of these four genes should result in a loss of the polysaccharide structure. Heptosyltransferase I and III were selected because one hypothetical anchor for the polysaccharide repeat was the third heptose residue in *N. sicca* 4320 LOS. Inactivation of either of these will result in no third heptose residue, which will give insight into the polysaccharide anchor location. The 4-α-glucanotransferase and the 1,4-α-glucan branching enzyme were chosen because they were associated with the initial shotgun clone sequencing. Finally, a fragment containing a putative O-antigen

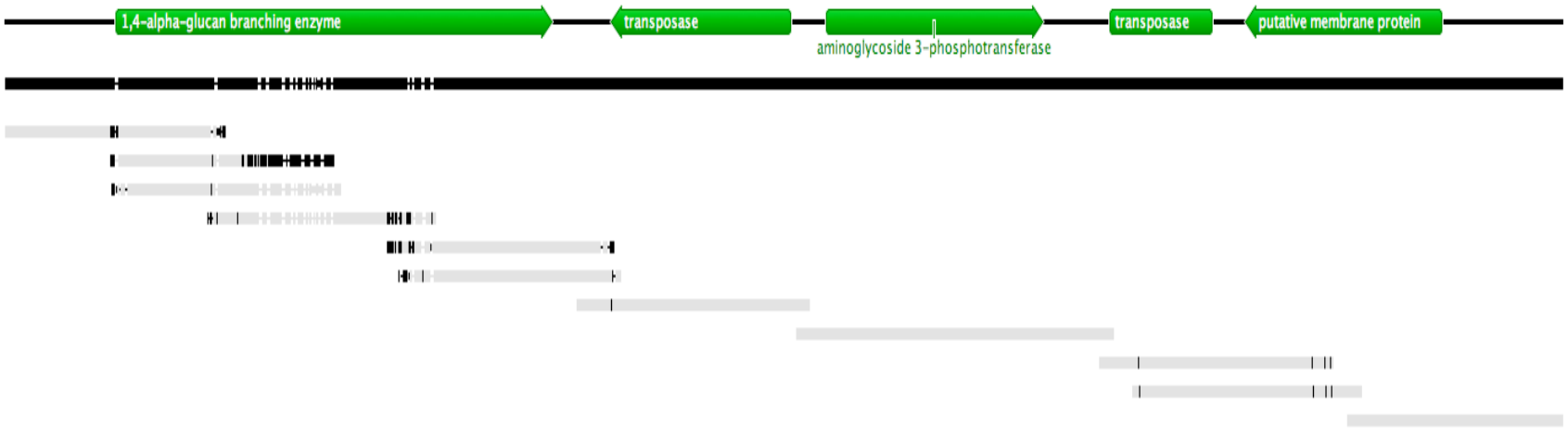


Figure 16. Inverse PCR consensus sequence. The sequence flanking E187 + E467 was determined by inverse PCR. The sequences used to determine the consensus sequence are shown below the consensus.

ligase/polymerase was chosen because it might be involved in polymerizing the disaccharides into the large repeating band structures or in ligation of the polysaccharide repeat onto its anchor. Knockout of either of these functions should result in loss of the polysaccharide structure.

The selected regions were amplified using PCR (Figure 17). The amplicons were digested with the appropriate enzymes and ligated into pUC19 (Figure 18A). A second set of primers was used to amplify the plasmid containing the cloned region. This introduced a XhoI site in the middle of the ROI. The Ω cassette was ligated into the middle of the ROI using the XhoI sites (Figure 18B). The Ω cassette contains inverted transcriptional terminators and a spectinomycin resistance gene, thus any gene it is inserted into will become inactive. The cloned regions carrying the transcriptional terminators in the middle were transformed into chemically competent *N. sicca* 4320 to generate strains carrying inactivated ROI. No spectinomycin resistant colonies were generated. The spectinomycin resistance marker in the Ω cassette was replaced with the kanamycin marker. After transformation, no kanamycin resistant colonies were generated.

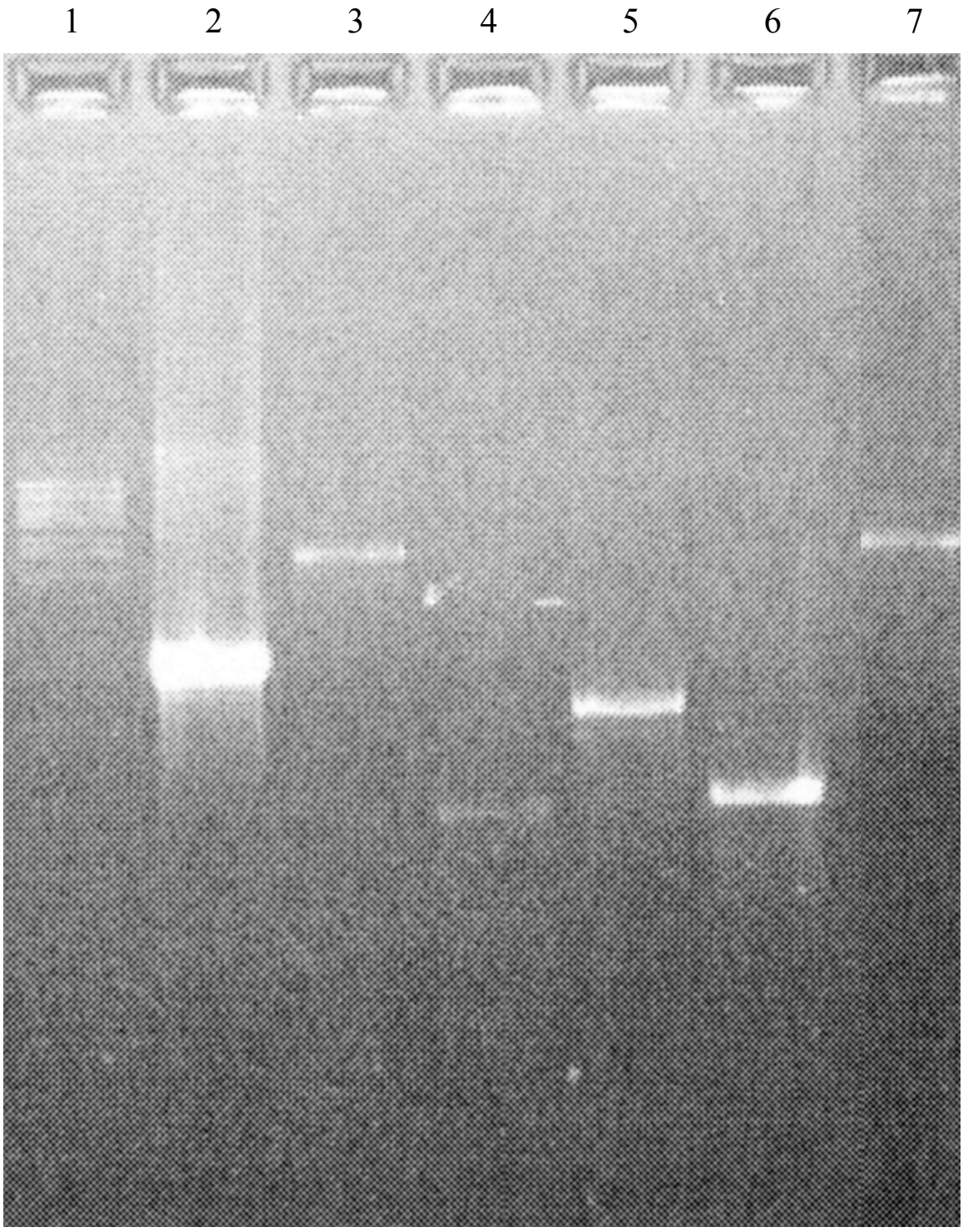
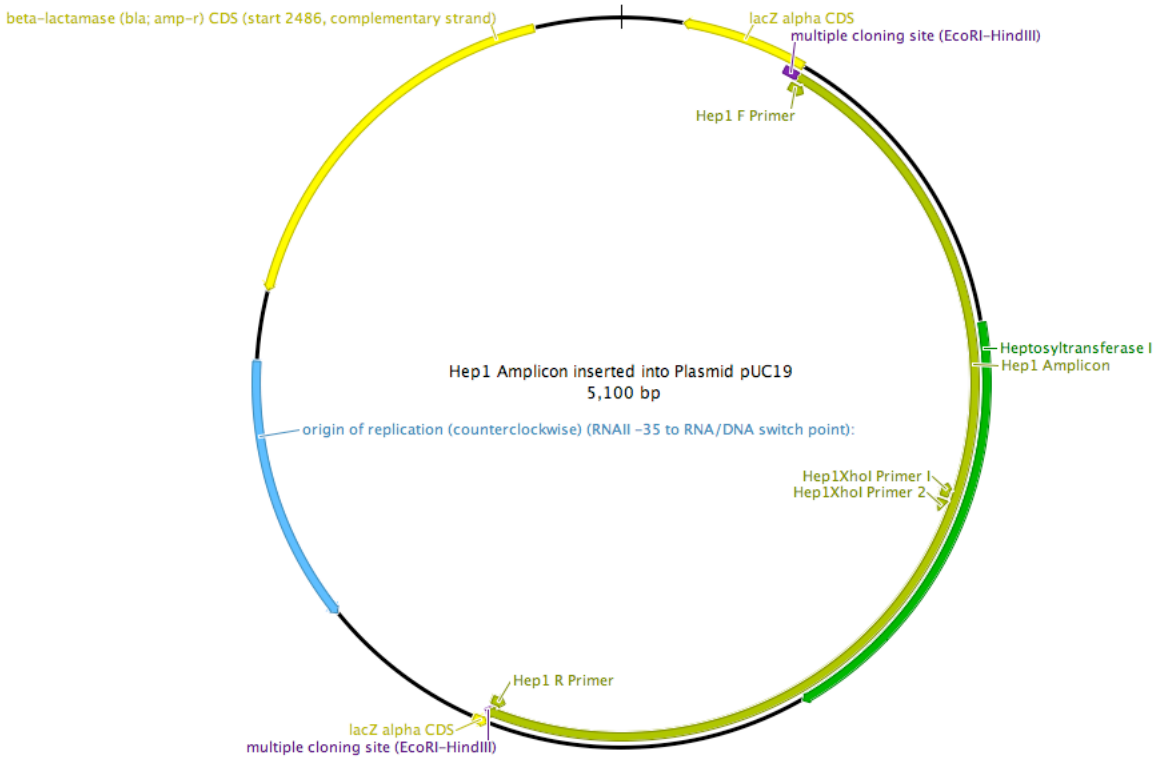


Figure 17. ROI PCR amplification. A subset of the ROI identified in chapter 1 were amplified by PCR in preparation for cloning. Lane 1: λ DNA BstEII digest. Lane 2: Hep3. Lane 3: GT4. Lane 4: R1. Lane 5: R2. Lane 6: R3. Lane 7: Branch.

A


beta-lactamase (bla; amp-r) CDS (start 2486, complementary strand)
lacZ alpha CDS
multiple cloning site (EcoRI-HindIII)
Hep1 F Primer
Heptosyltransferase I
Hep1 Amplicon
Hep1 Amplicon inserted into Plasmid pUC19
5,100 bp
origin of replication (counterclockwise) (RNAII -35 to RNA/DNA switch point):
Hep1XhoI Primer I
Hep1XhoI Primer 2
Hep1 R Primer
lacZ alpha CDS
multiple cloning site (EcoRI-HindIII)

B

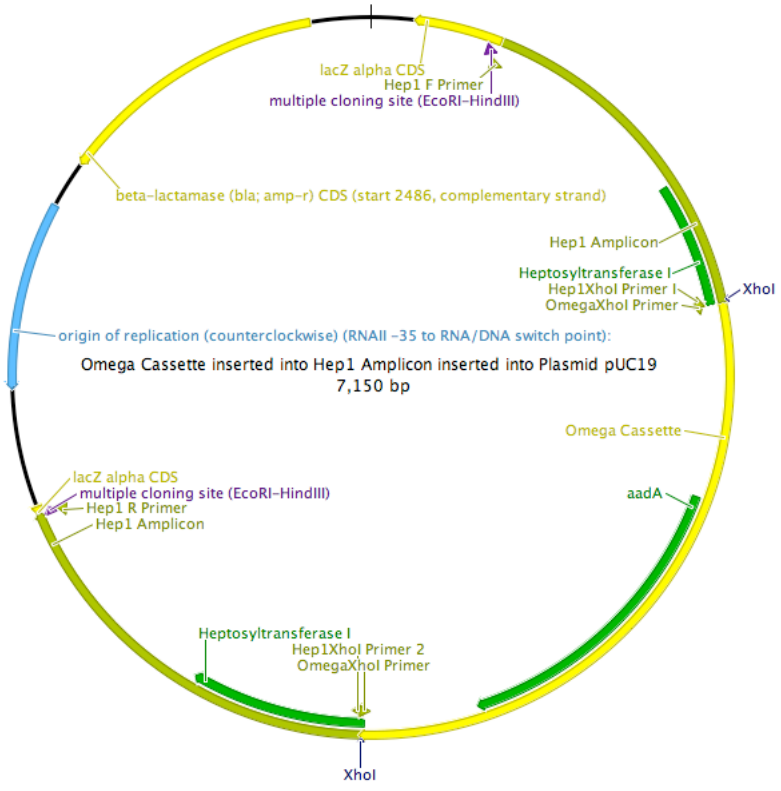

lacZ alpha CDS
Hep1 F Primer
multiple cloning site (EcoRI-HindIII)
beta-lactamase (bla; amp-r) CDS (start 2486, complementary strand)
Hep1 Amplicon
Heptosyltransferase I
Hep1XhoI Primer I
OmegaXhoI Primer
XhoI
origin of replication (counterclockwise) (RNAII -35 to RNA/DNA switch point):
Omega Cassette inserted into Hep1 Amplicon inserted into Plasmid pUC19
7,150 bp
Omega Cassette
lacZ alpha CDS
multiple cloning site (EcoRI-HindIII)
Hep1 R Primer
Hep1 Amplicon
aadA
Heptosyltransferase I
Hep1XhoI Primer 2
OmegaXhoI Primer
XhoI

Figure 18. ROI cloning schematic. The cloning of heptosyltransferase I is used as an example. A: The amplified ROI is cloned into the multiple cloning site on pUC19. The plasmid is then amplified with primers which will add a XhoI site to the middle of the ROI. B: The Ω cassette is ligated into the middle of the ROI, thus inactivating the putative gene. This new plasmid can be transformed into *N. sicca* 4320 to generate specific gene knockouts.

Discussion

Lectin GS-II and polymyxin B screen

Quick methods to screen hundreds of transformants or mutants would increase the speed and ease of identifying polysaccharide biosynthetic genes. Two methods, one relying on the lectin GS-II and the other on the antimicrobial peptide polymyxin B, were used to screen colonies. The lectin screen involves using a lectin that is specific for the terminal sugar in the polysaccharide repeat chain. The validation of the screen showed that the lectin specifically binds the polysaccharide and not the LOS of *N. sicca* 4320. It also showed that a *Neisseria* species not producing the polysaccharide failed to bind the lectin. Knocking out a gene that resulted in the loss of rhamnose, loss of the synthesis of disaccharide, loss of the polymerization of the disaccharide, loss of the ligation of the polymerized disaccharide to its anchor, loss of the anchor, or a loss in the transport of the components of the polysaccharide structure would result in no GS-II binding. Therefore, any colonies showing GS-II binding that is different from the wild-type are potential polysaccharide repeat biosynthetic mutants and worthy of further study.

The polymyxin B screen takes advantage of the affinity of polymyxin B for the bacterial cell surface. As the sugar structures on the surface of bacteria become truncated polymyxin B losses affinity for the surface and the survivability of the organism in the presence of polymyxin B increases. Thus *N. sicca* 4320 polysaccharide mutants would be more resistant to polymyxin B. The validation of the screen showed that polymyxin B resistant *N. sicca* 4320 could be generated and in one case the polysaccharide structure was lost. It is interesting to note that many of the polymyxin B resistant mutants still

bound the lectin, indicating that other changes can result in increased polymyxin B tolerance.

These two screens can be used in combination to test new mutants. Transformed *N. sicca* 4320 could be plated on polymyxin B plates then screened using GS-II. The polymyxin B would restrict the results to mutants with altered surfaces while GS-II would identify those with a loss of the polysaccharide repeat. This would greatly ease random mutational analysis of *N. sicca* 4320 and could also be useful when trying to generate specific gene knockouts.

Shotgun clone analysis

Analysis of the shotgun clones was undertaken prior to full genomic sequencing and thus represented the only set of available *N. sicca* 4320 sequence data at the beginning of the project. The four clones chosen for study each had similarity to sugar structure modification enzymes. This was important because the exact enzymes that are required for the O-repeat biosynthesis are unknown. Therefore any sugar structure modification enzyme could possibly play a role in synthesis of the O-repeat. It was unfortunate that the two clones showing similarity to known glycosyltransferases were found to have undergone a deletion event because one of the major classes of genes involved in LPS/LOS biosynthesis are glycosyltransferases. It is possible that the sequence carried on these two clones interfered with essential *E. coli* functions and the deletion of the clone was favored.

The two remaining clones were sequenced because it was not known how far into the clone the glucan branching enzyme extended. This made it impossible to determine

where the <KAN-2> would have to insert to cause insertional inactivation of the glucan branching enzyme. The two clones were found to represent adjacent sections of the glucan branching enzyme. It is interesting to note that such small coverage sequencing would result in two clones from the same gene. Further sequencing, by inverse PCR, revealed the full sequence of the glucan branching enzyme and its flanking sequence. This allowed the determination of the <KAN-2> insertions that gave *N. sicca* 4320 transformants. None of the insertions were in the glucan branching enzyme. This small-scale sequencing was insufficient to locate O-repeat biosynthesis genes and was superceded by the sequencing of the *N. sicca* 4320 chromosome.

Chromosomal <KAN-2> insertion and cloning regions of interest

The insertion of <KAN-2> into *N. sicca* 4320 chromosomal DNA and the cloning of a subset of the regions of interest were undertaken to generate polysaccharide repeat knockout mutants. The chromosomal <KAN-2> insertion generated a pool of random mutants that could be screened for deficiencies in polysaccharide biosynthesis genes. This approach was nice because there was no bias in the insertion, unlike the identified regions of interest, which were chosen based on similarity to other known LPS/LOS biosynthesis genes. Thus, having screened sufficient numbers of colonies to ensure coverage of the chromosome, genes which were involved in polysaccharide biosynthesis but with very little or no similarity to previously identified LPS/LOS biosynthesis genes would be knocked-out and found in the lectin screen. However, none of the colonies examined failed to bind GS-II during the lectin screen indicating an intact polysaccharide repeat.

The cloning and insertional inactivation of the regions of interest also failed to produce *N. sicca* 4320 transformants. One possibility for this transformation barrier could be restriction of the incoming plasmid DNA. *N. sicca* 4320 has five putative restriction/modification loci, and these could present a restriction barrier to transformation with exogenous DNA. Plasmid DNA that made it into *N. sicca* 4320 would be restricted and thus not transformable.

Another possibility for the difficulties in transforming *N. sicca* 4320 could be the antibiotic resistance markers used for selecting transformed *N. sicca* 4320. Alterations in the surface of the bacteria could result in an increased susceptibility to the antibiotic. Since the concentration of the antibiotic used is close to the minimum inhibitory concentration, increasing susceptibility because of an altered surface would result in mutants that could not be selected using antibiotics.

N. sicca 4320 has been a hard bacterium in which to study polysaccharide biosynthetic genes. The transformation and selection barrier present towards genes that alter the surface of the bacteria has made it impossible so far to generate relevant knockouts. However, future methods which address any restriction barrier and do not rely on antibacterial selection should be able to generate the mutants necessary to correlate knockout to polysaccharide structure.

Future Directions

The most important future direction for this project is overcoming the transformation and selection barrier for surface structure mutants. If a transformation barrier exists because of restriction of incoming DNA then the transforming DNA can be methylated pre-transformation by the appropriate methyltransferase. A more complete search of the *N. sicca* 4320 chromosome should reveal the locations of methyltransferase/restriction enzymes. The transforming DNA could then be incubated with the appropriate commercial methyltransferases to methylate the transforming DNA like *N. sicca* 4320 endogenous DNA. This would allow the transforming DNA to bypass the restriction barrier and transform *N. sicca* 4320.

If the use of antibiotic selection is not possible because of an increase in susceptibility then the O-repeat mutants will have to be selected by a method not requiring the use of antibiotics. One possible alternative would be to use a visual selectable marker instead of an antibiotic marker. GFP, for example, could be swapped for the spectinomycin resistance gene in the Ω cassette and transformants selected based on green fluorescence.

Another future direction is to characterize the polymyxin B resistant mutant identified in the screen. Complementation studies will give insight into what gene has been altered in the mutant.

Appendix A

Glimmer3 ORF predictions of *N. sicca* 4320.

The contig sequences of *N. sicca* 4320 were analyzed using the Glimmer3 ORF prediction program. Start: Beginning of ORF. End: End of ORF. Frame: Reading frame of identified ORF.

Contig	ORF	Start	End	Frame
>contig00001				
	orf00001	-2	1032	1
	orf00003	1162	1554	1
	orf00004	1682	2227	2
	orf00005	2429	3532	2
	orf00007	3529	3633	1
	orf00008	3639	5312	3
	orf00010	5381	6361	2
	orf00012	8672	6516	-3
	orf00013	8989	8783	-2
	orf00015	9705	9049	-1
	orf00016	9819	10379	3
	orf00019	10550	12397	2
	orf00020	12948	12502	-1
>contig00002				
	orf00001	116	334	2
	orf00003	473	1570	2
	orf00005	1878	2009	3
	orf00006	2013	2210	3
	orf00007	2291	2509	2
	orf00008	2522	2734	2
>contig00003				
	orf00001	1077	286	-1
>contig00004				
	orf00003	2110	44	-2
	orf00005	2385	2206	-1
	orf00006	2428	3336	1
	orf00008	3523	3362	-2
	orf00009	3494	5518	2
>contig00005				
	orf00001	1723	62	-2
	orf00002	3177	1981	-1
	orf00003	3280	3453	1
	orf00006	3660	4007	3
	orf00007	4007	4204	2
	orf00008	4201	5523	1
>contig00006				
	orf00001	665	45	-3
	orf00003	2063	753	-3
	orf00007	2874	2395	-1
	orf00009	5701	3317	-2
	orf00010	6121	6942	1
	orf00011	7446	7559	3
	orf00012	7562	7726	2
	orf00013	7902	8702	3
>contig00007				
	orf00001	1578	703	-1
>contig00008				

Contig	ORF	Start	End	Frame
	orf00001	605	57	-3
	orf00004	774	643	-1
	orf00005	808	1596	1
	orf00007	1875	1765	-1
	orf00008	1878	2330	3
	orf00009	2437	2553	1
	orf00011	3469	2564	-2
	orf00014	5272	3629	-2
	orf00016	5442	6101	3
	orf00017	6126	6338	3
	orf00020	6364	6567	1
	orf00022	6670	8094	1
	orf00025	8236	8096	-2
	orf00026	8856	8233	-1
	orf00028	9027	9197	3
	orf00032	10248	9250	-1
	orf00034	10306	10428	1
	orf00037	10655	10807	2
	orf00039	10822	13836	1
	orf00040	13940	13833	-3
	orf00041	14148	13942	-1
	orf00043	14464	15678	1
	orf00046	15850	17109	1
	orf00047	17277	17408	3
	orf00048	17411	18055	2
	orf00049	18055	18675	1
	orf00050	18666	18986	3
	orf00052	18992	19825	2
	orf00053	20002	20109	1
	orf00054	20118	20447	3
	orf00055	20457	21152	3
	orf00056	21382	21552	1
	orf00057	21552	21743	3
	orf00058	22681	22935	1
	orf00059	23332	23484	1
	orf00060	23487	23792	3
	orf00062	24435	24749	3
	orf00064	25882	26262	1
	orf00065	26276	27589	2
	orf00066	28270	28380	1
	orf00067	29450	30436	2
	orf00070	31365	32459	3
	orf00071	32527	32985	1
	orf00072	33128	33775	2
	orf00075	33856	34410	1
	orf00076	35546	34527	-3
	orf00077	35699	36004	2
	orf00079	36020	36562	2

Contig	ORF	Start	End	Frame
	orf00080	36668	36862	2
	orf00081	37076	37864	2
	orf00083	38132	40858	2
	orf00085	41761	41874	1
	orf00086	41957	43330	2
	orf00087	43331	43558	2
	orf00090	43920	43618	-1
	orf00091	44700	44044	-1
	orf00094	45300	44803	-1
	orf00096	45512	46285	2
	orf00097	46293	46655	3
	orf00098	46976	47374	2
	orf00100	48074	47451	-3
	orf00102	48699	48085	-1
	orf00103	49076	49579	2
	orf00104	51077	49707	-3
	orf00106	51092	52000	2
	orf00107	52199	52089	-3
>contig00009				
	orf00001	-2	255	1
	orf00003	2065	533	-2
	orf00004	3703	2306	-2
	orf00005	5352	3745	-1
	orf00006	7066	5411	-2
>contig00010				
	orf00001	61	240	1
	orf00003	1025	273	-3
	orf00004	1081	4221	1
	orf00007	4349	4894	2
	orf00008	5113	5009	-2
	orf00009	7255	5135	-2
	orf00012	8598	7489	-1
	orf00013	9785	8712	-3
	orf00015	11237	9801	-3
	orf00018	14034	11554	-1
	orf00020	16240	14240	-2
	orf00021	16376	16215	-3
	orf00022	17475	16420	-1
	orf00024	18005	17496	-3
	orf00025	19767	18733	-1
	orf00027	20425	19835	-2
	orf00030	20700	20512	-1
	orf00032	21213	20743	-1
	orf00033	21323	21210	-3
	orf00035	22384	21320	-2
	orf00036	23370	22381	-1
	orf00038	24108	23758	-1
	orf00039	24558	24118	-1

Contig	ORF	Start	End	Frame
	orf00040	24844	24548	-2
	orf00041	25855	24854	-2
	orf00042	26641	25865	-2
	orf00043	26892	26656	-1
	orf00045	27500	26925	-3
	orf00047	27771	27502	-1
	orf00049	27939	27823	-1
	orf00050	28362	28003	-1
	orf00051	28598	28359	-3
	orf00053	29576	29175	-3
	orf00055	30367	29984	-2
	orf00056	31059	31205	3
	orf00057	31379	31191	-3
	orf00058	31561	31788	1
	orf00059	32291	32605	2
	orf00061	32610	33392	3
	orf00062	33385	33561	1
	orf00063	33610	33756	1
	orf00065	33788	34072	2
	orf00067	34066	34434	1
	orf00068	34717	35115	1
	orf00069	35172	35609	3
	orf00071	36354	36842	3
	orf00072	36914	38335	2
	orf00073	38332	40479	1
	orf00074	40578	41693	3
	orf00075	41776	43236	1
	orf00076	43290	43607	3
	orf00077	43610	44140	2
	orf00078	44140	44622	1
	orf00079	44619	45047	3
	orf00081	45076	45849	1
	orf00082	45909	46238	3
	orf00084	46250	46516	2
	orf00085	46517	47116	2
	orf00086	47143	48399	1
	orf00087	48412	48843	1
	orf00088	48833	49372	2
	orf00090	49389	53948	3
	orf00091	53986	54282	1
	orf00092	54326	57439	2
	orf00093	57558	57971	3
	orf00095	57968	58279	2
	orf00096	58522	58806	1
	orf00097	58953	59297	3
	orf00100	59717	59508	-3
	orf00101	59982	59710	-1
	orf00102	60426	60040	-1

Contig	ORF	Start	End	Frame
	orf00103	61742	60549	-3
	orf00104	62234	61899	-3
	orf00106	62377	63255	1
	orf00107	63555	63322	-1
	orf00109	64034	63807	-3
	orf00111	64101	65729	3
	orf00112	65747	65917	2
	orf00113	66638	66057	-3
	orf00114	66796	68202	1
	orf00115	68359	69051	1
	orf00116	69064	69735	1
	orf00117	69735	70709	3
	orf00120	71354	71800	2
	orf00123	72807	71971	-1
	orf00126	73891	72980	-2
	orf00127	74226	75017	3
	orf00128	75167	76420	2
	orf00129	76629	76423	-1
	orf00130	76870	76685	-2
	orf00131	77112	77005	-1
	orf00133	77498	77139	-3
	orf00134	77735	77550	-3
	orf00135	77885	77760	-3
	orf00136	78759	78172	-1
	orf00137	79688	78774	-3
	orf00138	79810	80214	1
	orf00139	80325	80747	3
>contig00011				
	orf00001	830	988	2
	orf00002	811	32	-2
	orf00003	2228	1185	-3
	orf00004	2661	2260	-1
	orf00005	2672	2902	2
	orf00008	2938	3636	1
	orf00010	3831	4985	3
	orf00011	5168	6589	2
	orf00012	7199	6684	-3
	orf00013	7450	7340	-2
	orf00014	7483	7698	1
	orf00015	7870	9522	1
	orf00019	10331	9843	-3
	orf00020	10714	10328	-2
	orf00021	11076	10714	-1
	orf00022	12117	11266	-1
	orf00024	13371	12166	-1
	orf00026	14246	13740	-3
	orf00027	14245	14349	1
	orf00028	15094	14375	-2

Contig	ORF	Start	End	Frame
	orf00030	15793	15278	-2
	orf00031	16508	17149	2
	orf00033	17262	17747	3
	orf00034	17744	19054	2
	orf00036	20976	19504	-1
	orf00038	23138	21243	-3
	orf00039	23362	23162	-2
	orf00041	24285	23566	-1
	orf00043	25553	24699	-3
	orf00045	26388	25675	-1
	orf00047	26819	26577	-3
	orf00048	26897	27487	2
	orf00049	27571	28158	1
	orf00050	28229	28363	2
	orf00051	28338	28523	3
	orf00052	28534	30009	1
	orf00055	31413	30409	-1
	orf00057	31510	33891	1
	orf00058	33888	34874	3
	orf00060	34880	35116	2
	orf00063	35736	35473	-1
	orf00064	35870	35733	-3
	orf00066	35962	36078	1
	orf00068	36182	36412	2
	orf00069	36459	37409	3
	orf00070	37491	38465	3
	orf00072	40147	39011	-2
	orf00075	40503	43130	3
	orf00077	43375	43226	-2
	orf00078	43374	44177	3
	orf00082	44294	44815	2
	orf00083	44812	45090	1
	orf00084	45830	46702	2
	orf00087	49549	46934	-2
	orf00088	49818	49925	3
	orf00090	51014	50007	-3
	orf00094	52419	51139	-1
	orf00095	52770	53720	3
	orf00097	54536	53817	-3
	orf00099	54718	54533	-2
	orf00101	54782	55684	2
	orf00102	56331	56020	-1
>contig00012				
	orf00001	1263	79	-1
	orf00002	2007	1561	-1
	orf00003	2987	2013	-3
	orf00004	3062	3181	2
	orf00005	3236	3556	2

Contig	ORF	Start	End	Frame
	orf00007	3582	3854	3
	orf00009	6352	4382	-2
	orf00010	7953	6688	-1
	orf00012	8201	9190	2
	orf00013	9332	9655	2
	orf00015	9665	9967	2
	orf00017	10442	10843	2
	orf00018	10853	11245	2
	orf00020	12141	11800	-1
	orf00022	12520	14508	1
>contig00013				
	orf00001	-1	172	2
	orf00002	237	620	3
	orf00004	1317	751	-1
	orf00006	2026	1466	-2
	orf00009	4636	2189	-2
	orf00012	6171	4807	-1
	orf00013	6804	7277	3
	orf00014	7925	7365	-3
	orf00016	8499	8053	-1
>contig00014				
	orf00002	1525	338	-2
	orf00004	1663	1535	-2
	orf00005	2195	1947	-3
>contig00015				
	orf00001	765	148	-1
>contig00016				
	orf00001	784	47	-2
	orf00003	2299	1286	-2
	orf00004	2678	3439	2
	orf00006	4948	3653	-2
	orf00007	5221	5532	1
	orf00008	5622	5831	3
	orf00009	5838	6068	3
	orf00010	6085	6537	1
	orf00013	6632	7732	2
	orf00015	8568	7855	-1
	orf00017	8767	10962	1
	orf00019	11106	11441	3
	orf00021	11619	12524	3
	orf00024	13100	12606	-3
	orf00025	13366	13557	1
	orf00026	13588	13911	1
	orf00028	14280	14158	-1
	orf00029	14503	14282	-2
	orf00030	15667	14528	-2
	orf00033	15810	17144	3
	orf00035	17309	18037	2

Contig	ORF	Start	End	Frame
	orf00038	18091	18468	1
>contig00017				
	orf00002	974	123	-3
	orf00003	1603	1478	-2
	orf00006	2174	2707	2
	orf00007	2726	3223	2
	orf00008	3612	3307	-1
	orf00009	4348	3743	-2
	orf00011	5601	4780	-1
	orf00012	5613	5762	3
	orf00016	5865	8552	3
	orf00019	9846	8965	-1
	orf00020	10302	10189	-1
	orf00021	10411	10692	1
	orf00024	10879	11649	1
>contig00018				
	orf00001	0	218	3
	orf00002	697	392	-2
	orf00010	1209	7955	3
>contig00019				
	orf00001	400	945	1
>contig00020				
	orf00001	906	40	-1
	orf00004	1967	2476	2
	orf00005	1924	1076	-2
	orf00006	2671	2850	1
	orf00007	3031	3894	1
	orf00008	4407	4276	-1
	orf00009	4683	4429	-1
	orf00010	5046	4846	-1
>contig00021				
	orf00001	127	17	-2
	orf00002	210	326	3
	orf00003	323	1705	2
	orf00004	2859	1900	-1
	orf00005	3651	3061	-1
	orf00009	5466	4315	-1
	orf00010	6323	5523	-3
	orf00011	6598	6320	-2
	orf00014	7287	6697	-1
	orf00016	7893	7327	-1
	orf00019	8651	7875	-3
	orf00020	8772	8668	-1
	orf00022	9591	8791	-1
	orf00026	10460	10005	-3
	orf00027	11944	10751	-2
	orf00028	13414	12170	-2
	orf00030	14220	13495	-1

Contig	ORF	Start	End	Frame
	orf00032	15124	14210	-2
	orf00035	16701	15292	-1
	orf00037	17792	16965	-3
	orf00040	18994	17927	-2
	orf00042	20155	18998	-2
	orf00045	20403	20230	-1
	orf00047	21652	20432	-2
	orf00049	21954	21649	-1
	orf00051	22353	22144	-1
	orf00052	23744	22407	-3
	orf00054	24406	23831	-2
	orf00055	25125	24637	-1
	orf00057	25257	25138	-1
>contig00022				
	orf00001	269	114	-3
	orf00002	435	298	-1
	orf00005	2337	808	-1
	orf00007	3716	2526	-3
	orf00009	5569	4358	-2
	orf00011	6972	5803	-1
	orf00013	9206	7380	-3
	orf00014	9990	9193	-1
	orf00016	11027	10083	-3
	orf00019	12069	11281	-1
	orf00020	13127	12075	-3
	orf00021	14399	13245	-3
	orf00025	15282	14482	-1
	orf00026	15356	15523	2
	orf00027	15736	15605	-2
	orf00028	16306	16184	-2
	orf00029	16359	16469	3
	orf00031	18084	16573	-1
>contig00023				
	orf00001	1625	123	-3
	orf00003	3127	1886	-2
	orf00004	3509	3700	2
	orf00005	3839	4279	2
	orf00007	4398	5720	3
	orf00008	5802	5927	3
	orf00009	5937	6059	3
	orf00012	6526	6383	-2
	orf00013	7377	6838	-1
	orf00014	8645	7425	-3
	orf00015	8827	8657	-2
	orf00016	8898	9221	3
	orf00018	9276	9782	3
	orf00019	9994	10893	1
	orf00020	11665	10970	-2

Contig	ORF	Start	End	Frame
	orf00022	12245	11790	-3
	orf00023	12742	12305	-2
	orf00025	13658	13083	-3
	orf00026	13797	14828	3
	orf00029	17026	14894	-2
	orf00030	17334	18068	3
	orf00034	20951	18363	-3
	orf00036	22451	21183	-3
	orf00040	22781	23713	2
	orf00041	23724	24602	3
>contig00024				
	orf00002	187	80	-2
	orf00005	2993	201	-3
	orf00006	2997	3104	3
	orf00007	3224	3454	2
	orf00010	3538	4326	1
	orf00012	4556	5488	2
	orf00014	5490	6233	3
	orf00016	6863	6345	-3
	orf00019	8424	7039	-1
	orf00021	9252	8938	-1
	orf00023	10152	9319	-1
	orf00024	10670	10176	-3
	orf00026	11651	10917	-3
	orf00028	12273	11743	-1
	orf00029	12796	12254	-2
	orf00031	13368	12832	-1
	orf00032	14707	13769	-2
	orf00033	14938	15687	1
	orf00034	15810	16391	3
	orf00035	16410	17759	3
	orf00036	17759	18559	2
	orf00037	19543	18776	-2
	orf00038	19745	19861	2
	orf00040	19942	20976	1
	orf00042	20966	21964	2
	orf00043	22120	23985	1
	orf00044	24044	24667	2
	orf00045	24741	25499	3
	orf00047	25746	25973	3
	orf00049	27216	26173	-1
	orf00051	27243	28475	3
>contig00025				
	orf00003	2395	155	-2
>contig00026				
	orf00001	108	836	3
	orf00003	1148	2053	2
	orf00005	3585	3692	3

Contig	ORF	Start	End	Frame
	orf00008	3866	3711	-3
	orf00010	4694	4804	2
	orf00011	5026	5286	1
	orf00012	5874	6194	3
	orf00014	6253	6918	1
	orf00016	7048	8709	1
	orf00019	12930	9097	-1
	orf00020	13696	13475	-2
	orf00021	14196	15887	3
	orf00023	15907	16023	1
	orf00024	16067	16615	2
	orf00026	16770	17858	3
	orf00029	17945	18115	2
	orf00030	18702	18400	-1
	orf00031	18701	19096	2
	orf00032	19109	19360	2
	orf00034	20412	21197	3
>contig00027				
	orf00001	262	65	-2
	orf00002	557	267	-3
	orf00003	1952	603	-3
	orf00005	2731	2108	-2
	orf00006	2771	2902	2
	orf00007	2913	3038	3
	orf00008	3035	3862	2
	orf00011	3908	4870	2
	orf00014	4931	5578	2
	orf00015	6925	5645	-2
	orf00016	7769	7143	-3
	orf00017	7904	8011	2
	orf00018	8244	8834	3
	orf00019	8877	9602	3
	orf00020	9640	12057	1
	orf00023	12726	13163	3
	orf00024	13479	14393	3
	orf00026	14686	15687	1
	orf00027	15801	16439	3
	orf00031	18836	16851	-3
	orf00033	19430	18906	-3
	orf00034	19566	19456	-1
	orf00035	19778	20572	2
	orf00036	20691	22190	3
	orf00038	23656	22265	-2
	orf00039	24948	23983	-1
	orf00040	24947	25069	2
>contig00028				
	orf00001	-1	367	2
	orf00002	883	449	-2

Contig	ORF	Start	End	Frame
	orf00003	1166	909	-3
	orf00005	1346	1197	-3
	orf00006	1660	3153	1
	orf00008	3566	4237	2
	orf00011	4321	5652	1
	orf00013	6460	5714	-2
	orf00014	7701	6661	-1
	orf00015	8721	7711	-1
	orf00017	9913	8846	-2
	orf00018	10750	9917	-2
	orf00019	12714	10861	-1
	orf00020	13944	13018	-1
	orf00023	15253	13964	-2
	orf00025	15447	15301	-1
	orf00027	16580	15618	-3
	orf00028	16634	16741	2
	orf00029	17506	16781	-2
	orf00030	17595	18377	3
	orf00032	18713	18841	2
	orf00033	19424	18831	-3
	orf00035	20256	19543	-1
	orf00037	22109	20529	-3
	orf00039	22297	22121	-2
	orf00040	22471	23097	1
	orf00041	23111	23470	2
	orf00042	23658	23554	-1
	orf00043	23705	24139	2
	orf00044	24341	24225	-3
	orf00045	25334	24471	-3
	orf00047	25591	25346	-2
	orf00048	25590	25718	3
	orf00050	26719	25715	-2
	orf00052	27528	26878	-1
	orf00055	28729	27728	-2
	orf00056	29208	28729	-1
	orf00057	29341	29210	-2
	orf00058	29366	30301	2
	orf00059	30526	30359	-2
	orf00060	30669	31088	3
	orf00062	31188	31712	3
	orf00066	35417	31812	-3
	orf00067	37210	35693	-2
	orf00070	37736	39247	2
	orf00074	39551	39420	-3
	orf00075	39596	39916	2
	orf00079	39930	41426	3
	orf00081	41751	41960	3
	orf00082	42462	42232	-1

Contig	ORF	Start	End	Frame
	orf00084	42677	42790	2
	orf00086	42787	43878	1
	orf00087	43931	44533	2
	orf00089	44901	45725	3
	orf00091	46555	45845	-2
	orf00092	47204	46614	-3
	orf00093	47259	47759	3
	orf00094	47794	47973	1
	orf00095	48133	48660	1
	orf00097	48896	48768	-3
	orf00098	48975	50009	3
	orf00101	52639	50498	-2
	orf00102	53652	52756	-1
	orf00104	53784	53656	-1
	orf00105	53841	54635	3
	orf00107	54632	54736	2
>contig00029				
	orf00002	949	782	-2
	orf00003	1259	1477	2
	orf00006	1616	2284	2
	orf00010	4959	2812	-1
	orf00011	5313	5164	-1
	orf00013	6016	5849	-2
	orf00014	5990	6910	2
	orf00016	6920	7378	2
	orf00018	7678	9090	1
	orf00020	9599	9751	2
	orf00021	10324	9839	-2
	orf00023	10333	10494	1
	orf00025	10535	11425	2
	orf00028	12971	11868	-3
	orf00032	14350	13097	-2
	orf00035	15018	14554	-1
	orf00037	15600	15076	-1
>contig00030				
	orf00002	-2	2331	1
	orf00004	2558	2665	2
	orf00005	2769	2897	3
	orf00008	3106	4407	1
	orf00009	4569	4462	-1
	orf00011	4872	4705	-1
>contig00031				
	orf00002	26	1054	2
	orf00005	3092	1374	-3
	orf00007	4071	3262	-1
	orf00010	4842	4075	-1
	orf00011	4954	5130	1
	orf00014	6843	5494	-1

Contig	ORF	Start	End	Frame
	orf00016	7335	7162	-1
	orf00017	7782	7630	-1
	orf00018	8268	8152	-1
	orf00021	9383	9156	-3
	orf00022	9637	9515	-2
	orf00023	10025	10522	2
>contig00032				
	orf00002	1549	230	-2
	orf00005	3477	2590	-1
	orf00006	3845	3573	-3
	orf00007	4117	3911	-2
	orf00008	5648	4467	-3
	orf00009	6064	6378	1
	orf00011	7057	9246	1
	orf00012	10039	9599	-2
	orf00013	10531	10046	-2
	orf00016	11503	10754	-2
>contig00033				
	orf00003	6362	0	-3
	orf00007	7613	7762	2
	orf00010	10080	8113	-1
>contig00034				
>contig00035				
>contig00036				
	orf00002	868	242	-2
	orf00003	1022	918	-3
	orf00005	1355	1026	-3
	orf00006	2464	1745	-2
	orf00008	3894	2581	-1
	orf00010	4685	3891	-3
	orf00011	4936	6798	1
	orf00013	6879	7241	3
	orf00014	7326	7667	3
	orf00015	8349	7741	-1
	orf00016	8682	8879	3
	orf00018	9222	10100	3
	orf00020	10290	12515	3
	orf00022	13478	12759	-3
	orf00023	13614	13501	-1
	orf00025	14815	13745	-2
	orf00026	15048	16082	3
>contig00037				
	orf00002	352	1173	1
	orf00003	1379	1618	2
	orf00004	1712	1828	2
	orf00006	1974	2099	3
	orf00008	3872	2421	-3
	orf00009	5598	4129	-1

Contig	ORF	Start	End	Frame
	orf00012	6474	5611	-1
	orf00013	7777	6557	-2
	orf00014	8766	7801	-1
	orf00016	9620	8937	-3
>contig00038				
	orf00001	221	331	2
>contig00039				
	orf00001	-1	724	2
	orf00004	1925	924	-3
	orf00005	2197	2018	-2
	orf00007	2212	3534	1
	orf00010	4729	4094	-2
	orf00011	5327	4854	-3
	orf00012	5839	6333	1
	orf00013	6342	7832	3
	orf00014	10610	8517	-3
	orf00015	11064	12173	3
	orf00016	12352	12789	1
	orf00018	13794	14048	3
	orf00019	14023	16203	1
	orf00021	17344	18453	1
	orf00023	19593	18550	-1
	orf00024	20876	19878	-3
	orf00026	20972	22348	2
	orf00028	22449	23945	3
	orf00029	23973	25067	3
	orf00030	25227	25616	3
	orf00031	26135	26263	2
	orf00032	26303	26662	2
	orf00033	27422	27529	2
	orf00034	27770	28405	2
	orf00036	28383	28505	3
>contig00040				
	orf00001	1185	67	-1
	orf00003	1477	1169	-2
	orf00005	2872	1598	-2
	orf00006	4158	3199	-1
	orf00008	4605	4198	-1
	orf00011	6060	4738	-1
	orf00012	7959	6190	-1
	orf00014	8211	10433	3
	orf00015	10671	11447	3
>contig00041				
	orf00001	245	33	-3
	orf00004	1542	1396	-1
	orf00006	2849	1752	-3
	orf00007	3174	3037	-1
	orf00010	5498	3249	-3

Contig	ORF	Start	End	Frame
>contig00042				
	orf00001	262	59	-2
	orf00002	548	276	-3
	orf00004	1647	601	-1
	orf00006	2154	1924	-1
	orf00007	2416	3873	1
	orf00008	3973	3857	-2
	orf00009	4437	3970	-1
	orf00013	6592	4577	-2
	orf00014	6655	6849	1
	orf00016	7810	7004	-2
	orf00017	7940	8578	2
	orf00020	8789	9439	2
	orf00022	9449	9880	2
>contig00043				
>contig00044				
	orf00001	-1	754	2
	orf00003	891	1115	3
	orf00006	1117	1995	1
	orf00008	2023	2448	1
	orf00009	3714	3845	3
	orf00010	3701	2523	-3
	orf00013	4517	5881	2
	orf00016	6073	6657	1
	orf00017	6848	6678	-3
	orf00018	7252	7046	-2
	orf00020	7714	8484	1
	orf00021	8647	8528	-2
	orf00022	9473	8694	-3
	orf00024	10181	9582	-3
	orf00026	10862	10251	-3
	orf00028	11528	10935	-3
	orf00030	11880	11533	-1
	orf00031	11936	12823	2
	orf00033	12887	13258	2
	orf00035	13242	13361	3
	orf00037	13355	14134	2
	orf00038	14121	14465	3
	orf00040	14476	15006	1
	orf00042	15267	16076	3
	orf00044	16148	16648	2
	orf00046	17050	17343	1
	orf00048	17479	20307	1
	orf00050	21177	20395	-1
	orf00051	21620	21303	-3
	orf00052	22744	21998	-2
	orf00053	23238	22909	-1
	orf00054	23463	23242	-1

Contig	ORF	Start	End	Frame
>contig00045				
	orf00001	561	394	-1
	orf00002	1242	568	-1
	orf00003	1241	1360	2
	orf00005	1357	1992	1
	orf00006	2028	2996	3
	orf00008	3253	3972	1
	orf00009	3983	4918	2
	orf00010	4981	5592	1
	orf00011	5962	5645	-2
	orf00012	6118	7389	1
	orf00013	7415	8014	2
	orf00014	8758	8312	-2
	orf00017	9154	11469	1
	orf00018	11876	12064	2
	orf00019	11809	11654	-2
	orf00020	14058	12196	-1
	orf00022	14322	14212	-1
	orf00025	14400	16169	3
	orf00028	18388	16238	-2
	orf00030	19077	18811	-1
	orf00032	19281	19871	3
	orf00033	19890	20060	3
	orf00035	20142	20246	3
	orf00036	20497	20991	1
	orf00038	21488	21156	-3
	orf00039	22345	21620	-2
	orf00042	22957	22493	-2
	orf00044	23639	23022	-3
	orf00046	23716	24519	1
	orf00048	24687	26186	3
	orf00051	26446	27234	1
	orf00054	29126	27558	-3
	orf00057	29272	30723	1
	orf00060	31552	30866	-2
	orf00061	32384	31542	-3
	orf00062	32788	32492	-2
	orf00065	33280	32870	-2
	orf00066	34379	33513	-3
	orf00068	35324	34596	-3
	orf00069	35531	36238	2
	orf00071	36247	36384	1
	orf00075	38349	36979	-1
	orf00076	39043	38450	-2
	orf00077	39476	39312	-3
	orf00079	40732	39509	-2
	orf00081	41032	42870	1
	orf00083	43018	43413	1

Contig	ORF	Start	End	Frame
	orf00084	43447	43575	1
	orf00086	43600	44094	1
	orf00089	44697	48797	3
	orf00090	49569	48946	-1
	orf00091	49940	50296	2
	orf00092	50287	50769	1
	orf00093	50782	51375	1
	orf00095	51365	52621	2
	orf00096	52621	53094	1
	orf00097	53343	54707	3
	orf00098	54692	55081	2
	orf00099	55167	55292	3
	orf00101	55293	55604	3
	orf00104	55919	58180	2
	orf00105	58177	59259	1
	orf00108	59339	59818	2
	orf00109	59830	60501	1
	orf00110	60498	60803	3
	orf00113	60840	61415	3
	orf00117	61690	63714	1
	orf00120	63784	64089	1
	orf00121	64314	64634	3
	orf00123	64875	66371	3
	orf00125	66381	67856	3
	orf00127	68250	68140	-1
	orf00128	68243	68482	2
	orf00130	68537	69661	2
	orf00132	69773	69889	2
	orf00133	70165	71583	1
	orf00137	71707	72852	1
	orf00138	72907	73356	1
	orf00140	73437	73745	3
	orf00141	73745	74404	2
	orf00145	74659	75216	1
	orf00146	75274	76020	1
	orf00148	76023	76817	3
	orf00150	76936	76823	-2
	orf00151	76940	78124	2
	orf00154	78337	79677	1
	orf00157	79682	82081	2
	orf00158	82242	82135	-1
	orf00159	82235	82747	2
	orf00160	82943	83986	2
	orf00162	84111	84560	3
	orf00164	84686	85447	2
	orf00165	85490	86266	2
	orf00167	86398	86517	1
	orf00170	86571	87602	3

Contig	ORF	Start	End	Frame
	orf00172	88353	87688	-1
	orf00174	88714	88355	-2
	orf00178	88895	89386	2
	orf00180	89720	90370	2
	orf00181	90367	91284	1
	orf00184	91375	93990	1
	orf00185	94680	94874	3
	orf00186	95194	95730	1
	orf00189	96456	95920	-1
	orf00191	96688	96816	1
	orf00193	97451	96999	-3
	orf00196	98924	97731	-3
	orf00197	99136	98960	-2
	orf00199	100101	99133	-1
	orf00201	100359	101066	3
	orf00202	101120	101458	2
	orf00203	101549	102346	2
	orf00204	102349	102903	1
	orf00205	102888	103007	3
	orf00206	103097	103513	2
>contig00046				
	orf00003	560	315	-3
	orf00004	813	694	-1
	orf00005	1118	954	-3
	orf00006	1242	2669	3
	orf00008	2849	2685	-3
	orf00010	2848	4359	1
	orf00012	4623	5288	3
	orf00013	5316	6131	3
	orf00015	6150	6410	3
	orf00017	6414	7334	3
	orf00018	7423	7307	-2
	orf00021	8248	7439	-2
	orf00022	8647	8264	-2
	orf00023	8849	9292	2
	orf00027	9568	10293	1
	orf00029	10893	10432	-1
	orf00031	11927	11088	-3
	orf00032	12269	12000	-3
	orf00033	12559	12269	-2
	orf00034	13216	12563	-2
	orf00037	13438	15915	1
	orf00038	15958	16107	1
	orf00039	16148	16858	2
	orf00040	17560	18645	1
	orf00042	18990	19157	3
	orf00043	19420	19247	-2
	orf00044	19847	19737	-3

Contig	ORF	Start	End	Frame
	orf00045	20151	20029	-1
	orf00047	20414	20307	-3
	orf00048	20493	20612	3
	orf00052	23341	20951	-2
	orf00054	23547	23347	-1
	orf00055	24415	23561	-2
	orf00058	24961	24440	-2
	orf00060	25885	24986	-2
	orf00061	26316	25888	-1
	orf00063	26528	27592	2
	orf00067	28989	28261	-1
	orf00068	30081	29176	-1
	orf00069	30063	30185	3
	orf00070	30273	30950	3
	orf00071	30947	31390	2
	orf00072	31384	32223	1
	orf00077	33941	32721	-3
	orf00080	35068	34724	-2
	orf00081	34745	34023	-3
>contig00047				
	orf00001	1017	202	-1
	orf00003	3398	1248	-3
	orf00005	4899	3568	-1
	orf00007	6156	5119	-1
	orf00008	6418	8076	1
	orf00011	8370	8233	-1
	orf00012	9740	8394	-3
	orf00013	10195	9947	-2
	orf00015	12650	10188	-3
	orf00017	12639	12797	3
	orf00019	13022	13498	2
	orf00021	13925	15337	2
	orf00023	15530	16033	2
	orf00027	16030	17829	1
	orf00030	17918	18895	2
	orf00032	19280	19843	2
	orf00033	20088	19885	-1
	orf00034	20090	21478	2
	orf00035	22137	21571	-1
	orf00036	22379	22269	-3
	orf00037	22456	23247	1
	orf00038	23302	23478	1
	orf00041	23666	24928	2
	orf00042	24948	25718	3
>contig00048				
	orf00001	2202	97	-1
	orf00003	2658	2221	-1
	orf00004	3036	2809	-1

Contig	ORF	Start	End	Frame
	orf00007	7709	3534	-3
	orf00008	7813	7706	-2
	orf00010	12061	7877	-2
	orf00011	12616	12245	-2
	orf00012	12950	12675	-3
	orf00013	14096	13401	-3
	orf00014	14530	14096	-2
	orf00015	15149	14637	-3
	orf00016	15280	15173	-2
>contig00049				
	orf00001	399	1736	3
	orf00003	2864	1857	-3
	orf00004	2994	3113	3
	orf00005	4186	3110	-2
	orf00006	5011	4325	-2
	orf00008	5750	5013	-3
	orf00009	6178	5978	-2
	orf00010	7537	6296	-2
	orf00011	7586	7771	2
	orf00012	7860	8594	3
	orf00014	9123	8674	-1
	orf00016	10489	9269	-2
	orf00021	13187	10650	-3
	orf00022	14590	13334	-2
	orf00023	15374	14829	-3
	orf00024	15389	16525	2
	orf00026	18306	16606	-1
	orf00028	18762	18487	-1
	orf00030	19020	19133	3
	orf00031	19501	19130	-2
	orf00032	19693	19797	1
	orf00035	20042	21313	2
	orf00036	22009	21545	-2
	orf00039	22203	22979	3
	orf00041	22981	23439	1
	orf00043	23545	24432	1
	orf00046	24608	25939	2
	orf00049	26078	27301	2
>contig00050				
	orf00001	325	62	-2
	orf00002	3331	1310	-2
	orf00003	3761	3429	-3
	orf00004	3871	3758	-2
	orf00006	5481	3913	-1
	orf00008	7198	5657	-2
	orf00009	7302	7195	-1
	orf00011	8334	7312	-1
	orf00013	8554	8378	-2

Contig	ORF	Start	End	Frame
	orf00014	9642	8590	-1
	orf00016	10384	9734	-2
	orf00017	10383	10547	3
	orf00019	11257	11063	-2
	orf00022	12339	11410	-1
	orf00023	12803	12327	-3
	orf00025	12952	12812	-2
	orf00027	13003	13125	1
	orf00028	13188	14744	3
	orf00031	16354	15053	-2
	orf00033	16641	16537	-1
	orf00035	18907	17735	-2
	orf00037	19672	18998	-2
	orf00038	20790	19804	-1
	orf00041	22297	20930	-2
	orf00043	22694	22317	-3
	orf00045	23320	23799	1
	orf00047	23927	23796	-3
	orf00049	24075	28391	3
>contig00051				
	orf00001	407	69	-3
	orf00004	2147	912	-3
	orf00005	2575	2159	-2
	orf00007	4187	2733	-3
	orf00008	7096	4301	-2
	orf00009	9104	7182	-3
	orf00010	9625	9311	-2
	orf00011	10124	9789	-3
	orf00012	10951	10796	-2
	orf00013	10787	10167	-3
	orf00014	12227	11130	-3
	orf00015	13551	12322	-1
	orf00017	14387	13548	-3
	orf00018	15124	14384	-2
	orf00019	15243	15124	-1
	orf00020	15479	15324	-3
	orf00021	15965	15504	-3
	orf00022	16993	15989	-2
	orf00023	17235	17029	-1
	orf00024	17864	17256	-3
	orf00026	20357	18075	-3
	orf00028	21134	20817	-3
	orf00029	21277	21131	-2
	orf00032	22030	21878	-2
	orf00034	24324	23197	-1
	orf00036	24380	24508	2
	orf00038	24512	25213	2
	orf00040	25256	27148	2

Contig	ORF	Start	End	Frame
	orf00041	27148	28167	1
	orf00044	28481	29365	2
	orf00045	29689	30666	1
	orf00046	31085	32002	2
	orf00049	32177	32974	2
	orf00051	32962	33666	1
	orf00053	34875	35972	3
	orf00054	36523	36086	-2
	orf00056	37401	36628	-1
	orf00058	38105	37524	-3
	orf00060	39231	38107	-1
	orf00061	39230	40036	2
	orf00063	41183	40149	-3
	orf00064	41674	41240	-2
	orf00065	41732	41893	2
	orf00067	41890	43137	1
	orf00068	43228	43890	1
	orf00070	44450	43962	-3
	orf00071	44496	44654	3
	orf00073	45723	44764	-1
	orf00075	48034	45869	-2
	orf00078	48343	48134	-2
	orf00079	48491	48883	2
	orf00080	49024	49353	1
	orf00081	49590	49781	3
	orf00083	50048	50359	2
	orf00084	50538	51407	3
	orf00085	51440	51748	2
	orf00086	51748	51861	1
	orf00087	52325	53854	2
	orf00088	54706	53924	-2
	orf00089	54953	54846	-3
	orf00090	55033	55383	1
	orf00091	55391	55789	2
	orf00092	55985	56770	2
	orf00093	57962	57027	-3
	orf00095	58308	58072	-1
	orf00096	59501	58320	-3
	orf00099	59545	59985	1
	orf00100	59982	60281	3
	orf00102	61205	60402	-3
	orf00106	61434	64313	3
	orf00107	64345	65343	1
>contig00052				
	orf00001	1255	245	-2
	orf00003	1667	1804	2
	orf00005	1816	2730	1
	orf00008	3157	2993	-2

Contig	ORF	Start	End	Frame
	orf00010	4939	3170	-2
	orf00013	5417	6865	2
	orf00018	8072	7122	-3
	orf00019	8368	8586	1
	orf00022	8759	9019	2
	orf00023	9184	9513	1
	orf00025	10998	9661	-1
	orf00026	11419	11592	1
	orf00027	11755	11970	1
	orf00028	12270	12458	3
	orf00029	12537	12641	3
	orf00030	12737	12955	2
	orf00031	12974	13195	2
	orf00033	13369	13593	1
	orf00034	13571	13678	2
	orf00036	13737	15029	3
	orf00037	15026	15490	2
	orf00039	15501	17126	3
	orf00041	17315	17518	2
	orf00043	18633	17539	-1
	orf00046	18898	20292	1
	orf00047	21236	20637	-3
	orf00049	21262	22050	1
	orf00053	24240	22384	-1
	orf00055	24647	24519	-3
	orf00057	25552	24716	-2
	orf00058	25917	25546	-1
	orf00062	27603	26092	-1
	orf00064	28481	28588	2
	orf00066	28760	28864	2
	orf00068	29090	29197	2
	orf00070	30256	29315	-2
	orf00074	31201	30323	-2
	orf00076	31360	31956	1
	orf00078	32014	32625	1
	orf00080	32693	33079	2
	orf00081	33261	33157	-1
	orf00082	33278	33748	2
	orf00085	34617	34342	-1
	orf00087	34730	34855	2
	orf00088	34866	35264	3
	orf00090	35328	35792	3
	orf00092	35881	35777	-2
	orf00093	35874	36008	3
	orf00094	36304	36023	-2
	orf00095	37346	36282	-3
	orf00096	37853	38689	2
	orf00097	38744	39907	2

Contig	ORF	Start	End	Frame
	orf00099	40376	40254	-3
	orf00101	40449	41720	3
>contig00053				
	orf00002	271	-1	-2
	orf00005	748	605	-2
	orf00006	1497	721	-1
	orf00009	1727	1623	-3
	orf00010	1737	3371	3
	orf00011	3746	5803	2
	orf00014	6055	5951	-2
	orf00016	7657	6203	-2
	orf00018	7917	7813	-1
	orf00021	8217	9569	3
	orf00025	9706	11949	1
	orf00028	11962	12627	1
	orf00030	13151	12720	-3
	orf00032	14204	13392	-3
	orf00034	15078	14395	-1
	orf00036	15508	15149	-2
	orf00038	16117	15530	-2
	orf00039	16196	16351	2
	orf00040	16484	17620	2
	orf00041	17690	17842	2
>contig00054				
>contig00055				
	orf00001	0	707	3
	orf00003	704	1633	2
	orf00005	1620	2429	3
	orf00007	2486	3679	2
	orf00008	3787	4479	1
	orf00010	5728	4715	-2
	orf00011	6098	6343	2
	orf00013	7690	6497	-2
	orf00014	7942	8406	1
	orf00016	8403	8981	3
	orf00018	9228	10034	3
	orf00021	11798	10164	-3
	orf00023	12182	11895	-3
	orf00026	12616	14631	1
	orf00027	14828	14679	-3
	orf00028	14844	15803	3
	orf00029	16562	15879	-3
	orf00032	16746	17318	3
	orf00033	17419	18711	1
	orf00035	19060	20538	1
	orf00037	22998	21160	-1
	orf00039	24362	23265	-3
	orf00040	24969	24433	-1

Contig	ORF	Start	End	Frame
	orf00042	25411	25004	-2
	orf00044	26454	25612	-1
	orf00045	26925	26542	-1
	orf00047	27533	27168	-3
	orf00049	27843	27544	-1
	orf00050	27922	28035	1
	orf00052	28704	28036	-1
	orf00053	29369	28701	-3
	orf00054	29388	29567	3
	orf00055	29548	30186	1
	orf00058	30865	30260	-2
	orf00060	31801	30974	-2
	orf00061	31904	32155	2
	orf00062	32229	33071	3
	orf00065	33361	35109	1
	orf00066	35472	36056	3
	orf00068	37186	37037	-2
	orf00069	37364	37257	-3
	orf00070	37353	37469	3
>contig00056				
	orf00004	8029	7916	-2
	orf00005	7013	0	-3
	orf00008	9846	9226	-1
	orf00009	10291	10013	-2
	orf00011	11178	10288	-1
	orf00012	11299	11955	1
	orf00013	12315	12530	3
	orf00014	12555	12719	3
	orf00015	12968	14275	2
	orf00018	14440	15858	1
	orf00020	16028	17305	2
	orf00023	17319	18392	3
	orf00025	18389	19579	2
	orf00026	19572	20189	3
	orf00028	20224	21150	1
	orf00029	21137	21823	2
	orf00030	21890	22654	2
	orf00031	22647	23822	3
	orf00034	24015	25907	3
	orf00037	25995	27128	3
	orf00039	27204	27743	3
	orf00040	27791	29983	2
	orf00041	30909	30214	-1
	orf00042	31314	30922	-1
	orf00043	31402	31935	1
	orf00045	32173	33300	1
	orf00046	33297	33956	3
	orf00047	34015	34125	1

Contig	ORF	Start	End	Frame
	orf00048	35309	34122	-3
	orf00049	35587	35399	-2
	orf00050	36957	35590	-1
	orf00052	37849	36989	-2
	orf00053	37968	38072	3
	orf00054	38640	38056	-1
	orf00057	40243	38765	-2
	orf00059	42016	40268	-2
	orf00061	42366	42103	-1
	orf00062	43375	42422	-2
	orf00063	43806	43372	-1
	orf00064	44296	45336	1
	orf00067	46923	45919	-1
	orf00068	47079	47729	3
	orf00070	48659	47823	-3
	orf00071	48929	50044	2
	orf00074	50723	51769	2
	orf00077	51780	52547	3
	orf00078	52717	53148	1
	orf00080	54120	53224	-1
	orf00082	54243	54644	3
	orf00083	54740	55345	2
	orf00085	55854	55582	-1
	orf00086	55837	55953	1
	orf00087	56589	57329	3
	orf00088	57453	58892	3
	orf00091	59197	58982	-2
	orf00092	59405	59190	-3
	orf00093	60823	59480	-2
	orf00094	61369	60983	-2
	orf00096	61459	62271	1
>contig00057				
	orf00001	386	273	-3
	orf00004	899	1105	2
	orf00008	1112	4327	2
	orf00009	4609	4436	-2
	orf00010	4580	6139	2
	orf00011	7318	6233	-2
	orf00013	7710	7925	3
	orf00015	9513	7993	-1
	orf00018	11262	9709	-1
	orf00020	11257	11391	1
	orf00021	12065	11433	-3
	orf00026	14343	12175	-1
	orf00027	14482	15270	1
	orf00029	16195	15371	-2
	orf00031	16712	16197	-3
	orf00034	16887	17264	3

Contig	ORF	Start	End	Frame
	orf00035	17311	18249	1
	orf00037	18585	19754	3
	orf00038	19872	20075	3
	orf00040	22109	20757	-3
	orf00041	22616	22167	-3
	orf00044	22749	23609	3
	orf00045	24885	23923	-1
	orf00047	25390	25286	-2
>contig00058				
	orf00002	959	42	-3
	orf00003	1932	1006	-1
	orf00005	2719	2000	-2
	orf00006	2992	3315	1
	orf00008	3392	3871	2
	orf00011	4017	4448	3
	orf00012	5347	4859	-2
	orf00013	5457	6716	3
	orf00014	6868	6701	-2
	orf00016	8297	6960	-3
	orf00019	9710	8370	-3
	orf00020	9916	10077	1
	orf00023	11599	10052	-2
	orf00024	12276	11626	-1
	orf00026	14108	12729	-3
	orf00027	14973	15101	3
	orf00028	15221	16231	2
	orf00029	16228	16500	1
	orf00031	16536	18035	3
	orf00032	18138	18500	3
	orf00033	18550	19575	1
	orf00034	19641	20549	3
	orf00035	20560	21591	1
	orf00036	21588	22379	3
	orf00038	22422	22592	3
	orf00039	22651	22974	1
	orf00040	23084	23959	2
	orf00041	24156	25616	3
	orf00042	25739	26524	2
	orf00043	27238	26876	-2
	orf00044	29510	27795	-3
	orf00045	29559	31073	3
	orf00047	33281	31527	-3
	orf00049	33408	33298	-1
	orf00050	33699	33475	-1
	orf00051	34561	34286	-2
	orf00052	35145	34714	-1
	orf00053	35450	35139	-3
	orf00054	35745	35629	-1

Contig	ORF	Start	End	Frame
	orf00055	36115	35798	-2
	orf00056	36401	36099	-3
	orf00058	38838	36475	-1
	orf00059	40057	38867	-2
	orf00061	40809	40060	-1
	orf00062	41155	40784	-2
	orf00063	41570	41145	-3
	orf00065	42621	41587	-1
	orf00067	43183	42824	-2
	orf00068	43489	43196	-2
	orf00069	43944	43540	-1
	orf00070	45992	44079	-3
	orf00072	46163	46306	2
	orf00073	46380	47495	3
	orf00074	47605	48615	1
	orf00075	48694	49152	1
	orf00078	49285	50190	1
	orf00079	50466	50272	-1
	orf00081	52537	50456	-2
	orf00083	52567	52689	1
	orf00084	52954	52826	-2
	orf00085	54009	52969	-1
	orf00086	54171	55250	3
	orf00089	55329	56798	3
	orf00090	57689	56943	-3
	orf00091	57759	57899	3
	orf00093	58050	59402	3
	orf00096	59810	60007	2
	orf00097	60089	60247	2
	orf00102	63221	60369	-3
	orf00105	63924	63373	-1
	orf00107	64433	64032	-3
	orf00109	65638	64538	-2
	orf00111	66152	66637	2
	orf00112	67045	66920	-2
	orf00114	68467	67052	-2
	orf00115	68493	68789	3
	orf00117	68926	69168	1
	orf00119	70002	69361	-1
	orf00123	70304	72517	2
	orf00124	73928	72906	-3
	orf00125	73920	74069	3
	orf00127	74382	75857	3
	orf00129	76881	76627	-1
	orf00131	76951	77109	1
	orf00133	78597	77119	-1
	orf00135	82161	78727	-1
	orf00136	82174	82485	1

Contig	ORF	Start	End	Frame
	orf00137	82757	83545	2
	orf00138	84452	83913	-3
	orf00141	85352	87160	2
	orf00142	87484	87227	-2
	orf00143	87530	88444	2
	orf00144	88659	88492	-1
	orf00145	88631	88801	2
	orf00147	88907	89134	2
	orf00151	89532	89639	3
	orf00152	89510	89106	-3
	orf00154	89632	90315	1
	orf00155	90312	90482	3
	orf00156	90491	90676	2
	orf00157	90703	91500	1
	orf00158	91502	91747	2
	orf00159	91763	92284	2
	orf00162	93050	93454	2
	orf00165	93451	93930	1
	orf00168	94084	94590	1
	orf00169	94587	94760	3
	orf00171	94794	95036	3
	orf00172	95017	95427	1
	orf00174	95447	95641	2
	orf00175	95638	95967	1
	orf00176	95979	96242	3
	orf00177	96239	96436	2
	orf00179	96438	96941	3
	orf00180	96944	98590	2
	orf00182	98641	100086	1
	orf00184	100073	101368	2
	orf00185	101372	101671	2
	orf00186	101975	103051	2
	orf00187	103044	103373	3
	orf00189	103445	104404	2
	orf00191	104463	104873	3
	orf00193	104877	105308	3
	orf00194	105310	105774	1
	orf00195	105787	106545	1
	orf00197	106568	106687	2
	orf00198	106867	106694	-2
	orf00200	106921	110976	1
	orf00202	111077	111481	2
	orf00204	111528	113360	3
	orf00206	113364	115058	3
	orf00208	115227	115724	3
	orf00209	115746	116720	3
	orf00210	116721	117095	3
	orf00212	117107	118987	2

Contig	ORF	Start	End	Frame
	orf00215	119071	119301	1
	orf00218	119373	119711	3
	orf00219	119782	119907	1
	orf00221	119924	120430	2
	orf00222	120427	120792	1
	orf00223	120782	120922	2
	orf00225	121124	120987	-3
	orf00227	121174	121659	1
	orf00228	121790	121951	2
	orf00229	123775	122099	-2
	orf00231	127045	123992	-2
	orf00233	127921	127100	-2
	orf00235	130637	128490	-3
	orf00237	132772	131228	-2
	orf00240	133936	132824	-2
	orf00242	134139	135077	3
	orf00244	135334	135441	1
	orf00245	135438	135920	3
	orf00247	136020	136937	3
	orf00253	138069	137368	-1
	orf00254	138880	138071	-2
	orf00256	139124	140542	2
	orf00258	140747	140619	-3
	orf00260	140872	142017	1
	orf00261	143383	142241	-2
	orf00264	144412	143420	-2
	orf00267	145408	144770	-2
	orf00268	145707	145405	-1
	orf00270	146003	145869	-3
	orf00272	146429	146046	-3
	orf00273	146994	146479	-1
	orf00276	147686	147027	-3
	orf00278	148489	147851	-2
	orf00281	150584	148749	-3
	orf00282	151020	150916	-1
	orf00284	151049	152494	2
	orf00288	152709	153404	3
	orf00289	153385	154386	1
	orf00290	154436	155284	2
	orf00293	155504	157147	2
	orf00296	158196	157579	-1
	orf00297	159149	158247	-3
	orf00298	159814	159197	-2
	orf00299	159988	160146	1
	orf00301	160386	161327	3
	orf00303	161582	162841	2
	orf00305	162939	163337	3
	orf00307	163440	164630	3

Contig	ORF	Start	End	Frame
	orf00309	164795	166390	2
	orf00312	166997	166452	-3
	orf00313	167669	167001	-3
	orf00315	169039	167666	-2
	orf00317	169153	171228	1
	orf00318	171357	171509	3
	orf00319	173031	171613	-1
	orf00321	176306	173091	-3
	orf00323	177598	176318	-2
>contig00059				
	orf00001	-2	120	1
	orf00003	188	862	2
	orf00004	1021	1497	1
	orf00007	2029	3291	1
	orf00008	3284	5461	2
	orf00009	5463	6644	3
	orf00010	7067	7327	2
	orf00011	7329	8579	3
	orf00013	8843	8604	-3
>contig00060				
	orf00001	1539	10	-1
	orf00004	2413	1682	-2
	orf00005	3361	2420	-2
	orf00008	4820	3486	-3
	orf00009	5002	4859	-2
	orf00012	5014	6489	1
	orf00014	6715	7002	1
	orf00015	7212	8348	3
	orf00017	8538	8909	3
	orf00018	8882	8986	2
	orf00019	9005	9622	2
	orf00020	9665	9790	2
	orf00022	10002	12665	3
	orf00023	12905	12684	-3
	orf00024	12906	14501	3
	orf00027	15050	16837	2
	orf00029	17192	17899	2
	orf00031	17919	18548	3
	orf00032	18557	19423	2
	orf00035	20039	19611	-3
	orf00036	20220	20978	3
	orf00038	21153	21386	3
	orf00039	21641	21516	-3
	orf00040	21640	22791	1
	orf00041	22897	24195	1
	orf00042	24854	24477	-3
	orf00043	24908	25060	2
	orf00044	25057	25539	1

Contig	ORF	Start	End	Frame
	orf00046	25587	25817	3
	orf00047	25819	26439	1
	orf00049	26600	27475	2
	orf00051	27755	29152	2
>contig00061				
	orf00001	2075	300	-3
	orf00002	2687	2160	-3
	orf00004	4159	2948	-2
	orf00005	4253	4146	-3
	orf00006	4326	4928	3
	orf00009	5826	5026	-1
	orf00010	6759	5851	-1
	orf00011	6988	6878	-2
	orf00014	7826	6981	-3
	orf00015	9057	7834	-1
	orf00016	9308	9718	2
	orf00018	9822	11015	3
>contig00062				
	orf00002	338	703	2
	orf00004	3057	772	-1
	orf00005	3472	3059	-2
	orf00006	3682	3885	1
	orf00007	3968	4192	2
	orf00009	4623	4261	-1
	orf00010	5537	4644	-3
	orf00011	6273	5656	-1
	orf00014	9168	6607	-1
	orf00015	9537	9220	-1
	orf00017	10455	9883	-1
	orf00018	11505	10522	-1
	orf00019	12764	11919	-3
	orf00022	13379	12792	-3
	orf00023	15292	13433	-2
	orf00027	15492	16097	3
	orf00028	16290	17153	3
	orf00029	17270	18013	2
	orf00030	17266	17150	-2
	orf00032	18267	18142	-1
	orf00033	18481	19023	1
	orf00034	19023	19400	3
	orf00035	19836	20285	3
	orf00037	20289	21251	3
	orf00039	21232	22086	1
	orf00042	22235	22465	2
	orf00044	22622	23563	2
	orf00045	23825	23706	-3
	orf00046	23838	24983	3
	orf00047	25062	25817	3

Contig	ORF	Start	End	Frame
>contig00063				
	orf00002	2386	113	-2
	orf00005	3994	2552	-2
	orf00007	4239	4739	3
	orf00008	5000	5332	2
	orf00009	5353	5826	1
	orf00011	5861	5989	2
	orf00013	6150	6446	3
	orf00015	6965	6540	-3
	orf00017	7364	7020	-3
	orf00018	7493	7720	2
	orf00020	7891	8556	1
	orf00023	8635	9222	1
	orf00024	9228	9371	3
	orf00025	9465	9569	3
	orf00027	9960	10097	3
	orf00029	10156	11868	1
	orf00031	11994	15476	3
	orf00033	15984	15574	-1
	orf00036	17900	16362	-3
	orf00037	18216	18109	-1
	orf00039	19571	18312	-3
	orf00040	20029	19553	-2
	orf00041	20374	21489	1
	orf00044	21748	23880	1
>contig00064				
>contig00065				
>contig00066				
>contig00067				
	orf00001	233	0	-3
>contig00068				
>contig00069				
	orf00001	0	227	3
	orf00002	356	907	2
	orf00003	1095	904	-1
	orf00004	1321	1881	1
	orf00005	1963	2250	1
>contig00070				
	orf00002	1537	8	-2
	orf00003	1675	2130	1
	orf00004	2514	2305	-1
	orf00006	3045	4145	3
	orf00008	4236	4622	3
	orf00009	4714	4995	1
	orf00010	5118	7496	3
	orf00011	7835	8203	2
	orf00013	8200	9990	1
	orf00014	10003	10884	1

Contig	ORF	Start	End	Frame
	orf00015	10887	11549	3
>contig00071				
	orf00001	275	0	-3
	orf00003	522	632	3
>contig00072				
	orf00002	1188	-2	-1
	orf00003	1419	2111	3
>contig00073				
	orf00001	380	565	2
	orf00002	584	1540	2
	orf00004	2275	2748	1
>contig00074				
	orf00001	1179	1	-1
>contig00075				
	orf00002	560	1978	2
	orf00003	1982	2110	2
	orf00004	2161	3828	1
	orf00006	4660	4034	-2
	orf00007	4979	5245	2
	orf00008	5405	5271	-3
	orf00011	5419	7281	1
	orf00012	7281	7409	3
	orf00014	7526	10456	2
	orf00017	12146	10770	-3
	orf00018	12281	12994	2
	orf00022	14669	13047	-3
	orf00024	14853	14653	-1
	orf00026	14862	14981	3
	orf00027	16028	14991	-3
	orf00028	17019	16132	-1
	orf00029	17154	17813	3
	orf00032	18473	17874	-3
	orf00033	18601	19104	1
	orf00035	19985	19305	-3
	orf00036	20397	21659	3
	orf00038	21675	22640	3
	orf00039	22640	23527	2
	orf00041	23658	24953	3
	orf00043	25957	25130	-2
	orf00045	26371	26069	-2
	orf00047	27624	26491	-1
	orf00048	28762	27839	-2
	orf00050	31077	28798	-1
	orf00051	31942	31436	-2
	orf00053	32547	32206	-1
	orf00056	32840	32595	-3
	orf00058	33674	33288	-3
	orf00060	33872	33744	-3

Contig	ORF	Start	End	Frame
	orf00063	35172	33958	-1
	orf00064	35649	35203	-1
	orf00066	36007	37179	1
	orf00067	38093	37311	-3
	orf00068	38815	38267	-2
	orf00069	39458	38889	-3
	orf00070	40914	39571	-1
	orf00072	41967	41008	-1
	orf00073	41971	42132	1
	orf00075	42186	42587	3
	orf00077	42606	42740	3
	orf00078	43855	42737	-2
>contig00076				
	orf00001	-1	136	2
	orf00003	133	1176	1
	orf00005	2246	1338	-3
	orf00006	2245	2349	1
	orf00010	3675	2614	-1
	orf00011	3899	3693	-3
	orf00014	5067	4093	-1
	orf00016	5540	5145	-3
	orf00019	5689	7032	1
	orf00020	8126	7212	-3
	orf00022	8607	8236	-1
	orf00023	8726	9766	2
	orf00024	11147	10101	-3
	orf00025	12183	11371	-1
	orf00026	12844	12542	-2
	orf00028	15374	13089	-3
	orf00031	16265	15792	-3
	orf00032	16752	16288	-1
	orf00034	16892	17020	2
	orf00035	17218	19029	1
	orf00037	19900	21912	1
	orf00038	21909	22802	3
	orf00039	22805	23842	2
	orf00040	24165	24758	3
	orf00042	26922	25150	-1
	orf00043	27939	26959	-1
	orf00044	28556	27939	-3
	orf00045	28824	28558	-1
	orf00049	29025	31487	3
	orf00051	31687	31941	1
	orf00053	32618	32412	-3
	orf00054	33224	32646	-3
	orf00058	33481	33290	-2
	orf00059	33989	33558	-3
	orf00060	34361	35626	2

Contig	ORF	Start	End	Frame
	orf00061	36803	35961	-3
	orf00063	37443	36880	-1
	orf00064	37658	38020	2
	orf00065	38815	38126	-2
	orf00066	39531	38812	-1
	orf00067	39929	40411	2
	orf00068	40580	41023	2
>contig00077				
	orf00003	352	750	1
	orf00005	804	1592	3
	orf00006	1607	2164	2
	orf00007	2234	2398	2
>contig00078				
	orf00001	781	101	-2
	orf00002	1968	1087	-1
	orf00004	3238	2240	-2
	orf00005	3404	3279	-3
	orf00006	3627	3971	3
	orf00008	3984	5153	3
	orf00011	5201	5374	2
	orf00012	5973	8780	3
	orf00014	9636	8842	-1
	orf00016	10169	11506	2
	orf00018	11643	13004	3
	orf00019	13141	14055	1
	orf00020	14063	14170	2
	orf00021	15468	14281	-1
	orf00022	17413	15458	-2
	orf00023	17626	17510	-2
	orf00026	18362	17736	-3
	orf00027	18563	19198	2
	orf00029	19993	19571	-2
	orf00030	20671	20012	-2
	orf00031	21680	20739	-3
	orf00033	22654	22190	-2
	orf00034	22938	23204	3
	orf00036	23332	23225	-2
	orf00037	23316	24473	3
	orf00038	28191	24811	-1
	orf00040	28504	28379	-2
	orf00041	28517	29644	2
	orf00043	29793	29674	-1
	orf00044	29792	30049	2
	orf00045	30216	30605	3
>contig00079				
	orf00003	1116	220	-1
	orf00004	1148	1258	2
	orf00005	2046	1291	-1

Contig	ORF	Start	End	Frame
	orf00006	3016	2177	-2
	orf00008	3803	3201	-3
	orf00010	4129	5466	1
	orf00014	5564	7558	2
	orf00015	7649	7759	2
	orf00016	8639	7959	-3
	orf00019	8996	8685	-3
>contig00080				
	orf00001	168	302	3
	orf00002	363	683	3
	orf00003	778	1098	1
	orf00005	1195	2247	1
	orf00007	2252	2545	2
	orf00009	2549	3724	2
	orf00011	4030	4992	1
	orf00012	5842	5237	-2
	orf00016	8364	6403	-1
	orf00017	8882	8598	-3
	orf00018	9822	9046	-1
	orf00019	10505	9831	-3
	orf00020	10697	10509	-3
	orf00022	11066	10743	-3
	orf00023	11503	11180	-2
	orf00024	11656	11534	-2
	orf00025	12050	11643	-3
	orf00027	12885	12118	-1
	orf00028	13347	13030	-1
	orf00030	14442	13705	-1
	orf00031	15248	14604	-3
	orf00033	15263	15373	2
	orf00035	16964	15378	-3
	orf00037	18870	17305	-1
	orf00038	19335	18997	-1
	orf00040	19960	19514	-2
	orf00042	21713	20334	-3
	orf00044	23310	21808	-1
	orf00045	23316	23486	3
	orf00048	25329	23575	-1
	orf00049	25525	26073	1
	orf00050	26086	26634	1
	orf00051	26627	27103	2
	orf00054	28108	27197	-2
	orf00056	28331	29314	2
	orf00057	29507	29929	2
	orf00058	30531	29998	-1
	orf00060	31065	30664	-1
	orf00061	31071	31682	3
	orf00062	31722	31832	3

Contig	ORF	Start	End	Frame
	orf00063	31951	33402	1
	orf00066	33475	34218	1
	orf00067	35374	34286	-2
	orf00069	35522	35668	2
	orf00071	35777	36421	2
	orf00072	36437	37852	2
	orf00074	38173	40566	1
	orf00075	40643	40891	2
	orf00076	40937	41419	2
	orf00077	41419	42168	1
	orf00078	42182	42547	2
	orf00079	43331	42825	-3
	orf00081	44550	43324	-1
	orf00082	45855	44563	-1
	orf00083	46407	45973	-1
	orf00084	46834	46412	-2
	orf00085	47621	46893	-3
	orf00089	48418	47639	-2
	orf00091	49736	48597	-3
	orf00093	49894	49790	-2
	orf00094	49967	50716	2
	orf00095	50822	51571	2
	orf00098	53837	51885	-3
	orf00102	55830	54058	-1
	orf00105	56413	57771	1
	orf00109	59574	58108	-1
	orf00110	59590	59850	1
	orf00113	60776	59904	-3
	orf00114	64243	60977	-2
	orf00115	64478	64359	-3
	orf00116	64691	65371	2
	orf00118	65514	65410	-1
	orf00119	65642	66961	2
	orf00122	68561	67143	-3
	orf00125	68938	69495	1
	orf00127	69906	69706	-1
	orf00128	70858	69923	-2
	orf00130	72715	70862	-2
	orf00131	73045	72791	-2
	orf00132	73289	74386	2
	orf00133	74556	74446	-1
	orf00134	76297	74531	-2
	orf00136	77156	76533	-3
	orf00137	77239	77367	1
	orf00138	77618	77487	-3
	orf00139	77617	78153	1
	orf00140	78193	78792	1
	orf00141	78818	79432	2

Contig	ORF	Start	End	Frame
	orf00142	80779	79514	-2
	orf00145	81174	81884	3
	orf00146	82085	82555	2
	orf00149	83123	82629	-3
	orf00150	83543	83178	-3
	orf00152	84055	83669	-2
	orf00154	84164	85108	2
	orf00156	86806	85400	-2
	orf00158	87797	87060	-3
	orf00159	88631	88750	2
	orf00160	88618	87986	-2
	orf00161	89702	88860	-3
	orf00163	90601	89933	-2
	orf00166	91967	90765	-3
	orf00168	92077	92193	1
	orf00169	93713	92190	-3
	orf00171	94069	93929	-2
	orf00172	94538	95176	2
	orf00173	95173	96804	1
	orf00175	96801	97979	3
	orf00177	98232	98396	3
	orf00180	98898	100349	3
	orf00182	100353	100862	3
	orf00183	101163	101050	-1
	orf00184	102035	102202	2
	orf00186	102199	103611	1
	orf00187	103749	104480	3
	orf00188	105695	104574	-3
	orf00191	107772	106138	-1
	orf00195	108065	109453	2
	orf00197	110039	109587	-3
>contig00081				
	orf00001	114	10	-1
	orf00003	1983	271	-1
	orf00006	2433	3281	3
	orf00009	3316	3444	1
	orf00010	3467	4474	2
	orf00011	4721	6514	2
	orf00013	7439	6579	-3
	orf00017	8494	7952	-2
	orf00018	8702	8595	-3
	orf00019	8851	8726	-2
	orf00020	8841	8945	3
	orf00022	11925	8983	-1
	orf00024	12345	11956	-1
>contig00082				
	orf00001	928	509	-2
>contig00083				

Contig	ORF	Start	End	Frame
>contig00084				
>contig00085				
	orf00001	735	-2	-1
	orf00002	1398	1153	-1
	orf00004	2594	1434	-3
>contig00086				
	orf00001	0	917	3
>contig00087				
>contig00088				
	orf00001	1194	376	-1
	orf00003	1357	1929	1
	orf00005	1942	2052	1
	orf00007	2232	4163	3
	orf00008	4610	4335	-3
	orf00010	4789	4652	-2
	orf00011	5250	5011	-1
	orf00013	5610	7142	3
	orf00016	7886	9613	2
	orf00018	9649	10116	1
	orf00021	10180	10473	1
	orf00023	10547	11560	2
	orf00025	12027	11692	-1
	orf00027	12356	12069	-3
	orf00028	12327	13178	3
	orf00029	13210	14076	1
	orf00033	14165	16357	2
>contig00089				
	orf00001	320	1144	2
	orf00003	1134	1850	3
	orf00004	1860	2627	3
	orf00005	2761	2642	-2
	orf00006	2978	4900	2
	orf00007	5085	5402	3
	orf00009	5579	6109	2
	orf00010	7097	6264	-3
	orf00014	7219	8376	1
	orf00015	8470	8928	1
	orf00016	9145	8969	-2
	orf00017	9163	9942	1
	orf00019	9969	11159	3
	orf00022	11192	11353	2
	orf00024	11475	11350	-1
	orf00025	11887	11708	-2
	orf00026	11893	14364	1
	orf00028	14720	14571	-3
	orf00029	14814	14695	-1
>contig00090				
>contig00091				

Contig	ORF	Start	End	Frame
>contig00092				
	orf00001	672	-2	-1
	orf00003	2482	1097	-2
	orf00005	3307	2591	-2
	orf00007	3685	3317	-2
	orf00008	3684	3815	3
	orf00010	5417	3876	-3
	orf00011	5636	6043	2
	orf00013	7255	6116	-2
	orf00014	7434	7324	-1
	orf00016	8831	7443	-3
	orf00017	8943	9059	3
	orf00018	9925	9044	-2
	orf00019	10087	10827	1
	orf00020	11332	10904	-2
	orf00022	11618	12940	2
	orf00025	13042	13155	1
	orf00028	13349	14659	2
	orf00030	14656	16317	1
	orf00032	16317	16835	3
	orf00034	16860	17543	3
	orf00035	18686	17742	-3
	orf00036	18861	20240	3
	orf00037	20463	21104	3
	orf00039	21148	21282	1
	orf00041	21279	22964	3
	orf00042	22993	23289	1
	orf00046	23595	24731	3
	orf00048	24850	25275	1
	orf00049	25541	26635	2
	orf00050	26638	27393	1
	orf00051	27398	28270	2
	orf00053	28273	29538	1
	orf00055	29588	29719	2
	orf00056	30660	29905	-1
	orf00057	30864	30745	-1
	orf00060	32135	30942	-3
	orf00062	32672	34855	2
	orf00064	36335	35091	-3
	orf00066	36516	36623	3
	orf00067	37480	36620	-2
	orf00068	39036	37507	-1
	orf00070	40086	39091	-1
	orf00071	40658	40990	2
	orf00072	41025	42200	3
	orf00073	42367	42918	1
	orf00074	43308	43039	-1
	orf00075	43575	43339	-1

Contig	ORF	Start	End	Frame
	orf00076	43787	44272	2
	orf00077	45755	44337	-3
	orf00078	45772	45891	1
	orf00079	46060	45944	-2
>contig00093				
>contig00094				
	orf00001	48	251	3
	orf00003	307	1116	1
	orf00004	1245	1586	3
	orf00007	2437	1640	-2
	orf00009	3253	2675	-2
	orf00010	3968	3687	-3
	orf00011	4927	4235	-2
	orf00012	5222	5500	2
	orf00013	5708	8017	2
	orf00016	8183	9772	2
	orf00017	9789	11369	3
	orf00018	11540	11704	2
	orf00020	12123	13190	3
	orf00021	13260	14126	3
>contig00095				
	orf00001	287	673	2
	orf00003	1123	719	-2
	orf00004	1407	1120	-1
	orf00007	1883	1719	-3
	orf00009	2681	1914	-3
	orf00010	4342	4229	-2
	orf00011	4907	5191	2
	orf00013	6612	6890	3
	orf00014	7049	6894	-3
>contig00096				
	orf00001	359	9	-3
	orf00002	802	614	-2
	orf00003	1223	2416	2
	orf00005	2514	2675	3
	orf00006	2845	3015	1
	orf00007	3019	3291	1
	orf00008	3364	3609	1
	orf00010	3802	4212	1
	orf00011	4209	4445	3
	orf00013	4505	4972	2
>contig00097				
	orf00001	0	131	3
>contig00098				
>contig00099				
	orf00001	-2	195	1
	orf00002	1125	604	-1
	orf00003	1921	1457	-2

Contig	ORF	Start	End	Frame
	orf00005	3029	1929	-3
	orf00007	3736	3143	-2
	orf00008	4397	3729	-3
	orf00009	4812	6035	3
	orf00010	6105	7001	3
	orf00011	7196	7399	2
	orf00013	7473	7712	3
	orf00014	7729	8427	1
	orf00015	8496	9035	3
	orf00016	9323	9661	2
	orf00017	9804	10019	3
	orf00018	9805	9698	-2
	orf00019	10016	11137	2
	orf00023	11134	12882	1
	orf00025	13677	13432	-1
	orf00027	13971	14246	3
	orf00028	15052	14600	-2
	orf00029	15983	15024	-3
	orf00030	16349	16059	-3
	orf00033	17114	16638	-3
>contig00100				
>contig00101				
	orf00001	-1	130	2
	orf00002	1804	431	-2
	orf00003	2110	1919	-2
	orf00004	2508	2218	-1
	orf00007	3227	2571	-3
	orf00008	3290	4291	2
	orf00009	4362	4529	3
	orf00010	4776	5024	3
	orf00012	5202	6152	3
	orf00014	6156	7580	3
	orf00016	8038	8769	1
>contig00102				
	orf00003	-1	2212	2
>contig00103				
>contig00104				
	orf00001	0	275	3
>contig00105				
	orf00001	48	224	3
>contig00106				
	orf00001	113	607	2
	orf00002	801	1244	3
	orf00005	2650	1355	-2
	orf00006	3020	3184	2
	orf00007	4290	3199	-1
	orf00008	4484	5293	2
	orf00011	5866	5408	-2

Contig	ORF	Start	End	Frame
	orf00012	6217	5885	-2
	orf00014	8207	6582	-3
	orf00016	8559	8338	-1
	orf00017	9034	8900	-2
	orf00018	8897	8559	-3
	orf00021	9462	9088	-1
	orf00022	9461	11011	2
	orf00023	11161	12264	1
	orf00025	12871	12338	-2
	orf00027	12940	13053	1
	orf00028	13119	14480	3
	orf00030	14567	15748	2
	orf00031	15855	15745	-1
	orf00032	15872	16876	2
	orf00034	16963	17574	1
>contig00107				
	orf00001	-2	480	1
	orf00002	635	1030	2
	orf00004	1105	1398	1
	orf00007	1872	2294	3
	orf00008	3792	2377	-1
	orf00009	3962	3807	-3
	orf00010	4065	4979	3
	orf00012	6072	5335	-1
	orf00013	7274	6402	-3
	orf00014	7614	7384	-1
	orf00015	7642	8391	1
	orf00018	9217	8486	-2
	orf00019	10404	9346	-1
	orf00020	10404	10511	3
	orf00021	11344	10499	-2
	orf00022	11318	11443	2
	orf00023	11555	13315	2
>contig00108				
	orf00001	693	7	-1
	orf00002	1936	686	-2
	orf00003	2090	2434	2
	orf00004	3147	2527	-1
	orf00005	4759	3224	-2
	orf00006	5194	4841	-2
	orf00007	5474	6172	2
	orf00009	6304	8304	1
	orf00010	9253	9083	-2
	orf00012	10553	10353	-3
	orf00013	10552	10677	1
	orf00014	10695	11849	3
	orf00016	11846	12427	2
	orf00017	12496	12633	1

Contig	ORF	Start	End	Frame
	orf00019	14250	13036	-1
	orf00020	14254	14556	1
	orf00021	15429	14692	-1
	orf00022	15591	15472	-1
	orf00024	16052	15612	-3
	orf00025	16282	16049	-2
	orf00027	17697	16411	-1
	orf00028	18029	19357	2
	orf00029	19492	19677	1
	orf00030	19688	20356	2
	orf00032	20361	21095	3
	orf00033	21175	21660	1
	orf00035	21780	23687	3
	orf00036	25222	23759	-2
	orf00037	25515	25634	3
	orf00039	25886	27172	2
	orf00040	27189	27467	3
	orf00044	27766	27590	-2
	orf00045	27880	28374	1
	orf00047	29908	28535	-2
	orf00049	30245	31189	2
	orf00051	31227	31505	3
	orf00053	31554	32705	3
	orf00054	32746	33306	1
	orf00056	33314	33448	2
	orf00058	33488	36253	2
	orf00059	36342	37640	3
	orf00060	37944	38060	3
	orf00061	38120	41761	2
	orf00065	42549	43448	3
	orf00067	43499	43927	2
	orf00069	43998	44564	3
	orf00075	47252	45027	-3
	orf00079	48728	47391	-3
	orf00081	49047	50453	3
	orf00082	50602	50739	1
	orf00083	50772	50909	3
	orf00084	50998	51639	1
	orf00086	51736	52197	1
	orf00088	52290	52421	3
	orf00090	52432	53502	1
	orf00093	53774	54172	2
	orf00095	54259	55281	1
	orf00097	55463	55353	-3
	orf00099	55651	55547	-2
	orf00100	55654	57174	1
	orf00101	57178	57342	1
	orf00102	57339	57722	3

Contig	ORF	Start	End	Frame
	orf00104	57753	59408	3
	orf00107	59533	59973	1
	orf00109	60102	60923	3
	orf00111	60941	61126	2
	orf00114	61149	61775	3
	orf00115	62079	62624	3
	orf00117	63453	62746	-1
	orf00118	64209	63538	-1
	orf00121	64816	64280	-2
	orf00122	66835	65018	-2
	orf00124	68635	67181	-2
	orf00126	69333	68632	-1
	orf00128	70109	69330	-3
	orf00129	70537	71946	1
>contig00109				
	orf00002	119	1177	2
>contig00110				
>contig00111				
>contig00112				
>contig00113				
	orf00001	-1	898	2
	orf00002	1024	2445	1
	orf00004	2728	2528	-2
	orf00006	3613	2738	-2
	orf00008	4445	3720	-3
	orf00009	4573	4442	-2
	orf00011	5940	4972	-1
	orf00012	6270	7895	3
	orf00015	7991	9787	2
	orf00017	9818	10207	2
	orf00019	10201	11121	1
	orf00022	11194	12102	1
	orf00024	12125	13729	2
	orf00026	14867	14598	-3
	orf00027	15258	14869	-1
	orf00028	15890	15453	-3
	orf00029	17054	16164	-3
	orf00032	18231	17065	-1
	orf00034	18617	18330	-3
	orf00036	20250	18817	-1
	orf00042	20715	20446	-1
	orf00043	20714	20842	2
	orf00044	22180	20909	-2
	orf00049	25032	22204	-1
	orf00050	26541	25258	-1
	orf00051	26908	26660	-2
	orf00052	27619	26912	-2
	orf00053	29507	27744	-3

Contig	ORF	Start	End	Frame
	orf00054	29851	29510	-2
	orf00055	30114	29845	-1
	orf00057	31351	30869	-2
	orf00058	31690	32088	1
	orf00060	32659	32156	-2
	orf00062	33801	32866	-1
	orf00064	34535	33927	-3
	orf00066	35383	34532	-2
	orf00067	36266	35616	-3
	orf00068	37324	36284	-2
	orf00070	37943	37371	-3
	orf00073	39587	38208	-3
	orf00075	40097	39759	-3
	orf00076	40369	40238	-2
	orf00079	40537	44463	1
	orf00081	44876	45685	2
	orf00082	45901	46008	1
	orf00083	47032	45998	-2
	orf00085	47705	47103	-3
	orf00086	47901	47719	-1
	orf00087	48052	48366	1
	orf00088	48344	48664	2
	orf00089	49512	48736	-1
	orf00090	49873	49517	-2
	orf00092	50870	49893	-3
	orf00093	50853	51056	3
	orf00094	51156	51386	3
	orf00095	51540	52169	3
	orf00098	52653	52883	3
	orf00100	52893	53486	3
	orf00103	53544	54719	3
	orf00104	54904	55482	1
	orf00105	55815	56204	3
	orf00107	56285	57115	2
	orf00108	58269	57214	-1
	orf00109	58441	58322	-2
	orf00112	58509	59483	3
	orf00115	59572	60837	1
	orf00120	61376	61221	-3
	orf00123	61586	61702	2
	orf00124	62420	61809	-3
	orf00126	62631	62524	-1
	orf00128	63241	62621	-2
	orf00130	63870	63361	-1
	orf00133	64558	63965	-2
	orf00134	65271	64849	-1
	orf00136	65272	65382	1
	orf00138	65429	68182	2

Contig	ORF	Start	End	Frame
	orf00141	70422	68734	-1
	orf00143	71279	71422	2
	orf00144	71308	70532	-2
	orf00146	71943	71470	-1
	orf00147	72206	72042	-3
	orf00148	73349	72243	-3
	orf00149	73703	74134	2
	orf00150	73675	73565	-2
	orf00153	74172	75662	3
	orf00155	75674	78586	2
	orf00156	78885	79034	3
	orf00157	79654	80367	1
	orf00159	80561	81214	2
	orf00160	81423	82313	3
	orf00162	82310	83602	2
	orf00163	84756	83683	-1
	orf00166	85613	84753	-3
	orf00169	86094	85822	-1
	orf00170	86927	86091	-3
	orf00171	87162	87635	3
	orf00172	87735	88229	3
	orf00174	88588	89238	1
	orf00176	89374	89733	1
	orf00179	89730	91574	3
	orf00182	91795	95013	1
	orf00184	95618	97153	2
	orf00185	97150	98379	1
	orf00186	98626	98468	-2
>contig00114				
>contig00115				
	orf00001	109	744	1
	orf00002	2807	834	-3
	orf00004	3116	2976	-3
	orf00006	4041	3208	-1
	orf00008	5409	4573	-1
	orf00011	5918	5700	-3
	orf00013	6129	5896	-1
	orf00015	6738	8939	3
	orf00017	9591	9863	3
	orf00019	9965	11677	2
	orf00021	12032	11925	-3
	orf00022	12217	12071	-2
	orf00024	13013	12237	-3
	orf00027	13409	15052	2
	orf00028	15063	15176	3
	orf00033	15554	18196	2
>contig00116				
	orf00001	267	1436	3

Contig	ORF	Start	End	Frame
	orf00002	1614	1465	-1
	orf00003	1661	2512	2
	orf00005	5224	2600	-2
	orf00006	5438	6583	2
	orf00007	8187	8327	3
	orf00008	8178	6655	-1
	orf00010	9328	8324	-2
	orf00012	9885	9346	-1
	orf00013	11078	10068	-3
	orf00016	11339	13912	2
	orf00018	14919	14011	-1
	orf00021	15053	16138	2
	orf00022	16143	16340	3
	orf00024	16457	17023	2
	orf00025	17298	17152	-1
	orf00027	18345	17491	-1
	orf00029	19588	18458	-2
	orf00032	19901	20791	2
	orf00033	22442	20934	-3
	orf00035	22694	23323	2
	orf00036	23454	24836	3
	orf00037	24840	25355	3
	orf00038	25828	26904	1
	orf00039	26967	27869	3
	orf00041	28291	30330	1
	orf00043	32656	31325	-2
	orf00045	38021	32712	-3
	orf00046	39508	38090	-2
	orf00049	39672	39866	3
	orf00052	39879	40400	3
	orf00054	40973	41236	2
>contig00117				
	orf00001	-2	204	1
	orf00003	1298	3808	2
	orf00005	4496	3936	-3
	orf00006	4739	6544	2
	orf00007	6541	7197	1
	orf00009	7471	9276	1
	orf00012	9347	10039	2
	orf00013	10135	10632	1
	orf00014	11612	10842	-3
	orf00015	11934	11752	-1
	orf00016	12675	12568	-1
	orf00017	12778	13536	1
	orf00018	13545	14372	3
	orf00020	15570	15061	-1
	orf00022	17096	15678	-3
	orf00023	17547	18314	3

Contig	ORF	Start	End	Frame
	orf00025	19683	18613	-1
	orf00027	20795	19680	-3
	orf00028	20963	22372	2
	orf00030	22841	22479	-3
	orf00031	22993	23472	1
	orf00033	23717	23517	-3
	orf00035	23877	26075	3
	orf00037	26529	28439	3
>contig00118				
	orf00001	668	405	-3
>contig00119				
	orf00002	286	633	1
	orf00003	743	639	-3
	orf00004	975	715	-1
	orf00005	1103	975	-3
	orf00006	1679	1536	-3
	orf00007	2381	1731	-3
	orf00008	2507	2388	-3
	orf00009	3288	3446	3
	orf00010	3905	3564	-3
	orf00011	4192	3947	-2
	orf00013	4746	4615	-1
	orf00014	4966	5082	1
	orf00016	6084	5788	-1
>contig00120				
	orf00001	-1	709	2
>contig00121				
>contig00122				
	orf00002	1221	1352	3
	orf00004	2202	6101	3
	orf00005	6541	7077	1
	orf00008	7112	8893	2
	orf00009	8925	9053	3
	orf00010	9303	9055	-1
	orf00011	10379	9507	-3
	orf00012	10564	10761	1
	orf00013	10881	11372	3
>contig00123				
	orf00001	1535	0	-3
	orf00003	1794	1636	-1
	orf00004	1781	3802	2
>contig00124				
	orf00001	482	210	-3
	orf00002	2043	646	-1
	orf00004	2729	2082	-3
	orf00006	4529	2982	-3
	orf00007	5073	4540	-1
	orf00008	5548	5078	-2

Contig	ORF	Start	End	Frame
	orf00009	5856	5620	-1
	orf00010	6784	5918	-2
	orf00013	8250	7393	-1
	orf00014	8405	8974	2
	orf00015	11207	9777	-3
	orf00016	11520	12620	3
	orf00017	14094	12793	-1
	orf00018	14352	14185	-1
	orf00019	14968	14357	-2
	orf00021	16398	14992	-1
	orf00023	16770	18533	3
	orf00024	18520	19038	1
	orf00025	20119	19181	-2
	orf00027	22285	20372	-2
	orf00029	23332	22460	-2
	orf00030	23526	23329	-1
	orf00031	23543	24628	2
	orf00032	25074	24706	-1
	orf00033	25234	25782	1
	orf00034	25912	26781	1
	orf00036	27816	27631	-1
>contig00125				
	orf00001	230	0	-3
	orf00002	525	220	-1
	orf00003	782	531	-3
>contig00126				
	orf00001	209	427	2
>contig00127				
	orf00002	348	85	-1
	orf00003	593	342	-3
>contig00128				
	orf00001	209	24	-3
>contig00129				
>contig00130				
>contig00131				
	orf00001	66	1901	3
	orf00002	2777	1950	-3
	orf00004	2904	3362	3
	orf00006	3439	3576	1
	orf00008	3789	3568	-1
	orf00009	5256	4216	-1
	orf00011	5273	6232	2
	orf00013	6281	7834	2
	orf00015	8000	8761	2
	orf00016	9013	9861	1
	orf00019	11597	10254	-3
	orf00020	11589	11699	3
	orf00021	13379	14587	2

Contig	ORF	Start	End	Frame
	orf00024	15062	14640	-3
	orf00026	16094	15078	-3
	orf00027	17533	16421	-2
	orf00029	18025	17684	-2
	orf00030	18147	18022	-1
>contig00132				
	orf00001	138	-2	-1
	orf00002	1236	313	-1
	orf00004	2372	1428	-3
	orf00005	2692	2561	-2
>contig00133				
>contig00134				
	orf00001	1290	433	-1
	orf00002	3043	1757	-2
	orf00003	3097	3951	1
	orf00005	4394	5731	2
	orf00007	5930	6718	2
	orf00009	6967	6860	-2
	orf00010	6966	7958	3
	orf00011	7966	8757	1
	orf00015	9013	9969	1
	orf00016	9962	10450	2
	orf00017	10554	10922	3
	orf00019	11658	11176	-1
>contig00135				
	orf00003	1349	21	-3
	orf00005	1939	1553	-2
	orf00006	1982	2125	2
	orf00007	2173	3456	1
	orf00011	4679	3747	-3
	orf00015	5345	6370	2
>contig00136				
	orf00001	1190	48	-3
	orf00003	1371	1757	3
	orf00005	1998	1828	-1
	orf00006	1997	3217	2
	orf00008	3375	4076	3
	orf00009	4139	5947	2
	orf00011	6697	7932	1
	orf00013	8024	8728	2
	orf00015	10201	8834	-2
	orf00017	10741	11820	1
	orf00019	11850	12821	3
	orf00022	13964	13212	-3
	orf00024	15282	13999	-1
	orf00026	17593	15536	-2
	orf00027	18435	18013	-1
	orf00029	19318	18437	-2

Contig	ORF	Start	End	Frame
>contig00137				
>contig00138				
	orf00001	2	484	2
	orf00003	702	1214	3
	orf00005	1261	1839	1
	orf00008	1934	2116	2
	orf00009	2113	2874	1
	orf00012	2885	3403	2
	orf00014	3486	4133	3
	orf00015	4657	5388	1
	orf00016	5402	6052	2
	orf00017	6097	7059	1
	orf00019	7148	8152	2
	orf00020	9421	8234	-2
	orf00021	10797	9628	-1
	orf00022	12045	11119	-1
	orf00025	13169	12120	-3
	orf00027	14008	13376	-2
	orf00028	14007	14117	3
	orf00029	14114	14584	2
	orf00031	14751	16142	3
>contig00139				
	orf00001	0	146	3
	orf00003	1497	184	-1
	orf00004	1736	1587	-3
	orf00006	2876	1761	-3
>contig00140				
	orf00001	241	366	1
>contig00141				
	orf00002	1101	40	-1
	orf00004	1532	2581	2
	orf00006	2823	3044	3
	orf00008	4364	3195	-3
	orf00010	5305	6162	1
	orf00012	6475	6942	1
	orf00014	7227	8906	3
	orf00015	8978	10219	2
	orf00016	10329	11084	3
	orf00017	11086	11715	1
	orf00019	13338	12487	-1
	orf00020	13333	13455	1
	orf00021	13913	13521	-3
	orf00022	15028	14060	-2
	orf00023	15573	15055	-1
	orf00024	15803	16198	2
	orf00028	16536	17924	3
	orf00029	18192	18067	-1
	orf00032	18377	19756	2

Contig	ORF	Start	End	Frame
	orf00035	20122	21465	1
	orf00037	21468	22700	3
	orf00040	22693	23469	1
	orf00041	23478	24095	3
	orf00043	24123	24692	3
	orf00045	24706	25923	1
	orf00047	27294	26104	-1
>contig00142				
	orf00001	-1	352	2
	orf00003	757	653	-2
	orf00004	963	1439	3
	orf00006	2449	1562	-2
	orf00009	4296	2935	-1
	orf00010	4523	4332	-3
	orf00011	4770	4594	-1
>contig00143				
	orf00001	0	428	3
	orf00002	593	423	-3
>contig00144				
>contig00145				
	orf00001	745	44	-2
	orf00003	968	849	-3
	orf00004	1346	1083	-3
	orf00007	2895	1546	-1
>contig00146				
>contig00147				
>contig00148				
	orf00002	392	72	-3
	orf00003	1104	472	-1
	orf00005	2591	1908	-3
	orf00007	3750	2632	-1
	orf00009	5328	3898	-1
	orf00010	6302	5430	-3
	orf00012	7759	6302	-2
	orf00014	8221	7931	-2
	orf00016	8450	9487	2
	orf00017	9499	10338	1
	orf00018	10346	10849	2
	orf00019	10859	12898	2
	orf00022	12891	14054	3
	orf00023	14066	14722	2
	orf00026	16802	15030	-3
	orf00028	18806	17424	-3
	orf00030	19763	18927	-3
	orf00031	20338	19904	-2
	orf00034	21638	20331	-3
	orf00035	21622	21738	1
	orf00037	22033	22407	1

Contig	ORF	Start	End	Frame
	orf00041	22578	23072	3
	orf00042	23164	23045	-2
	orf00044	24206	23292	-3
	orf00046	25622	24372	-3
	orf00047	25657	25761	1
	orf00048	26131	25754	-2
	orf00050	26267	27424	2
	orf00052	28950	27637	-1
	orf00056	29172	28987	-1
	orf00057	29793	29275	-1
	orf00058	30512	30381	-3
	orf00059	30782	30660	-3
	orf00060	30792	31169	3
	orf00062	31250	32725	2
	orf00064	33208	32924	-2
	orf00065	33383	33937	2
	orf00067	34056	35957	3
	orf00068	37339	36389	-2
	orf00069	37468	37584	1
	orf00072	38618	37617	-3
	orf00075	39497	38772	-3
	orf00076	39902	39636	-3
	orf00077	40085	41626	2
	orf00079	43243	41678	-2
	orf00080	43249	43371	1
>contig00149				
	orf00001	751	428	-2
	orf00002	1367	801	-3
	orf00004	1640	1861	2
	orf00006	2023	2754	1
	orf00009	5200	2828	-2
	orf00010	5674	5219	-2
	orf00011	5846	5700	-3
	orf00013	6919	5852	-2
	orf00016	8634	7351	-1
	orf00017	10750	8627	-2
	orf00018	11293	10754	-2
	orf00019	12566	11313	-3
	orf00021	12745	12569	-2
	orf00022	12744	13028	3
	orf00023	13661	13140	-3
	orf00025	14721	13795	-1
	orf00028	15530	14949	-3
	orf00029	15772	17013	1
	orf00033	18090	17470	-1
	orf00035	20799	18979	-1
	orf00036	21901	21041	-2
	orf00037	23037	22108	-1

Contig	ORF	Start	End	Frame
	orf00038	23204	25102	2
	orf00040	26610	25147	-1
	orf00041	27058	27294	1
	orf00042	27469	28716	1
	orf00046	29607	29080	-1
	orf00047	29878	30468	1
	orf00050	32119	30608	-2
	orf00051	32425	32988	1
	orf00052	33275	33712	2
	orf00054	33760	34029	1
	orf00056	34038	35816	3
	orf00061	36385	39240	1
>contig00150				
	orf00001	-2	786	1
	orf00004	2077	2217	1
>contig00151				
	orf00001	182	286	2
	orf00002	283	387	1
	orf00003	393	1772	3
	orf00004	1796	2221	2
	orf00007	2354	2887	2
	orf00009	3481	4953	1
	orf00010	5097	5960	3
	orf00012	6239	7045	2
	orf00014	7130	7020	-3
	orf00015	8008	7127	-2
	orf00016	8467	9525	1
	orf00017	9802	9617	-2
	orf00018	9872	10144	2
	orf00020	10156	11514	1
	orf00023	11618	12085	2
	orf00024	12295	12402	1
	orf00026	12447	13163	3
	orf00028	13310	14392	2
	orf00030	14509	15279	1
	orf00032	15384	16484	3
	orf00033	16632	16465	-1
	orf00036	16714	17178	1
	orf00037	17185	17295	1
	orf00038	17391	17507	3
	orf00041	20356	17747	-2
	orf00042	21531	21037	-1
	orf00043	22358	21528	-3
	orf00044	23251	22355	-2
	orf00046	24837	23530	-1
	orf00050	27065	25095	-3
	orf00053	29543	27219	-3
	orf00054	30769	29894	-2

Contig	ORF	Start	End	Frame
	orf00056	31685	31801	2
	orf00057	31659	30829	-1
	orf00059	31960	32826	1
	orf00060	32908	34449	1
	orf00061	34723	35586	1
	orf00063	36164	35748	-3
	orf00064	36913	36413	-2
	orf00065	36992	37303	2
	orf00066	37430	38056	2
	orf00068	38310	38519	3
>contig00152				
	orf00001	-2	168	1
	orf00003	721	161	-2
	orf00005	1372	827	-2
	orf00006	2288	1719	-3
	orf00008	3812	2292	-3
	orf00010	3869	4027	2
	orf00011	4191	4075	-1
	orf00012	4462	4352	-2
	orf00014	4475	6454	2
	orf00016	6575	6465	-3
	orf00018	6745	8757	1
	orf00021	8920	9699	1
	orf00022	10221	10466	3
>contig00153				
>contig00154				
	orf00001	312	181	-1
	orf00002	774	331	-1
>contig00155				
	orf00001	665	165	-3
	orf00004	1339	1184	-2
>contig00156				
	orf00001	459	-2	-1
>contig00157				
	orf00001	1096	209	-2
>contig00158				
	orf00001	0	473	3
>contig00159				
>contig00160				
>contig00161				
	orf00001	1009	260	-2
	orf00003	1425	1117	-1
	orf00004	2132	1422	-3
	orf00005	2486	3367	2
	orf00006	3440	4567	2
	orf00007	4850	4728	-3
	orf00008	4862	5668	2
	orf00010	6332	5763	-3

Contig	ORF	Start	End	Frame
>contig00162				
	orf00001	1058	105	-3
	orf00002	1363	1256	-2
	orf00004	1398	2192	3
	orf00006	3384	2533	-1
	orf00007	4378	3455	-2
	orf00008	4454	5239	2
	orf00009	5569	5429	-2
	orf00010	5599	6738	1
	orf00011	6832	8961	1
	orf00012	9052	10278	1
	orf00014	10536	11846	3
	orf00016	11824	11928	1
	orf00020	13391	12099	-3
	orf00021	13843	13445	-2
	orf00022	16219	14174	-2
	orf00024	16624	17259	1
	orf00026	17443	17547	1
	orf00028	19298	19173	-3
	orf00029	19086	17608	-1
	orf00030	19855	19727	-2
	orf00032	21128	19869	-3
	orf00033	21407	21294	-3
	orf00037	22633	21611	-2
	orf00038	23393	22728	-3
	orf00039	23646	23473	-1
	orf00040	25262	23646	-3
	orf00041	26365	25475	-2
	orf00042	26959	26387	-2
	orf00043	27930	27136	-1
	orf00044	29058	27943	-1
	orf00045	29177	29055	-3
	orf00046	30007	29258	-2
	orf00048	30566	30135	-3
	orf00049	30887	32068	2
	orf00052	32165	34102	2
	orf00054	34196	34870	2
>contig00163				
	orf00001	165	-2	-1
>contig00164				
>contig00165				
	orf00001	138	1	-1
>contig00166				
>contig00167				
	orf00001	832	197	-2
	orf00002	836	997	2
	orf00004	1545	1051	-1
	orf00005	1935	1561	-1

Contig	ORF	Start	End	Frame
	orf00007	2557	1988	-2
	orf00009	2908	2639	-2
	orf00010	3232	3360	1
	orf00013	4858	3401	-2
	orf00015	5785	5156	-2
	orf00016	7105	5786	-2
	orf00017	7540	7406	-2
	orf00019	8379	9251	3
	orf00020	9256	9366	1
	orf00021	10621	9350	-2
	orf00022	10842	10717	-1
	orf00024	12051	10990	-1
	orf00026	13394	12171	-3
	orf00027	14905	13391	-2
	orf00028	15614	14892	-3
	orf00029	16205	15909	-3
	orf00032	17180	16221	-3
	orf00033	17721	17314	-1
	orf00035	17938	19014	1
	orf00036	19986	20183	3
	orf00038	20317	20799	1
	orf00039	21117	21338	3
	orf00041	22091	21561	-3
>contig00168				
	orf00001	0	461	3
>contig00169				
	orf00001	0	380	3

Appendix B

BLAST analysis of *N. sicca* 4320 ORFs with DanAnn database.

The amino acid sequences of the identified *N. sicca* 4320 ORFs were BLASTed against the DanAnn database. Query: *N. sicca* 4320 ORF. Subject: Database match to query. Subject ID: Identification number of match to query. %ID: Percent identity between query and subject. E Value: Expectation value; number of similar matches that would occur by chance.

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00001-orf00001	glutathione synthetase [Neisseria meningitidis MC58]	gi|15677410|ref|NP 274566.1|	93.67	8E-166
contig00001-orf00003	diacylglycerol kinase [Neisseria gonorrhoeae FA 1090]	gi|59801575|ref|YP 208287.1|	73.81	3E-46
contig00001-orf00004	hypothetical protein NMA1745 [Neisseria meningitidis Z2491]	gi|15794638|ref|NP 284460.1|	85.31	6E-67
contig00001-orf00005	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Neisseria meningitidis Z2491]	gi|15794637|ref|NP 284459.1|	94.81	0
contig00001-orf00008	long-chain-fatty-acid--CoA-ligase [Neisseria meningitidis MC58]	gi|15677406|ref|NP 274562.1|	89.67	0
contig00001-orf00010	PhoH-related protein [Neisseria meningitidis MC58]	gi|15676741|ref|NP 273886.1|	85.06	2E-143
contig00001-orf00012	guanosine-3',5'-bis(diphosphate) 3'-pyrophophohydrolase [Neisseria meningitidis Z2491]	gi|15794802|ref|NP 284624.1|	89.55	0
contig00001-orf00013	DNA-directed RNA polymerase omega chain [Neisseria meningitidis Z2491]	gi|15794803|ref|NP 284625.1|	92.65	1E-29
contig00001-orf00015	KguA [Neisseria gonorrhoeae FA 1090]	gi|59801662|ref|YP 208374.1|	78.54	2E-85
contig00001-orf00016	adenine phosphoribosyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801663|ref|YP 208375.1|	90.32	6E-91
contig00001-orf00019	putative soluble lytic murein transglycosylase [Neisseria meningitidis MC58]	gi|15677779|ref|NP 274943.1|	71.9	0
contig00001-orf00020	transposase [Haemophilus influenzae Rd KW20]	gi|30995473|ref|NP 439862.2|	52.11	3E-35
contig00002-orf00001	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	gi|59801514|ref|YP 208226.1|	44.93	2E-11
contig00002-orf00003	hypothetical protein NMA1999 [Neisseria meningitidis Z2491]	gi|15794879|ref|NP 284701.1|	58.22	5E-99
contig00002-orf00005	hypothetical protein NMA2000 [Neisseria meningitidis Z2491]	gi|15794880|ref|NP 284702.1|	69.44	2E-08
contig00002-orf00006	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801628|ref|YP 208340.1|	53.97	2E-10
contig00002-orf00007	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801627|ref|YP 208339.1|	75	1E-13
contig00002-orf00008	hypothetical protein NMA0778 [Neisseria meningitidis Z2491]	gi|15793753|ref|NP 283575.1|	78.57	2E-27
contig00003-orf00001	putative integrase [Shigella flexneri 5 str. 8401]	gi|110804320|ref|YP 687840.1|	53.71	7E-64
contig00004-orf00003	choline-glycine betaine transporter [Haemophilus influenzae 86-028NP]	gi|68250309|ref|YP 249421.1|	72.35	0
contig00004-orf00006	NH(3)-dependent NAD synthetase [Neisseria meningitidis Z2491]	gi|15794469|ref|NP 284291.1|	77.1	2E-113
contig00004-orf00008	heavy metal translocating P-type ATPase [Methylobacillus flagellatus KT]	gi|91774990|ref|YP 544746.1|	34.15	4.5
contig00004-orf00009	site-specific recombinase [Neisseria meningitidis Z2491]	gi|15794385|ref|NP 284207.1|	86.04	0
contig00005-orf00001	hypothetical protein NGO0318 [Neisseria gonorrhoeae FA 1090]	gi|59800765|ref|YP 207477.1|	89.49	0
contig00005-orf00002	acetate kinase [Neisseria meningitidis MC58]	gi|15677371|ref|NP 274526.1|	93.72	0
contig00005-orf00006	hypothetical protein NMA1717 [Neisseria meningitidis Z2491]	gi|15794610|ref|NP 284432.1|	74.26	1E-35
contig00005-orf00007	inner membrane protein [Neisseria meningitidis Z2491]	gi|15794609|ref|NP 284431.1|	95.83	6E-21
contig00005-orf00008	putative transporter [Neisseria meningitidis MC58]	gi|15677368|ref|NP 274523.1|	81.73	0
contig00006-orf00001	endopeptidase [Neisseria meningitidis Z2491]	gi|15794419|ref|NP 284241.1|	96.12	6E-102
contig00006-orf00003	trigger factor [Neisseria meningitidis Z2491]	gi|15794420|ref|NP 284242.1|	96.33	0
contig00006-orf00007	lipoprotein [Chromobacterium violaceum ATCC 12472]	gi|34498817|ref|NP 903032.1|	44.38	9E-35
contig00006-orf00009	phosphoenolpyruvate synthase [Neisseria meningitidis MC58]	gi|15676521|ref|NP 273662.1|	97.36	0
contig00006-orf00010	hypothetical protein NMA0827 [Neisseria meningitidis Z2491]	gi|15793798|ref|NP 283620.1|	87.18	2E-137
contig00006-orf00013	ABC transporter periplasmic protein [Haemophilus influenzae 86-028NP]	gi|68250044|ref|YP 249156.1|	53.82	2E-77
contig00007-orf00001	integrase/recombinase XerD [Neisseria meningitidis MC58]	gi|15676649|ref|NP 273793.1|	70.45	9E-109

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00008-orf00001	oligoribonuclease [Neisseria meningitidis Z2491]	gi|15793584|ref|NP 283406.1|	87.01	3E-88
contig00008-orf00005	enoyl-(acyl carrier protein) reductase [Neisseria meningitidis Z2491]	gi|15795023|ref|NP 284845.1|	96.54	1E-138
contig00008-orf00008	large conductance mechanosensitive channel protein [Methylobacillus flagellatus KT]	gi|91775002|ref|YP 544758.1|	63.83	6E-29
contig00008-orf00011	Hsp33-like chaperonin [Neisseria meningitidis Z2491]	gi|15793446|ref|NP 283268.1|	83.45	1E-118
contig00008-orf00014	ubiquinone biosynthesis protein [Chromobacterium violaceum ATCC 12472]	gi|34498422|ref|NP 902637.1|	43.97	1E-130
contig00008-orf00016	GNA2001 [Neisseria gonorrhoeae FA 1090]	gi|59801550|ref|YP 208262.1|	86.92	6E-62
contig00008-orf00017	hypothetical protein NMA0439 [Neisseria meningitidis Z2491]	gi|15793444|ref|NP 283266.1|	88.41	1E-30
contig00008-orf00022	amino-acid transport protein [Neisseria meningitidis Z2491]	gi|15793102|ref|NP 282924.1|	87.1	0
contig00008-orf00026	glucose-inhibited division protein B [Neisseria meningitidis Z2491]	gi|15793106|ref|NP 282928.1|	74.76	4E-85
contig00008-orf00028	hypothetical protein MK1300 [Methanopyrus kandleri AV19]	gi|20094736|ref|NP 614583.1|	52	2.6
contig00008-orf00032	ribosomal large subunit pseudouridine synthase C [Neisseria meningitidis Z2491]	gi|15793099|ref|NP 282921.1|	87.31	9E-153
contig00008-orf00039	ribonuclease E [Neisseria meningitidis MC58]	gi|15676123|ref|NP 273254.1|	78.95	0
contig00008-orf00041	hypothetical protein NMB1129 [Neisseria meningitidis MC58]	gi|15677006|ref|NP 274158.1|	76.47	1E-29
contig00008-orf00043	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793078|ref|NP 282900.1|	81.44	9E-167
contig00008-orf00046	integral membrane signal transducer protein [Neisseria meningitidis Z2491]	gi|15794998|ref|NP 284820.1|	73.25	5E-154
contig00008-orf00048	50S ribosomal protein L3 [Neisseria meningitidis Z2491]	gi|15793157|ref|NP 282979.1|	99.07	5E-106
contig00008-orf00049	50S ribosomal protein L4 [Neisseria meningitidis Z2491]	gi|15793156|ref|NP 282978.1|	99.03	1E-110
contig00008-orf00050	50S ribosomal protein L23 [Neisseria meningitidis Z2491]	gi|15793155|ref|NP 282977.1|	100	3E-27
contig00008-orf00052	50S ribosomal protein L2 [Neisseria meningitidis Z2491]	gi|15793154|ref|NP 282976.1|	99.28	6E-142
contig00008-orf00053	30S ribosomal protein S19 [Neisseria meningitidis Z2491]	gi|15793153|ref|NP 282975.1|	100	1E-09
contig00008-orf00054	50S ribosomal protein L22 [Neisseria meningitidis Z2491]	gi|15793152|ref|NP 282974.1|	99.08	2E-54
contig00008-orf00055	30S ribosomal protein S3 [Neisseria meningitidis Z2491]	gi|15793151|ref|NP 282973.1|	96.31	7E-115
contig00008-orf00056	50S ribosomal protein L16 [Neisseria meningitidis Z2491]	gi|15793150|ref|NP 282972.1|	96.43	5E-15
contig00008-orf00057	50S ribosomal protein L29 [Neisseria meningitidis Z2491]	gi|15793149|ref|NP 282971.1|	95.24	6E-27
contig00008-orf00058	50S ribosomal protein L24 [Neisseria meningitidis Z2491]	gi|15793146|ref|NP 282968.1|	94.03	8E-31
contig00008-orf00059	50S ribosomal protein L5 [Neisseria meningitidis Z2491]	gi|15793145|ref|NP 282967.1|	100	1E-11
contig00008-orf00060	30S ribosomal protein S14 [Neisseria meningitidis Z2491]	gi|15793144|ref|NP 282966.1|	94.06	2E-47
contig00008-orf00062	50S ribosomal protein L6 [Neisseria meningitidis Z2491]	gi|15793142|ref|NP 282964.1|	96.08	6E-50
contig00008-orf00064	50S ribosomal protein L15 [Neisseria meningitidis MC58]	gi|15676088|ref|NP 273219.1|	83.53	5E-34
contig00008-orf00065	preprotein translocase subunit SecY [Neisseria meningitidis Z2491]	gi|15793137|ref|NP 282959.1|	86.27	0
contig00008-orf00066	30S ribosomal protein S13 [Neisseria meningitidis Z2491]	gi|15793134|ref|NP 282956.1|	100	1E-12
contig00008-orf00067	DNA-directed RNA polymerase subunit alpha [Neisseria meningitidis Z2491]	gi|15793131|ref|NP 282953.1|	94.21	2E-174
contig00008-orf00070	oxidoreductase [Neisseria meningitidis Z2491]	gi|15793372|ref|NP 283194.1|	93.41	1E-174
contig00008-orf00071	hypothetical protein PFL 2399 [Pseudomonas fluorescens Pf-5]	gi|70729767|ref|YP 259506.1|	45.39	8E-32
contig00008-orf00072	hypothetical protein MS2110 [Mannheimia succiniciproducens MBEL55E]	gi|52426165|ref|YP 089302.1|	53.42	6E-60
contig00008-orf00075	thiamin-phosphate pyrophosphorylase [Neisseria meningitidis MC58]	gi|15677891|ref|NP 275059.1|	95.08	2E-84

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contig00008-orf00076	putative oxidoreductase [Gluconobacter oxydans 621H]	gi|58038345|ref|YP 190314.1|	59.23	9E-100
contig00008-orf00077	hypothetical protein Atu0997 [Agrobacterium tumefaciens str. C58]	gi|17934905|ref|NP 531695.1|	63.74	9E-28
contig00008-orf00079	cysteinyl-tRNA synthetase [Mesoplasma florum L1]	gi|50364902|ref|YP 053327.1|	31.09	0.54
contig00008-orf00080	thiamine biosynthesis protein ThiS [Neisseria meningitidis MC58]	gi|15677892|ref|NP 275060.1|	93.75	6E-27
contig00008-orf00081	thiazole synthase [Neisseria meningitidis MC58]	gi|15677893|ref|NP 275061.1|	98.09	2E-145
contig00008-orf00083	DNA polymerase I [Neisseria meningitidis Z2491]	gi|15793464|ref|NP 283286.1|	92.21	0
contig00008-orf00086	hypothetical protein NMB2064 [Neisseria meningitidis MC58]	gi|15677886|ref|NP 275054.1|	81.61	0
contig00008-orf00087	hypothetical protein NMA0371 [Neisseria meningitidis Z2491]	gi|15793379|ref|NP 283201.1|	72	2E-23
contig00008-orf00090	hypothetical protein NMA0573 [Neisseria meningitidis Z2491]	gi|15793564|ref|NP 283386.1|	80.81	1E-42
contig00008-orf00091	protein-L-isoaspartate O-methyltransferase [Neisseria meningitidis Z2491]	gi|15793563|ref|NP 283385.1|	92.2	2E-108
contig00008-orf00094	hypothetical protein NMB1886 [Neisseria meningitidis MC58]	gi|15677721|ref|NP 274882.1|	95.71	2E-86
contig00008-orf00096	triosephosphate isomerase [Neisseria meningitidis MC58]	gi|15677722|ref|NP 274883.1|	97.25	3E-139
contig00008-orf00097	preprotein translocase subunit SecG [Neisseria meningitidis Z2491]	gi|15793560|ref|NP 283382.1|	93.48	6E-16
contig00008-orf00098	putative prophage integrase [Escherichia coli CFT073]	gi|26250313|ref|NP 756353.1|	48.06	6E-30
contig00008-orf00100	hypothetical protein NMB2018 [Neisseria meningitidis MC58]	gi|15677843|ref|NP 275010.1|	70.35	6E-77
contig00008-orf00102	hypothetical protein Sfri 0575 [Shewanella frigidimarina NCIMB 400]	gi|114561761|ref|YP 749274.1|	54.95	4E-45
contig00008-orf00103	hypothetical protein Bamb 4365 [Burkholderia ambifaria AMMD]	gi|115359113|ref|YP 776251.1|	40.54	9E-18
contig00008-orf00104	putative signal recognition particle protein [Neisseria gonorrhoeae FA 1090]	gi|59802021|ref|YP 208733.1|	91.45	0
contig00008-orf00106	CcsA-related protein [Neisseria meningitidis MC58]	gi|15676218|ref|NP 273350.1|	78.73	4E-103
contig00009-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	91.67	3E-37
contig00009-orf00003	hypothetical protein NMA0426A [Neisseria meningitidis Z2491]	gi|15793431|ref|NP 283253.1|	78.67	2E-24
contig00009-orf00004	hypothetical protein PBPRB0630 [Photobacterium profundum SS9]	gi|54302310|ref|YP 132303.1|	44.1	6E-101
contig00009-orf00005	hypothetical protein PBPRB0631 [Photobacterium profundum SS9]	gi|54302311|ref|YP 132304.1|	52.46	8E-134
contig00009-orf00006	HrpA [Neisseria gonorrhoeae FA 1090]	gi|59801559|ref|YP 208271.1|	93.42	0
contig00010-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	100	7E-20
contig00010-orf00003	hypothetical protein NMB1066 [Neisseria meningitidis MC58]	gi|15676950|ref|NP 274099.1|	62.22	5E-74
contig00010-orf00004	cell-division protein [Neisseria meningitidis Z2491]	gi|15794199|ref|NP 284021.1|	92.99	0
contig00010-orf00007	hypothetical protein NGO0899 [Neisseria gonorrhoeae FA 1090]	gi|59801297|ref|YP 208009.1|	94.3	2E-63
contig00010-orf00009	polynucleotide phosphorylase/polyadenylase [Neisseria meningitidis Z2491]	gi|15793926|ref|NP 283748.1|	96.83	0
contig00010-orf00012	hypothetical protein NGO0532 [Neisseria gonorrhoeae FA 1090]	gi|59800970|ref|YP 207682.1|	61.11	2E-124
contig00010-orf00013	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794379|ref|NP 284201.1|	60.17	3E-115
contig00010-orf00015	polysaccharide modification protein [Neisseria meningitidis Z2491]	gi|15794378|ref|NP 284200.1|	75.94	0
contig00010-orf00018	glycogen phosphorylase [Haemophilus somnus 129PT]	gi|113461028|ref|YP 719095.1|	61.04	0
contig00010-orf00020	Glgx [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602407|ref|NP 245479.1|	53.23	0
contig00010-orf00021	#N/A	#N/A	#N/A	#N/A
contig00010-orf00022	AcrA protein [Mannheimia succiniciproducens MBEL55E]	gi|52425356|ref|YP 088493.1|	49.28	2E-69
contig00010-orf00024	extracellular solute-binding protein [Mycobacterium sp. MCS]	gi|108801003|ref|YP 641200.1|	33.33	2.3

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contig00010-orf00025	anthranilate phosphoribosyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801562|ref|YP 208274.1|	88.01	2E-146
contig00010-orf00027	anthranilate synthase component II [Neisseria gonorrhoeae FA 1090]	gi|59801563|ref|YP 208275.1|	89.58	6E-98
contig00010-orf00030	prophage CP4-57 regulatory [Ralstonia eutropha JMP134]	gi|73542058|ref|YP 296578.1|	40.32	3E-08
contig00010-orf00032	hypothetical protein SAR11 0011 [Candidatus Pelagibacter ubique HTCC1062]	gi|71082720|ref|YP 265439.1|	38.53	5E-14
contig00010-orf00035	modification methylase Bsp6I-like [Haemophilus influenzae 86-028NP]	gi|68249848|ref|YP 248960.1|	56.96	3E-114
contig00010-orf00036	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801944|ref|YP 208656.1|	84.92	5E-156
contig00010-orf00038	imidazoleglycerol-phosphate dehydratase [Sulfolobus acidocaldarius DSM 639]	gi|70607313|ref|YP 256183.1|	32.84	0.41
contig00010-orf00039	single-stranded binding protein [Neisseria meningitidis Z2491]	gi|15794566|ref|NP 284388.1|	60.47	2E-50
contig00010-orf00040	TonB-dependent receptor [Xanthomonas campestris pv. campestris str. ATCC 33913]	gi|77747725|ref|NP 635445.2|	33.96	0.24
contig00010-orf00041	hypothetical protein BURPS1710b A1695 [Burkholderia pseudomallei 1710b]	gi|76817970|ref|YP 336852.1|	28.22	0.03
contig00010-orf00042	exonuclease VIII [Escherichia coli APEC O1]	gi|117623600|ref|YP 852513.1|	37.64	1E-38
contig00010-orf00043	putative periplasmic protein [Dehalococcoides sp. CBDB1]	gi|73748881|ref|YP 308120.1|	30.16	2
contig00010-orf00045	putative lipoprotein [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]	gi|29142378|ref|NP 805720.1|	32.43	0.056
contig00010-orf00047	hypothetical protein pNG6182 [Haloarcula marismortui ATCC 43049]	gi|55376571|ref|YP 134423.1|	40.43	1.2
contig00010-orf00050	type III restriction enzyme, res subunit [Silicibacter sp. TM1040]	gi|99078512|ref|YP 611770.1|	28.79	2.6
contig00010-orf00051	hypothetical protein BLi02293 [Bacillus licheniformis ATCC 14580]	gi|52786037|ref|YP 091866.1|	44.83	3.5
contig00010-orf00053	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801955|ref|YP 208667.1|	90.91	1E-65
contig00010-orf00055	transcriptional regulator [Haemophilus influenzae 86-028NP]	gi|68250056|ref|YP 249168.1|	60.32	6E-43
contig00010-orf00056	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801959|ref|YP 208671.1|	97.22	0.00003
contig00010-orf00057	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801960|ref|YP 208672.1|	79.03	2E-18
contig00010-orf00058	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801479|ref|YP 208191.1|	77.33	3E-27
contig00010-orf00059	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801963|ref|YP 208675.1|	65.28	2E-20
contig00010-orf00061	putative DNA replication protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801964|ref|YP 208676.1|	80.98	1E-83
contig00010-orf00062	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801476|ref|YP 208188.1|	56.52	5E-10
contig00010-orf00065	hypothetical protein lmo2268 [Listeria monocytogenes EGD-e]	gi|16804307|ref|NP 465792.1|	58.33	5.9
contig00010-orf00067	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800927|ref|YP 207639.1|	63.11	3E-32
contig00010-orf00068	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801470|ref|YP 208182.1|	41.98	2E-25
contig00010-orf00069	hypothetical protein Nmul A1530 [Nitrosospira multiformis ATCC 25196]	gi|82702659|ref|YP 412225.1|	32.73	0.037
contig00010-orf00071	hypothetical protein UTI89 C2655 [Escherichia coli UTI89]	gi|91211666|ref|YP 541652.1|	63.08	1E-45
contig00010-orf00072	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800933|ref|YP 207645.1|	90.49	0
contig00010-orf00073	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800934|ref|YP 207646.1|	88.66	0
contig00010-orf00074	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800935|ref|YP 207647.1|	83.96	4E-137
contig00010-orf00075	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800936|ref|YP 207648.1|	91.32	0
contig00010-orf00076	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800937|ref|YP 207649.1|	82.54	6E-23
contig00010-orf00077	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800938|ref|YP 207650.1|	72.73	3E-69

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contig00010-orf00078	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800939|ref|YP 207651.1|	70	3E-38
contig00010-orf00079	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800940|ref|YP 207652.1|	89.44	1E-72
contig00010-orf00081	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800941|ref|YP 207653.1|	82.88	1E-120
contig00010-orf00082	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800942|ref|YP 207654.1|	85.26	6E-40
contig00010-orf00084	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800943|ref|YP 207655.1|	92.05	2E-43
contig00010-orf00085	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800944|ref|YP 207656.1|	92.96	3E-106
contig00010-orf00086	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800945|ref|YP 207657.1|	89.53	8E-75
contig00010-orf00087	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800946|ref|YP 207658.1|	71.11	6E-55
contig00010-orf00088	DNA topoisomerase IV subunit A [Geobacillus kaustophilus HTA426]	gi|56420285|ref|YP 147603.1|	30.3	0.18
contig00010-orf00090	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800948|ref|YP 207660.1|	85.11	0
contig00010-orf00091	hypothetical protein NGO0511 [Neisseria gonorrhoeae FA 1090]	gi|59800949|ref|YP 207661.1|	36.17	4E-11
contig00010-orf00092	putative tail length tape measure protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800960|ref|YP 207672.1|	73.79	0
contig00010-orf00093	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800951|ref|YP 207663.1|	53.49	7E-36
contig00010-orf00095	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800952|ref|YP 207664.1|	52.13	4E-14
contig00010-orf00096	peptidase M15A [Pseudomonas putida KT2440]	gi|26988833|ref|NP 744258.1|	38.04	0.0000008
contig00010-orf00097	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801977|ref|YP 208689.1|	53.1	1E-25
contig00010-orf00100	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801148|ref|YP 207860.1|	39.68	0.0003
contig00010-orf00101	AbpK sensory transduction histidine kinase [Lactobacillus salivarius UCC118]	gi|90962885|ref|YP 536800.1|	31.25	1.2
contig00010-orf00102	hypothetical protein PCP51 [Clostridium perfringens str. 13]	gi|15081531|ref|NP 150044.1|	32.63	0.53
contig00010-orf00103	prophage PSPPH01, site-specific recombinase phage integrase family protein [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71734594|ref|YP 272965.1|	42.34	8E-77
contig00010-orf00104	hypothetical protein XOO 2892 [Xanthomonas oryzae pv. oryzae MAFF 311018]	gi|84624549|ref|YP 451921.1|	54.55	1.2
contig00010-orf00106	hypothetical protein Bxe A4326 [Burkholderia xenovorans LB400]	gi|91781520|ref|YP 556726.1|	31.25	1E-19
contig00010-orf00107	hypothetical protein CV 3590 [Chromobacterium violaceum ATCC 12472]	gi|34499045|ref|NP 903260.1|	45.65	0.003
contig00010-orf00109	hypothetical protein NGO0818 [Neisseria gonorrhoeae FA 1090]	gi|59801229|ref|YP 207941.1|	49.23	5E-10
contig00010-orf00111	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677112|ref|NP 274264.1|	97.6	0
contig00010-orf00113	superoxide dismutase [Neisseria meningitidis Z2491]	gi|15794051|ref|NP 283873.1|	98.45	1E-102
contig00010-orf00114	replicative DNA helicase [Neisseria meningitidis Z2491]	gi|15794052|ref|NP 283874.1|	94.23	0
contig00010-orf00115	hypothetical protein NMA1106 [Neisseria meningitidis Z2491]	gi|15794053|ref|NP 283875.1|	53.92	2E-61
contig00010-orf00116	putative type IV pilus assembly protein PilV [Neisseria meningitidis MC58]	gi|15676783|ref|NP 273928.1|	46.27	8E-31
contig00010-orf00117	membrane protein [Neisseria meningitidis Z2491]	gi|15794055|ref|NP 283877.1|	45.32	5E-70
contig00010-orf00120	pilin [Neisseria meningitidis Z2491]	gi|15794057|ref|NP 283879.1|	47.71	3E-30
contig00010-orf00123	pantoate--beta-alanine ligase [Neisseria meningitidis MC58]	gi|15676767|ref|NP 273912.1|	85.2	3E-132
contig00010-orf00126	3-methyl-2-oxobutanoate hydroxymethyltransferase [Neisseria meningitidis Z2491]	gi|15794036|ref|NP 283858.1|	92.75	5E-116

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contig00010-orf00127	spermidine synthase [Neisseria meningitidis Z2491]	gi|15794035|ref|NP 283857.1|	88.21	5E-136
contig00010-orf00128	glutamyl-tRNA reductase [Neisseria gonorrhoeae FA 1090]	gi|59801748|ref|YP 208460.1|	84.82	0
contig00010-orf00129	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	90.24	4E-15
contig00010-orf00130	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	100	1E-23
contig00010-orf00133	hypothetical protein Sden 1113 [Shewanella denitrificans OS217]	gi|91792473|ref|YP 562124.1|	35.44	9E-09
contig00010-orf00134	hypothetical protein SCO7003 [Streptomyces coelicolor A3(2)]	gi|21225289|ref|NP 631068.1|	41.67	6
contig00010-orf00136	galactose mutarotase-like protein [Lactobacillus brevis ATCC 367]	gi|116333449|ref|YP 794976.1|	31.91	5.4
contig00010-orf00137	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801141|ref|YP 207853.1|	25.89	7E-11
contig00010-orf00138	hypothetical protein NTHI0420 [Haemophilus influenzae 86-028NP]	gi|68248909|ref|YP 248021.1|	41.43	7E-25
contig00010-orf00139	putative transposase [Neisseria meningitidis MC58]	gi|15677452|ref|NP 274608.1|	55.32	0.000001
contig00011-orf00001	cell wall biosynthesis glycosyltransferase-like protein [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	gi|78355477|ref|YP 386926.1|	50	0.004
contig00011-orf00002	glycosyltransferase [Lactobacillus salivarius UCC118]	gi|90962544|ref|YP 536460.1|	27.54	3E-14
contig00011-orf00003	virulence factor MviN [Neisseria meningitidis MC58]	gi|15676201|ref|NP 273333.1|	93.04	6E-169
contig00011-orf00004	putative virulence factor, membrane protein [Pseudomonas aeruginosa UCBPP-PA14]	gi|116052705|ref|YP 793021.1|	75.79	3E-47
contig00011-orf00005	virulence factor MviN [Neisseria meningitidis MC58]	gi|15676201|ref|NP 273333.1|	94.44	0.18
contig00011-orf00008	thiol:disulphide interchange protein [Neisseria meningitidis Z2491]	gi|15795078|ref|NP 284900.1|	85.05	7E-84
contig00011-orf00010	GTPase ObgE [Neisseria gonorrhoeae FA 1090]	gi|59802298|ref|YP 209010.1|	97.14	0
contig00011-orf00011	cysteinyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793358|ref|NP 283180.1|	97.46	0
contig00011-orf00012	putative acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802423|ref|YP 209135.1|	67.06	2E-55
contig00011-orf00014	50S ribosomal protein L31 [Neisseria meningitidis Z2491]	gi|15793494|ref|NP 283316.1|	91.55	4E-35
contig00011-orf00015	hypothetical protein NGO2128 [Neisseria gonorrhoeae FA 1090]	gi|59802426|ref|YP 209138.1|	73.36	0
contig00011-orf00019	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793492|ref|NP 283314.1|	75.71	1E-58
contig00011-orf00020	hypothetical protein NMA0492 [Neisseria meningitidis Z2491]	gi|15793491|ref|NP 283313.1|	60.63	1E-37
contig00011-orf00021	hypothetical protein NMA0491 [Neisseria meningitidis Z2491]	gi|15793490|ref|NP 283312.1|	95.83	2E-65
contig00011-orf00022	TonB-dependent receptor protein [Neisseria meningitidis Z2491]	gi|15795063|ref|NP 284885.1|	88.03	3E-146
contig00011-orf00024	putative TonB-dependent receptor [Neisseria meningitidis MC58]	gi|15676215|ref|NP 273347.1|	93.28	0
contig00011-orf00026	phosphopantetheine adenylyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802386|ref|YP 209098.1|	77.64	7E-71
contig00011-orf00028	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793425|ref|NP 283247.1|	71.49	3E-79
contig00011-orf00030	TbpB [Neisseria gonorrhoeae FA 1090]	gi|59801834|ref|YP 208546.1|	25.97	0.00009
contig00011-orf00031	orotate phosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15793573|ref|NP 283395.1|	91.51	8E-99
contig00011-orf00033	hypothetical protein NMB1875 [Neisseria meningitidis MC58]	gi|15677710|ref|NP 274871.1|	49.07	6E-27
contig00011-orf00034	N-acetylglutamate synthase [Neisseria meningitidis Z2491]	gi|15793571|ref|NP 283393.1|	64.02	3E-135
contig00011-orf00036	hypothetical protein VP2903 [Vibrio parahaemolyticus RIMD 2210633]	gi|28899677|ref|NP 799282.1|	40.27	1E-85
contig00011-orf00038	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA [Neisseria meningitidis Z2491]	gi|15793103|ref|NP 282925.1|	97.29	0

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00011-orf00039	#N/A	#N/A	#N/A	#N/A
contig00011-orf00041	uridylate kinase [Neisseria gonorrhoeae FA 1090]	gi|59802282|ref|YP 208994.1|	99.16	7E-116
contig00011-orf00043	elongation factor Ts [Neisseria meningitidis Z2491]	gi|15793339|ref|NP 283161.1|	97.01	5E-135
contig00011-orf00045	30S ribosomal protein S2 [Neisseria meningitidis Z2491]	gi|15793340|ref|NP 283162.1|	98.19	7E-121
contig00011-orf00047	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793341|ref|NP 283163.1|	84.85	2E-25
contig00011-orf00048	hypothetical protein NMA0330 [Neisseria meningitidis Z2491]	gi|15793342|ref|NP 283164.1|	87.56	2E-89
contig00011-orf00049	hypothetical protein NMA0331 [Neisseria meningitidis Z2491]	gi|15793343|ref|NP 283165.1|	71.35	3E-71
contig00011-orf00051	#N/A	#N/A	#N/A	#N/A
contig00011-orf00052	malate:quinone oxidoreductase [Neisseria meningitidis Z2491]	gi|15793344|ref|NP 283166.1|	90.57	0
contig00011-orf00055	hypothetical protein NMA2208 [Neisseria meningitidis Z2491]	gi|15795077|ref|NP 284899.1|	88.32	4E-153
contig00011-orf00057	solvent tolerance protein [Neisseria meningitidis Z2491]	gi|15795076|ref|NP 284898.1|	62.17	0
contig00011-orf00058	peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58]	gi|15676205|ref|NP 273337.1|	67.2	5E-105
contig00011-orf00063	putative signalling protein [Xanthomonas campestris pv. vesicatoria str. 85-10]	gi|78048416|ref|YP 364591.1|	30.77	2.6
contig00011-orf00068	phosphoesterase, PA-phosphatase-related protein [Deinococcus geothermalis DSM 11300]	gi|94972215|ref|YP 594255.1|	58.33	5E-18
contig00011-orf00069	hypothetical protein NMB0276 [Neisseria meningitidis MC58]	gi|15676200|ref|NP 273332.1|	72.03	6E-119
contig00011-orf00070	putative protease [Neisseria meningitidis MC58]	gi|15677940|ref|NP 275112.1|	66.15	2E-103
contig00011-orf00072	DnaJ protein [Neisseria meningitidis Z2491]	gi|15793233|ref|NP 283055.1|	81.75	3E-162
contig00011-orf00075	leucyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59800478|ref|YP 207190.1|	93.62	0
contig00011-orf00077	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.74	1E-14
contig00011-orf00078	type II restriction enzyme DpnI [Neisseria meningitidis MC58]	gi|15677728|ref|NP 274891.1|	95.51	6E-151
contig00011-orf00082	putative modification methylase [Neisseria gonorrhoeae FA 1090]	gi|59800480|ref|YP 207192.1|	88.07	6E-70
contig00011-orf00083	putative modification methylase [Neisseria gonorrhoeae FA 1090]	gi|59800480|ref|YP 207192.1|	90.24	1E-39
contig00011-orf00084	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15793483|ref|NP 283305.1|	59.17	2E-91
contig00011-orf00087	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603318|ref|NP 246392.1|	79.43	0
contig00011-orf00088	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	93.75	0.00007
contig00011-orf00090	hypothetical protein NMB0086 [Neisseria meningitidis MC58]	gi|15676018|ref|NP 273148.1|	56	5E-92
contig00011-orf00094	sodium/glutamate symport carrier protein [Neisseria meningitidis Z2491]	gi|15793211|ref|NP 283033.1|	89.55	1E-177
contig00011-orf00095	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793077|ref|NP 282899.1|	84.44	7E-131
contig00011-orf00097	3-demethylubiquinone-9 3-methyltransferase [Neisseria meningitidis Z2491]	gi|15793415|ref|NP 283237.1|	78.02	3E-106
contig00011-orf00101	hypothetical protein MS1484 [Mannheimia succiniciproducens MBEL55E]	gi|52425539|ref|YP 088676.1|	65.68	8E-102
contig00011-orf00102	30S ribosomal protein S10 [Neisseria meningitidis Z2491]	gi|15793161|ref|NP 282983.1|	99.03	1E-51
contig00012-orf00001	hypothetical protein NMA2164 [Neisseria meningitidis Z2491]	gi|15795035|ref|NP 284857.1|	90.61	0
contig00012-orf00002	hypothetical protein NMA2160 [Neisseria meningitidis Z2491]	gi|15795031|ref|NP 284853.1|	83.67	2E-65
contig00012-orf00003	octaprenyl-diphosphate synthase [Neisseria meningitidis Z2491]	gi|15795032|ref|NP 284854.1|	89.51	2E-159
contig00012-orf00005	50S ribosomal protein L21 [Neisseria meningitidis Z2491]	gi|15795033|ref|NP 284855.1|	99.02	2E-50

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contig00012-orf00007	50S ribosomal protein L27 [Neisseria meningitidis Z2491]	gi|15795034|ref|NP 284856.1|	98.89	5E-45
contig00012-orf00009	thiamine biosynthesis protein ThiC [Neisseria meningitidis Z2491]	gi|15793405|ref|NP 283227.1|	97.63	0
contig00012-orf00010	CcpR [Neisseria gonorrhoeae FA 1090]	gi|59802088|ref|YP 208800.1|	82.76	5E-180
contig00012-orf00012	glycerol-3-phosphate dehydrogenase [Neisseria meningitidis Z2491]	gi|15793383|ref|NP 283205.1|	91.79	2E-167
contig00012-orf00013	hypothetical protein NMA0376 [Neisseria meningitidis Z2491]	gi|15793384|ref|NP 283206.1|	67.59	3E-31
contig00012-orf00015	hypothetical protein NGO2023 [Neisseria gonorrhoeae FA 1090]	gi|59802331|ref|YP 209043.1|	67	2E-30
contig00012-orf00017	50S ribosomal protein L13 [Neisseria meningitidis Z2491]	gi|15793386|ref|NP 283208.1|	99.25	4E-72
contig00012-orf00018	30S ribosomal protein S9 [Neisseria meningitidis Z2491]	gi|15793387|ref|NP 283209.1|	97.69	1E-66
contig00012-orf00020	hypothetical protein NGO2162 [Neisseria gonorrhoeae FA 1090]	gi|59802456|ref|YP 209168.1|	64.6	2E-34
contig00012-orf00022	glutathione-regulated potassium-efflux system protein [Neisseria meningitidis MC58]	gi|15676136|ref|NP 273267.1|	83.99	0
contig00013-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676806|ref|NP 273951.1|	75.76	0.0000009
contig00013-orf00002	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794704|ref|NP 284526.1|	85.37	2E-54
contig00013-orf00004	peptidyl-prolyl cis-trans isomerase A [Neisseria meningitidis Z2491]	gi|15794370|ref|NP 284192.1|	69.7	3E-60
contig00013-orf00006	hypothetical protein NMB1030 [Neisseria meningitidis MC58]	gi|15676917|ref|NP 274064.1|	91.62	2E-87
contig00013-orf00009	cell division protein FtsK [Neisseria meningitidis MC58]	gi|15677180|ref|NP 274333.1|	83.23	0
contig00013-orf00012	putative sodium-dependent transport protein [Neisseria gonorrhoeae FA 1090]	gi|59801034|ref|YP 207746.1|	94.69	0
contig00013-orf00013	FxsA [Neisseria meningitidis Z2491]	gi|15793898|ref|NP 283720.1|	59.59	2E-42
contig00013-orf00014	hypothetical protein NMB1369 [Neisseria meningitidis MC58]	gi|15677234|ref|NP 274387.1|	83.33	5E-47
contig00013-orf00016	hypothetical protein NMA1582 [Neisseria meningitidis Z2491]	gi|15794475|ref|NP 284297.1|	62.2	2E-38
contig00014-orf00002	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801974|ref|YP 208686.1|	40.34	2E-64
contig00014-orf00005	molybdopterin-guanine dinucleotide biosynthesis protein A [Roseobacter denitrificans OCh 114]	gi|110680580|ref|YP 683587.1|	31.43	0.71
contig00015-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	88.54	3E-96
contig00016-orf00001	hypothetical protein NGO2139 [Neisseria gonorrhoeae FA 1090]	gi|59802436|ref|YP 209148.1|	91.19	2E-118
contig00016-orf00003	transcriptional regulator CysB-like protein [Neisseria meningitidis Z2491]	gi|15794980|ref|NP 284802.1|	84.49	4E-153
contig00016-orf00004	Omp3 [Neisseria gonorrhoeae FA 1090]	gi|59801906|ref|YP 208618.1|	75	1E-83
contig00016-orf00006	seryl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15794826|ref|NP 284648.1|	94.2	0
contig00016-orf00007	30S ribosomal protein S6 [Neisseria meningitidis Z2491]	gi|15794430|ref|NP 284252.1|	96.81	5E-39
contig00016-orf00008	primosomal replication protein [Neisseria meningitidis Z2491]	gi|15794429|ref|NP 284251.1|	75.36	2E-24
contig00016-orf00009	30S ribosomal protein S18 [Neisseria meningitidis Z2491]	gi|15794428|ref|NP 284250.1|	97.37	2E-35
contig00016-orf00010	50S ribosomal protein L9 [Neisseria gonorrhoeae FA 1090]	gi|59801015|ref|YP 207727.1|	94.03	2E-58
contig00016-orf00013	putative murein hydrolase [Neisseria gonorrhoeae FA 1090]	gi|59801054|ref|YP 207766.1|	70.69	2E-141
contig00016-orf00015	aldose 1-epimerase [Salmonella typhimurium LT2]	gi|16764640|ref|NP 460255.1|	29.73	0.0000004
contig00016-orf00017	DNA polymerase III subunits gamma and tau [Neisseria meningitidis MC58]	gi|15678010|ref|NP 274455.1|	72.09	0
contig00016-orf00019	hypothetical protein NMA1657 [Neisseria meningitidis Z2491]	gi|15794551|ref|NP 284373.1|	85.59	8E-50
contig00016-orf00021	DNA repair protein (recombination protein o) [Neisseria meningitidis MC58]	gi|15676358|ref|NP 273494.1|	70.25	3E-92

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contig00016-orf00024	hypothetical protein NMB0541 [Neisseria meningitidis MC58]	gi|15676447|ref|NP 273586.1|	59.26	5E-52
contig00016-orf00025	hypothetical protein NMA0721 [Neisseria meningitidis Z2491]	gi|15793698|ref|NP 283520.1|	56.25	1E-18
contig00016-orf00026	(p)ppGpp synthetase [Streptococcus thermophilus LMG 18311]	gi|55820243|ref|YP 138685.1|	29.33	0.93
contig00016-orf00029	hypothetical protein NGO1421 [Neisseria gonorrhoeae FA 1090]	gi|59801765|ref|YP 208477.1|	91.67	6E-14
contig00016-orf00030	thiamine biosynthesis lipoprotein ApbE [Neisseria meningitidis MC58]	gi|15676468|ref|NP 273607.1|	73.31	1E-133
contig00016-orf00033	S-adenosylmethionine synthetase [Neisseria gonorrhoeae FA 1090]	gi|59800567|ref|YP 207279.1|	98.16	0
contig00016-orf00035	pyridoxal phosphate biosynthetic protein PdxJ [Neisseria meningitidis MC58]	gi|15676359|ref|NP 273495.1|	95.45	9E-127
contig00016-orf00038	holo-(acyl-carrier protein) synthase [Neisseria meningitidis Z2491]	gi|15794913|ref|NP 284735.1|	95.2	1E-53
contig00017-orf00002	methylenetetrahydrofolate dehydrogenase/cyclohydrolase [Neisseria meningitidis Z2491]	gi|15793364|ref|NP 283186.1|	85.87	4E-137
contig00017-orf00006	isochorismatase hydrolase [Psychrobacter cryohalolentis K5]	gi|93007049|ref|YP 581486.1|	40.56	7E-30
contig00017-orf00007	GCN5-related N-acetyltransferase [Psychrobacter cryohalolentis K5]	gi|93006865|ref|YP 581302.1|	47.73	2E-41
contig00017-orf00008	ClpXP protease specificity-enhancing factor [Neisseria meningitidis Z2491]	gi|15793498|ref|NP 283320.1|	66.34	3E-30
contig00017-orf00009	stringent starvation protein A [Neisseria meningitidis MC58]	gi|15677783|ref|NP 274947.1|	94.03	3E-107
contig00017-orf00011	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Neisseria meningitidis Z2491]	gi|15795024|ref|NP 284846.1|	98.53	5E-140
contig00017-orf00012	#N/A	#N/A	#N/A	#N/A
contig00017-orf00016	glutamate-ammonia-ligase adenylyltransferase [Neisseria meningitidis Z2491]	gi|15793067|ref|NP 282889.1|	96.75	0
contig00017-orf00019	lipid A biosynthesis lauroyl acyltransferase [Neisseria meningitidis MC58]	gi|15677639|ref|NP 274798.1|	72.5	9E-111
contig00017-orf00021	ArsR family transcriptional regulator [Neisseria meningitidis MC58]	gi|15676312|ref|NP 273447.1|	68.82	5E-29
contig00017-orf00024	exodeoxyribonuclease III [Neisseria meningitidis MC58]	gi|15676313|ref|NP 273448.1|	89.8	4E-136
contig00018-orf00002	hypothetical protein NMA0256 [Neisseria meningitidis Z2491]	gi|15793274|ref|NP 283096.1|	92.68	8E-37
contig00018-orf00010	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	25.15	1E-115
contig00019-orf00001	hypothetical protein MS0981 [Mannheimia succiniciproducens MBEL55E]	gi|52425036|ref|YP 088173.1|	81.32	5E-82
contig00020-orf00001	phosphoribosylaminoimidazole-succinocarboxamide synthase [Neisseria gonorrhoeae FA 1090]	gi|59800779|ref|YP 207491.1|	89.9	2E-149
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	46.41	6E-32
contig00020-orf00006	#N/A	#N/A	#N/A	#N/A
contig00020-orf00007	putative reductase [Neisseria gonorrhoeae FA 1090]	gi|59800778|ref|YP 207490.1|	70.63	1E-106
contig00020-orf00009	hypothetical protein NMB0753 [Neisseria meningitidis MC58]	gi|15676651|ref|NP 273795.1|	78.95	8E-32
contig00020-orf00010	ferredoxin [Neisseria meningitidis Z2491]	gi|15793922|ref|NP 283744.1|	80.3	5E-26
contig00021-orf00001	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	97.14	1E-13
contig00021-orf00003	hypothetical protein NMA0184 [Neisseria meningitidis Z2491]	gi|15793212|ref|NP 283034.1|	47.85	1E-94
contig00021-orf00004	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793875|ref|NP 283697.1|	78.34	6E-96
contig00021-orf00005	ribonuclease HII [Neisseria meningitidis Z2491]	gi|15793104|ref|NP 282926.1|	82.81	1E-84
contig00021-orf00009	lipid-A-disaccharide synthase [Neisseria meningitidis Z2491]	gi|15793098|ref|NP 282920.1|	82.01	2E-168
contig00021-orf00010	hypothetical protein NGO2121 [Neisseria gonorrhoeae FA 1090]	gi|59802419|ref|YP 209131.1|	73.26	1E-111

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contig00021-orf00011	hypothetical protein NMA0489 [Neisseria meningitidis Z2491]	gi|15793488|ref|NP 283310.1|	83.33	1E-35
contig00021-orf00014	periplasmic transport protein [Neisseria meningitidis Z2491]	gi|15793487|ref|NP 283309.1|	93.37	2E-77
contig00021-orf00016	hypothetical protein NGO2118 [Neisseria gonorrhoeae FA 1090]	gi|59802416|ref|YP 209128.1|	85.11	3E-73
contig00021-orf00019	ABC transport inner membrane subunit [Neisseria meningitidis Z2491]	gi|15793485|ref|NP 283307.1|	98.06	8E-126
contig00021-orf00022	ABC transport ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793484|ref|NP 283306.1|	98.12	2E-144
contig00021-orf00026	hypothetical protein NGO1701 [Neisseria gonorrhoeae FA 1090]	gi|59802022|ref|YP 208734.1|	62.91	2E-30
contig00021-orf00027	cell division protein FtsZ [Neisseria meningitidis Z2491]	gi|15794935|ref|NP 284757.1|	81.41	1E-157
contig00021-orf00028	cell division protein [Neisseria meningitidis Z2491]	gi|15794936|ref|NP 284758.1|	73.67	3E-170
contig00021-orf00030	cell division protein [Neisseria meningitidis Z2491]	gi|15794937|ref|NP 284759.1|	60.33	6E-72
contig00021-orf00032	D-alanine--D-alanine ligase [Neisseria meningitidis MC58]	gi|15676336|ref|NP 273472.1|	93.09	3E-153
contig00021-orf00035	UDP-N-acetylmuramate--L-alanine ligase [Neisseria meningitidis Z2491]	gi|15794939|ref|NP 284761.1|	94.67	0
contig00021-orf00037	TcmP [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603187|ref|NP 246260.1|	55.15	2E-83
contig00021-orf00040	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentape pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Neisseria meningitidis Z2491]	gi|15794940|ref|NP 284762.1|	95.49	0
contig00021-orf00042	cell division protein [Neisseria meningitidis Z2491]	gi|15794941|ref|NP 284763.1|	61.63	1E-123
contig00021-orf00045	periplasmic sensor hybrid histidine kinase [Rhodobacter sphaeroides 2.4.1]	gi|77462965|ref|YP 352469.1|	38.78	0.71
contig00021-orf00047	6-aminohexanoate-cyclic-dimer hydrolase [Deinococcus radiodurans R1]	gi|15805271|ref|NP 293959.1|	40.51	1E-56
contig00021-orf00049	amidase family protein [Myxococcus xanthus DK 1622]	gi|108763797|ref|YP 631063.1|	47.37	2E-10
contig00021-orf00051	response regulator aspartate phosphatase inhibitor [Bacillus cereus ATCC 14579]	gi|30021621|ref|NP 833252.1|	37.5	4.6
contig00021-orf00052	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [Neisseria meningitidis MC58]	gi|15676332|ref|NP 273468.1|	97.08	0
contig00021-orf00054	hypothetical protein NMB0419 [Neisseria meningitidis MC58]	gi|15676331|ref|NP 273467.1|	74.47	3E-79
contig00021-orf00055	hypothetical protein Daro 1997 [Dechloromonas aromatica RCB]	gi|71907626|ref|YP 285213.1|	50.82	5E-31
contig00022-orf00001	50S ribosomal protein L33 [Neisseria meningitidis Z2491]	gi|15795036|ref|NP 284858.1|	98.04	1E-22
contig00022-orf00002	50S ribosomal protein L28 [Neisseria meningitidis Z2491]	gi|15795037|ref|NP 284859.1|	100	5E-18
contig00022-orf00005	multidrug resistance translocase [Neisseria meningitidis Z2491]	gi|15795039|ref|NP 284861.1|	81.4	0
contig00022-orf00007	multidrug resistance translocase [Neisseria meningitidis Z2491]	gi|15795040|ref|NP 284862.1|	64.38	3E-111
contig00022-orf00009	acetate kinase [Neisseria meningitidis MC58]	gi|15676347|ref|NP 273483.1|	94.49	0
contig00022-orf00011	hypothetical protein NMA2051 [Neisseria meningitidis Z2491]	gi|15794929|ref|NP 284751.1|	96.14	0
contig00022-orf00013	aconitate hydratase [Neisseria meningitidis Z2491]	gi|15794930|ref|NP 284752.1|	96.38	0
contig00022-orf00014	aconitate hydratase [Neisseria meningitidis MC58]	gi|15676345|ref|NP 273481.1|	97.83	7E-133
contig00022-orf00016	hypothetical protein PFL 2353 [Pseudomonas fluorescens Pf-5]	gi|70729721|ref|YP 259460.1|	42.66	2E-38
contig00022-orf00019	hypothetical protein NMA2053 [Neisseria meningitidis Z2491]	gi|15794931|ref|NP 284753.1|	98.85	1E-101
contig00022-orf00020	cephalosporin hydroxylase [Rickettsia bellii RML369-C]	gi|91205293|ref|YP 537648.1|	25.83	0.001
contig00022-orf00021	methylcitrate synthase [Neisseria meningitidis Z2491]	gi|15794932|ref|NP 284754.1|	93.75	0
contig00022-orf00025	2-methylisocitrate lyase [Neisseria meningitidis MC58]	gi|15676342|ref|NP 273478.1|	97.37	9E-144
contig00022-orf00031	LmrB [Bacillus licheniformis ATCC 14580]	gi|52785922|ref|YP 091751.1|	38.81	7E-82

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contig00023-orf00001	putative phosphate acetyltransferase Pta [Neisseria meningitidis MC58]	gi|15676533|ref|NP 273674.1|	85.4	0
contig00023-orf00003	amino-acid transport protein [Neisseria meningitidis Z2491]	gi|15793414|ref|NP 283236.1|	92.49	0
contig00023-orf00004	carbonate dehydratase [Cytophaga hutchinsonii ATCC 33406]	gi|110636727|ref|YP 676934.1|	61.02	1E-15
contig00023-orf00005	carbonate dehydratase [Cytophaga hutchinsonii ATCC 33406]	gi|110636727|ref|YP 676934.1|	67.15	1E-47
contig00023-orf00007	integral membrane sulfate transportor [Haemophilus ducreyi 35000HP]	gi|33152170|ref|NP 873523.1|	53.83	1E-107
contig00023-orf00008	hypothetical protein NGO1163 [Neisseria gonorrhoeae FA 1090]	gi|59801529|ref|YP 208241.1|	57.14	0.24
contig00023-orf00013	dTDP-4-keto-6-deoxy-D-glucose-3,6-epimerase [Neisseria meningitidis MC58]	gi|15676014|ref|NP 273144.1|	93.3	2E-89
contig00023-orf00014	diaminopimelate decarboxylase [Neisseria meningitidis Z2491]	gi|15793470|ref|NP 283292.1|	94.58	0
contig00023-orf00015	hypothetical protein NMB1977 [Neisseria meningitidis MC58]	gi|15677806|ref|NP 274970.1|	83.33	6E-13
contig00023-orf00016	frataxin-like protein [Neisseria gonorrhoeae FA 1090]	gi|59802401|ref|YP 209113.1|	95.33	2E-54
contig00023-orf00018	S-ribosylhomocysteinase [Neisseria meningitidis Z2491]	gi|15793465|ref|NP 283287.1|	95.83	2E-89
contig00023-orf00019	rarD protein [Psychrobacter cryohalolentis K5]	gi|93005188|ref|YP 579625.1|	46.67	2E-60
contig00023-orf00020	sugar-phosphate nucleotidyl transferase [Neisseria meningitidis Z2491]	gi|15793605|ref|NP 283427.1|	68.83	5E-84
contig00023-orf00022	NADH:FMN oxidoreductase [Neisseria meningitidis Z2491]	gi|15793604|ref|NP 283426.1|	77.48	5E-67
contig00023-orf00023	MarR family transcriptional regulator [Neisseria meningitidis Z2491]	gi|15793603|ref|NP 283425.1|	93.39	4E-58
contig00023-orf00025	thioredoxin [Neisseria meningitidis MC58]	gi|15677681|ref|NP 274842.1|	50	5E-46
contig00023-orf00026	glyceraldehyde-3-phosphate dehydrogenase [Neisseria meningitidis MC58]	gi|15676134|ref|NP 273265.1|	88.34	4E-175
contig00023-orf00029	hypothetical protein NMA1951 [Neisseria meningitidis Z2491]	gi|15794834|ref|NP 284656.1|	50.79	0
contig00023-orf00030	chorismate mutase-related protein [Neisseria meningitidis MC58]	gi|15677540|ref|NP 274696.1|	50.41	4E-61
contig00023-orf00034	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Neisseria meningitidis Z2491]	gi|15794654|ref|NP 284476.1|	97.44	0
contig00023-orf00036	ATP-dependent protease ATP-binding subunit [Neisseria meningitidis MC58]	gi|15677237|ref|NP 274390.1|	87.17	0
contig00023-orf00040	putative D-alanyl-D-alanine-endopeptidase [Neisseria gonorrhoeae FA 1090]	gi|59800773|ref|YP 207485.1|	80.36	1E-117
contig00023-orf00041	hypothetical protein NMA0562 [Neisseria meningitidis Z2491]	gi|15793554|ref|NP 283376.1|	50.59	2E-65
contig00024-orf00005	isoleucyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677669|ref|NP 274830.1|	94.52	0
contig00024-orf00007	putative hemin degrading factor [Pseudomonas aeruginosa UCBPP-PA14]	gi|116052855|ref|YP 793172.1|	45.76	0.0000003
contig00024-orf00010	hypothetical protein PM1078 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602943|ref|NP 246015.1|	48.97	3E-68
contig00024-orf00012	hypothetical protein PM1079 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602944|ref|NP 246016.1|	61.69	2E-79
contig00024-orf00014	hypothetical protein PM1080 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602945|ref|NP 246017.1|	46.55	3E-50
contig00024-orf00016	glucokinase [Neisseria meningitidis Z2491]	gi|15793417|ref|NP 283239.1|	84.3	1E-82
contig00024-orf00019	gluconate permease [Neisseria meningitidis Z2491]	gi|15793418|ref|NP 283240.1|	87.64	9E-174
contig00024-orf00021	sigma-54 modulation protein [Chromobacterium violaceum ATCC 12472]	gi|34498788|ref|NP 903003.1|	56.7	2E-27
contig00024-orf00023	RNA polymerase factor sigma-54 [Dechloromonas aromatica RCB]	gi|71909758|ref|YP 287345.1|	40.07	3E-46
contig00024-orf00024	putative RNA polymerase sigma-54 factor RpoN [Neisseria meningitidis MC58]	gi|15676143|ref|NP 273274.1|	75.25	1E-48
contig00024-orf00026	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676271|ref|NP 273405.1|	94.26	2E-124
contig00024-orf00028	hypothetical protein NGO1606 [Neisseria gonorrhoeae FA 1090]	gi|59801934|ref|YP 208646.1|	80.11	1E-61
contig00024-orf00029	hypothetical protein NMB0354 [Neisseria meningitidis MC58]	gi|15676269|ref|NP 273403.1|	75.56	8E-77

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contig00024-orf00031	hypothetical protein NMA2134 [Neisseria meningitidis Z2491]	gi|15795005|ref|NP 284827.1|	93.26	5E-91
contig00024-orf00032	transcriptional activator protein METR [Neisseria meningitidis Z2491]	gi|15793389|ref|NP 283211.1|	91.5	1E-153
contig00024-orf00033	hypothetical protein NGO2028 [Neisseria gonorrhoeae FA 1090]	gi|59802336|ref|YP 209048.1|	72.29	7E-106
contig00024-orf00034	ubiquinol-cytochrome c reductase iron-sulfur subunit [Neisseria meningitidis Z2491]	gi|15793391|ref|NP 283213.1|	91.19	4E-91
contig00024-orf00035	PetB [Neisseria gonorrhoeae FA 1090]	gi|59802338|ref|YP 209050.1|	96.66	0
contig00024-orf00036	cytochrome C1 precursor [Neisseria meningitidis MC58]	gi|15677873|ref|NP 275041.1|	94.74	7E-149
contig00024-orf00037	hypothetical protein NGO2019 [Neisseria gonorrhoeae FA 1090]	gi|59802327|ref|YP 209039.1|	70.08	2E-78
contig00024-orf00040	iron(III) ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15677818|ref|NP 274982.1|	86.11	3E-112
contig00024-orf00042	iron(III) ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15677819|ref|NP 274983.1|	88.36	6E-126
contig00024-orf00043	lipopolysaccharide modification acyltransferase [Neisseria meningitidis Z2491]	gi|15793609|ref|NP 283431.1|	37.95	1E-94
contig00024-orf00044	hypothetical protein NMB1992 [Neisseria meningitidis MC58]	gi|15677820|ref|NP 274984.1|	85.1	3E-90
contig00024-orf00045	iron(III) ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677821|ref|NP 274985.1|	83.73	4E-118
contig00024-orf00047	lipoprotein [Neisseria meningitidis Z2491]	gi|15793663|ref|NP 283485.1|	84	6E-31
contig00024-orf00049	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Neisseria meningitidis MC58]	gi|15677694|ref|NP 274855.1|	89.18	8E-176
contig00024-orf00051	hypothetical protein NMA0611 [Neisseria meningitidis Z2491]	gi|15793601|ref|NP 283423.1|	82.73	9E-161
contig00025-orf00003	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	96.64	0
contig00026-orf00001	hypothetical protein NMA1902 [Neisseria meningitidis Z2491]	gi|15794787|ref|NP 284609.1|	98.35	5E-124
contig00026-orf00003	putative adhesin [Neisseria meningitidis MC58]	gi|15676491|ref|NP 273630.1|	81.25	4E-130
contig00026-orf00005	membrane protein [Neisseria meningitidis Z2491]	gi|15794022|ref|NP 283844.1|	74.07	0.00008
contig00026-orf00008	membrane protein [Neisseria meningitidis Z2491]	gi|15794022|ref|NP 283844.1|	80	0.0000005
contig00026-orf00011	hypothetical protein NMA1072 [Neisseria meningitidis Z2491]	gi|15794020|ref|NP 283842.1|	91.89	2E-35
contig00026-orf00012	hypothetical protein NGO0162 [Neisseria gonorrhoeae FA 1090]	gi|59800618|ref|YP 207330.1|	89.74	8E-35
contig00026-orf00014	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794015|ref|NP 283837.1|	86.7	2E-102
contig00026-orf00016	electron transfer flavoprotein-ubiquinone oxidoreductase [Neisseria meningitidis MC58]	gi|15676486|ref|NP 273625.1|	96.93	0
contig00026-orf00019	oxidoreductase [Neisseria meningitidis Z2491]	gi|15794150|ref|NP 283972.1|	96.95	0
contig00026-orf00020	sugar transporter [Chromohalobacter salexigens DSM 3043]	gi|92112633|ref|YP 572561.1|	49.06	0.0000005
contig00026-orf00021	D-lactate dehydrogenase [Neisseria meningitidis MC58]	gi|15676888|ref|NP 274033.1|	96.8	0
contig00026-orf00023	macrophage infectivity potentiator-related protein [Neisseria meningitidis MC58]	gi|15676886|ref|NP 274031.1|	68.42	2.7
contig00026-orf00024	hypothetical protein NMA1203 [Neisseria meningitidis Z2491]	gi|15794147|ref|NP 283969.1|	92.31	5E-90
contig00026-orf00026	acyl-CoA dehydrogenase family protein [Neisseria meningitidis MC58]	gi|15676885|ref|NP 274030.1|	87.02	3E-172
contig00026-orf00029	putative rubredoxin [Neisseria gonorrhoeae FA 1090]	gi|59801284|ref|YP 207996.1|	98.21	2E-30
contig00026-orf00030	hypothetical protein NMB1701 [Neisseria meningitidis MC58]	gi|15677549|ref|NP 274705.1|	58.95	1E-26
contig00026-orf00031	putative acyltransferase [Neisseria meningitidis MC58]	gi|15677546|ref|NP 274702.1|	63.86	6E-24
contig00026-orf00032	acyl carrier protein [Neisseria meningitidis MC58]	gi|15677544|ref|NP 274700.1|	82.5	4E-29

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contig00026-orf00034	hypothetical protein ACIAD2340 [Acinetobacter sp. ADP1]	gi|50085431|ref|YP 046941.1|	41.03	0.0000002
contig00027-orf00001	hypothetical protein NMA2001 [Neisseria meningitidis Z2491]	gi|15794881|ref|NP 284703.1|	100	2E-31
contig00027-orf00002	hypothetical protein NMA2000 [Neisseria meningitidis Z2491]	gi|15794880|ref|NP 284702.1|	97.92	1E-48
contig00027-orf00003	hypothetical protein NMA1999 [Neisseria meningitidis Z2491]	gi|15794879|ref|NP 284701.1|	95.35	0
contig00027-orf00005	outer membrane lipoprotein carrier protein [Neisseria meningitidis MC58]	gi|15676525|ref|NP 273666.1|	87.92	9E-95
contig00027-orf00008	hypothetical protein NMA0829 [Neisseria meningitidis Z2491]	gi|15793800|ref|NP 283622.1|	91.27	1E-143
contig00027-orf00011	potassium/proton-divalent cation antiporter [Bacillus subtilis subsp. subtilis str. 168]	gi|16079718|ref|NP 390542.1|	57.48	2E-100
contig00027-orf00014	phosphoglycolate phosphatase [Neisseria meningitidis MC58]	gi|15676523|ref|NP 273664.1|	88.84	4E-91
contig00027-orf00015	malate oxidoreductase (NAD) [Neisseria meningitidis MC58]	gi|15676569|ref|NP 273713.1|	97.18	0
contig00027-orf00016	thymidylate kinase [Neisseria meningitidis Z2491]	gi|15793838|ref|NP 283660.1|	84.39	3E-94
contig00027-orf00018	hypothetical protein Pcryo 1832 [Psychrobacter cryohalolentis K5]	gi|93006656|ref|YP 581093.1|	30.38	5E-08
contig00027-orf00019	pili assembly chaperone [Xanthomonas campestris pv. vesicatoria str. 85-10]	gi|78047039|ref|YP 363214.1|	40.26	2E-38
contig00027-orf00020	fimbrial biogenesis outer membrane usher protein [Psychrobacter cryohalolentis K5]	gi|93006655|ref|YP 581092.1|	32.71	5E-104
contig00027-orf00023	hypothetical protein Pcryo 1832 [Psychrobacter cryohalolentis K5]	gi|93006656|ref|YP 581093.1|	34.48	2E-13
contig00027-orf00024	hypothetical protein NMA1773 [Neisseria meningitidis Z2491]	gi|15794666|ref|NP 284488.1|	84.83	1E-135
contig00027-orf00026	hypothetical protein RSP 2309 [Rhodobacter sphaeroides 2.4.1]	gi|77462860|ref|YP 352364.1|	27.52	2E-14
contig00027-orf00027	hypothetical protein NMA1086 [Neisseria meningitidis Z2491]	gi|15794034|ref|NP 283856.1|	84.83	2E-100
contig00027-orf00031	DNA topoisomerase IV subunit B [Neisseria meningitidis Z2491]	gi|15794824|ref|NP 284646.1|	97.73	0
contig00027-orf00033	dinucleoside polyphosphate hydrolase [Neisseria meningitidis MC58]	gi|15677531|ref|NP 274687.1|	92.53	2E-96
contig00027-orf00035	hypothetical protein lmo0912 [Listeria monocytogenes EGD-e]	gi|16802953|ref|NP 464438.1|	52.02	3E-68
contig00027-orf00036	hypothetical protein FN0616 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	gi|19703951|ref|NP 603513.1|	50.1	4E-121
contig00027-orf00038	putative sodium/alanine symporter [Neisseria meningitidis MC58]	gi|15676104|ref|NP 273235.1|	91.14	0
contig00027-orf00039	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	93.77	1E-176
contig00027-orf00040	hypothetical protein NMB1100 [Neisseria meningitidis MC58]	gi|15676980|ref|NP 274131.1|	85.71	0.037
contig00028-orf00001	isrso11-transposase orfb protein [Ralstonia solanacearum GMI1000]	gi|17547808|ref|NP 521210.1|	52.07	2E-25
contig00028-orf00002	preprotein translocase subunit SecB [Neisseria gonorrhoeae FA 1090]	gi|59800576|ref|YP 207288.1|	89.58	2E-68
contig00028-orf00003	glutaredoxin [Neisseria meningitidis Z2491]	gi|15793656|ref|NP 283478.1|	82.35	2E-35
contig00028-orf00006	hypothetical protein NMA0672 [Neisseria meningitidis Z2491]	gi|15793655|ref|NP 283477.1|	94.77	0
contig00028-orf00008	two component transcriptional regulator [Dechloromonas aromatica RCB]	gi|71907917|ref|YP 285504.1|	66.67	8E-68
contig00028-orf00011	two-component system sensor kinase [Neisseria meningitidis Z2491]	gi|15793653|ref|NP 283475.1|	61.37	5E-120
contig00028-orf00013	3-ketoacyl-(acyl-carrier-protein) reductase [Neisseria meningitidis MC58]	gi|15677752|ref|NP 274915.1|	96.37	6E-120
contig00028-orf00014	hypothetical protein Psyc 1209 [Psychrobacter arcticus 273-4]	gi|71065767|ref|YP 264494.1|	36.73	9E-58
contig00028-orf00015	hypothetical protein Psyc 1209 [Psychrobacter arcticus 273-4]	gi|71065767|ref|YP 264494.1|	35.17	6E-48
contig00028-orf00017	glycosyl transferase [Pyrococcus abyssi GE5]	gi|14521365|ref|NP 126841.1|	28.7	2E-13

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contig00028-orf00018	putative glycosyl transferase [Burkholderia thailandensis E264]	gi|83721331|ref|YP 442023.1|	30.86	4E-23
contig00028-orf00019	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793530|ref|NP 283352.1|	77.74	0
contig00028-orf00020	acyl-carrier-protein S-malonyltransferase [Neisseria meningitidis Z2491]	gi|15793531|ref|NP 283353.1|	90.91	3E-141
contig00028-orf00023	cold shock DNA-binding domain-containing protein [Nitrosomonas europaea ATCC 19718]	gi|30248726|ref|NP 840796.1|	34.2	6E-22
contig00028-orf00027	3-oxoacyl-(acyl carrier protein) synthase III [Neisseria meningitidis Z2491]	gi|15793533|ref|NP 283355.1|	87.19	2E-158
contig00028-orf00029	hypothetical protein NMB1925 [Neisseria meningitidis MC58]	gi|15677755|ref|NP 274919.1|	72.5	6E-88
contig00028-orf00030	hypothetical protein NMA0529 [Neisseria meningitidis Z2491]	gi|15793526|ref|NP 283348.1|	88.08	3E-123
contig00028-orf00033	glutathione S-transferase [Rhodobacter sphaeroides 2.4.1]	gi|77464476|ref|YP 353980.1|	43.01	2E-35
contig00028-orf00035	hypothetical protein lpp2105 [Legionella pneumophila str. Paris]	gi|54298048|ref|YP 124417.1|	47.58	7E-46
contig00028-orf00037	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Neisseria meningitidis Z2491]	gi|15794127|ref|NP 283949.1|	96.04	0
contig00028-orf00040	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794260|ref|NP 284082.1|	79.02	6E-94
contig00028-orf00041	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794259|ref|NP 284081.1|	52.58	2E-21
contig00028-orf00042	lipoprotein [Ralstonia solanacearum GMI1000]	gi|17548896|ref|NP 522236.1|	71.88	0.000002
contig00028-orf00043	putative lipoprotein [Yersinia pseudotuberculosis IP 32953]	gi|51597012|ref|YP 071203.1|	63.04	1E-41
contig00028-orf00044	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	94.29	8E-13
contig00028-orf00045	hypothetical protein NGO1512 [Neisseria gonorrhoeae FA 1090]	gi|59801850|ref|YP 208562.1|	73.14	2E-103
contig00028-orf00047	factor-for-inversion-stimulation protein [Neisseria meningitidis Z2491]	gi|15794526|ref|NP 284348.1|	83.54	4E-35
contig00028-orf00050	hypothetical protein NMA1633 [Neisseria meningitidis Z2491]	gi|15794527|ref|NP 284349.1|	90.36	7E-175
contig00028-orf00052	hypothetical protein NMA1986 [Neisseria meningitidis Z2491]	gi|15794868|ref|NP 284690.1|	66.04	1E-69
contig00028-orf00055	DNA polymerase III subunit delta [Neisseria meningitidis MC58]	gi|15676606|ref|NP 273750.1|	80.18	4E-139
contig00028-orf00056	hypothetical protein NGO0282 [Neisseria gonorrhoeae FA 1090]	gi|59800731|ref|YP 207443.1|	59.49	3E-49
contig00028-orf00057	2-isopropylmalate synthase [Bacillus halodurans C-125]	gi|15615620|ref|NP 243924.1|	43.33	10
contig00028-orf00058	proline iminopeptidase [Neisseria gonorrhoeae FA 1090]	gi|59801340|ref|YP 208052.1|	81.49	1E-149
contig00028-orf00059	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	69.57	2E-11
contig00028-orf00060	membrane protein [Neisseria meningitidis Z2491]	gi|15793879|ref|NP 283701.1|	92.09	2E-53
contig00028-orf00062	hypothetical protein NGO0285 [Neisseria gonorrhoeae FA 1090]	gi|59800734|ref|YP 207446.1|	68.42	2E-55
contig00028-orf00066	proline dehydrogenase [Neisseria meningitidis Z2491]	gi|15794959|ref|NP 284781.1|	92.51	0
contig00028-orf00067	putative sodium/proline symporter, proline permease [Neisseria gonorrhoeae FA 1090]	gi|59801888|ref|YP 208600.1|	91.29	0
contig00028-orf00070	putative ubiquinone biosynthesis protein UbiB [Neisseria meningitidis MC58]	gi|15676464|ref|NP 273603.1|	92.71	0
contig00028-orf00075	hypothetical protein NMA2081 [Neisseria meningitidis Z2491]	gi|15794957|ref|NP 284779.1|	92.06	8E-26
contig00028-orf00079	chelatase [Neisseria meningitidis Z2491]	gi|15794956|ref|NP 284778.1|	93.98	0
contig00028-orf00082	IS1016C2 transposase [Neisseria meningitidis MC58]	gi|15677271|ref|NP 274424.1|	100	9E-41
contig00028-orf00086	hypothetical protein NMA2079 [Neisseria meningitidis Z2491]	gi|15794955|ref|NP 284777.1|	52.85	4E-21
contig00028-orf00087	thiol:disulfide interchange protein DsbA [Neisseria meningitidis MC58]	gi|15676320|ref|NP 273456.1|	66.32	2E-62

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contig00028-orf00089	hypothetical protein NGO1547 [Neisseria gonorrhoeae FA 1090]	gi|59801883|ref|YP 208595.1|	76.1	1E-110
contig00028-orf00091	hypothetical protein NMB1908 [Neisseria meningitidis MC58]	gi|15677739|ref|NP 274902.1|	88.14	8E-112
contig00028-orf00092	Maf-like protein [Neisseria gonorrhoeae FA 1090]	gi|59802468|ref|YP 209180.1|	71.43	7E-77
contig00028-orf00093	hypothetical protein NMA0545 [Neisseria meningitidis Z2491]	gi|15793539|ref|NP 283361.1|	84.43	1E-76
contig00028-orf00094	50S ribosomal protein L32 [Neisseria meningitidis MC58]	gi|15677742|ref|NP 274905.1|	96.61	4E-27
contig00028-orf00095	hypothetical protein NMA0543 [Neisseria meningitidis Z2491]	gi|15793537|ref|NP 283359.1|	91.95	4E-92
contig00028-orf00098	putative glycerol-3-phosphate acyltransferase PlsX [Neisseria meningitidis Z2491]	gi|15793536|ref|NP 283358.1|	84.38	5E-159
contig00028-orf00101	glycyl-tRNA synthetase subunit beta [Neisseria meningitidis MC58]	gi|15677760|ref|NP 274924.1|	85.73	0
contig00028-orf00102	glycyl-tRNA synthetase subunit alpha [Neisseria meningitidis Z2491]	gi|15793519|ref|NP 283341.1|	98.99	2E-174
contig00028-orf00105	hypothetical protein NMB1417 [Neisseria meningitidis MC58]	gi|15677276|ref|NP 274429.1|	85.55	4E-137
contig00029-orf00003	hypothetical protein NGO1387 [Neisseria gonorrhoeae FA 1090]	gi|59801735|ref|YP 208447.1|	97.22	1E-36
contig00029-orf00006	hypothetical protein NMB0372 [Neisseria meningitidis MC58]	gi|15676286|ref|NP 273421.1|	89.58	6E-74
contig00029-orf00010	hypothetical protein NMB0050 [Neisseria meningitidis MC58]	gi|15675988|ref|NP 273115.1|	77.01	0
contig00029-orf00011	hypothetical protein NMA0694 [Neisseria meningitidis Z2491]	gi|15793674|ref|NP 283496.1|	93.88	3E-23
contig00029-orf00014	aspartate carbamoyltransferase catalytic subunit [Neisseria meningitidis Z2491]	gi|15793195|ref|NP 283017.1|	91.83	2E-150
contig00029-orf00016	aspartate carbamoyltransferase regulatory subunit [Neisseria meningitidis Z2491]	gi|15793194|ref|NP 283016.1|	89.47	5E-75
contig00029-orf00018	hypothetical protein NMA0178 [Neisseria meningitidis Z2491]	gi|15793206|ref|NP 283028.1|	75.11	0
contig00029-orf00020	NADH dehydrogenase subunit H [Ralstonia metallidurans CH34]	gi|94309879|ref|YP 583089.1|	32.56	0.92
contig00029-orf00021	hypothetical protein NGO1694 [Neisseria gonorrhoeae FA 1090]	gi|59802018|ref|YP 208730.1|	68.94	2E-51
contig00029-orf00023	#N/A	#N/A	#N/A	#N/A
contig00029-orf00025	hypothetical protein PAM 636 [Onion yellows phytoplasma OY-M]	gi|39939122|ref|NP 950888.1|	26.79	4E-18
contig00029-orf00028	peptide chain release factor 2 [Neisseria meningitidis Z2491]	gi|15793246|ref|NP 283068.1|	98.91	0
contig00029-orf00032	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Neisseria meningitidis Z2491]	gi|15793276|ref|NP 283098.1|	89.93	0
contig00029-orf00035	putative acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802241|ref|YP 208953.1|	64.47	2E-53
contig00029-orf00037	methionyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793293|ref|NP 283115.1|	97.11	1E-90
contig00030-orf00002	DNA helicase II [Neisseria meningitidis Z2491]	gi|15793060|ref|NP 282882.1|	96.19	0
contig00030-orf00008	hypothetical protein tll0709 [Thermosynechococcus elongatus BP-1]	gi|22298251|ref|NP 681498.1|	46.15	5E-21
contig00030-orf00011	iron-sulfur cluster binding protein [Carboxydothermus hydrogenoformans Z-2901]	gi|78044449|ref|YP 360062.1|	34.29	2
contig00031-orf00002	ornithine carbamoyltransferase [Neisseria meningitidis MC58]	gi|15677423|ref|NP 274579.1|	93.96	2E-169
contig00031-orf00005	arginyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677359|ref|NP 274514.1|	96.96	0
contig00031-orf00007	hypothetical protein NGO0585 [Neisseria gonorrhoeae FA 1090]	gi|59801016|ref|YP 207728.1|	72.76	2E-96
contig00031-orf00010	phosphatidylserine synthase [Neisseria meningitidis Z2491]	gi|15794425|ref|NP 284247.1|	89.3	5E-108
contig00031-orf00011	hypothetical protein NMB1917 [Neisseria meningitidis MC58]	gi|15677748|ref|NP 274911.1|	66.67	6E-10
contig00031-orf00014	exodeoxyribonuclease VII large subunit [Neisseria meningitidis MC58]	gi|15677228|ref|NP 274381.1|	87.53	0

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contig00031-orf00016	urea transporter or sodium transporter [Rhodopirellula baltica SH 1]	gi|32477973|ref|NP 870967.1|	75	10
contig00031-orf00023	tetraacyldisaccharide 4'-kinase [Neisseria meningitidis Z2491]	gi|15793841|ref|NP 283663.1|	68.25	7E-39
contig00032-orf00002	MFS family transporter [Acinetobacter sp. ADP1]	gi|50083512|ref|YP 045022.1|	64.76	4E-149
contig00032-orf00005	glycine betaine/carnitine/choline ABC transporter, ATP-binding protein [Enterococcus faecalis V583]	gi|29375272|ref|NP 814425.1|	57.2	5E-75
contig00032-orf00006	lytic murein transglycosylase [Yersinia pseudotuberculosis IP 32953]	gi|51594946|ref|YP 069137.1|	36.23	7.8
contig00032-orf00008	Hmp protein [Mannheimia succiniciproducens MBEL55E]	gi|52424735|ref|YP 087872.1|	41	5E-76
contig00032-orf00009	LysR protein [Mannheimia succiniciproducens MBEL55E]	gi|52425458|ref|YP 088595.1|	67.68	1E-35
contig00032-orf00011	helicase, putative [Geobacter sulfurreducens PCA]	gi|39995869|ref|NP 951820.1|	46.98	0
contig00032-orf00012	potassium-tellurite ethidium and proflavin transporter [Neisseria meningitidis MC58]	gi|15677453|ref|NP 274609.1|	63.45	7E-20
contig00032-orf00013	potassium-tellurite ethidium and proflavin transporter [Neisseria meningitidis MC58]	gi|15677453|ref|NP 274609.1|	71.17	3E-52
contig00032-orf00016	hypothetical protein MXAN 7250 [Myxococcus xanthus DK 1622]	gi|108759038|ref|YP 635363.1|	35.54	1E-15
contig00033-orf00003	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	91.22	0
contig00033-orf00007	putative transposase [Neisseria meningitidis MC58]	gi|15677452|ref|NP 274608.1|	85.71	0.0000003
contig00033-orf00010	putative hemolysin activation protein HecB [Neisseria meningitidis MC58]	gi|15677604|ref|NP 274762.1|	85.59	0
contig00036-orf00002	hypothetical protein PA2459 [Pseudomonas aeruginosa PAO1]	gi|15597655|ref|NP 251149.1|	37.37	7E-34
contig00036-orf00005	hypothetical protein NGO1062 [Neisseria gonorrhoeae FA 1090]	gi|59801432|ref|YP 208144.1|	98.17	5E-58
contig00036-orf00006	short chain dehydrogenase [Neisseria meningitidis MC58]	gi|15677040|ref|NP 274192.1|	92.05	1E-123
contig00036-orf00008	hypothetical protein NMB1166 [Neisseria meningitidis MC58]	gi|15677041|ref|NP 274193.1|	72.16	4E-179
contig00036-orf00010	putative phytoene synthase [Neisseria meningitidis MC58]	gi|15677043|ref|NP 274195.1|	89.77	1E-136
contig00036-orf00011	chaperone protein HscA [Neisseria gonorrhoeae FA 1090]	gi|59801239|ref|YP 207951.1|	89.84	0
contig00036-orf00013	hypothetical protein LVIS 1846 [Lactobacillus brevis ATCC 367]	gi|116334413|ref|YP 795940.1|	64.17	3E-40
contig00036-orf00014	putative ferredoxin [Neisseria gonorrhoeae FA 1090]	gi|59801235|ref|YP 207947.1|	93.81	2E-48
contig00036-orf00015	hypothetical protein NMA1345 [Neisseria meningitidis Z2491]	gi|15794268|ref|NP 284090.1|	38.31	1E-27
contig00036-orf00016	hypothetical protein NMA1347 [Neisseria meningitidis Z2491]	gi|15794269|ref|NP 284091.1|	92.31	4E-30
contig00036-orf00018	5,10-methylenetetrahydrofolate reductase [Neisseria meningitidis Z2491]	gi|15794085|ref|NP 283907.1|	98.63	5E-165
contig00036-orf00020	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Neisseria meningitidis Z2491]	gi|15794086|ref|NP 283908.1|	98.11	0
contig00036-orf00022	5'-methylthioadenosine phosphorylase [Chromobacterium violaceum ATCC 12472]	gi|34499349|ref|NP 903564.1|	49.77	2E-58
contig00036-orf00025	integral membrane protein [Neisseria meningitidis Z2491]	gi|15794302|ref|NP 284124.1|	72.88	4E-110
contig00036-orf00026	phosphoribosylaminoimidazole synthetase [Neisseria meningitidis Z2491]	gi|15794333|ref|NP 284155.1|	92.73	0
contig00037-orf00002	hypothetical protein MM 0503 [Methanosarcina mazei Go1]	gi|21226605|ref|NP 632527.1|	31.93	2E-26
contig00037-orf00003	ferredoxin [Clostridium acetobutylicum ATCC 824]	gi|15893371|ref|NP 346720.1|	33.33	2
contig00037-orf00004	hypothetical protein CV 4086 [Chromobacterium violaceum ATCC 12472]	gi|34499541|ref|NP 903756.1|	78.26	0.003

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contig00037-orf00006	hypothetical protein CV 4086 [Chromobacterium violaceum ATCC 12472]	gi|34499541|ref|NP 903756.1|	89.29	0.0000007
contig00037-orf00008	amino acid carrier protein [Psychrobacter cryohalolentis K5]	gi|93006043|ref|YP 580480.1|	69.71	2E-165
contig00037-orf00009	aldehyde dehydrogenase [Psychrobacter cryohalolentis K5]	gi|93006044|ref|YP 580481.1|	66.6	3E-179
contig00037-orf00012	dihydrodipicolinate synthetase [Psychrobacter cryohalolentis K5]	gi|93006045|ref|YP 580482.1|	67.7	8E-112
contig00037-orf00013	FAD dependent oxidoreductase [Psychrobacter cryohalolentis K5]	gi|93006046|ref|YP 580483.1|	52.46	1E-118
contig00037-orf00014	hypothetical protein PA14 47840 [Pseudomonas aeruginosa UCBPP-PA14]	gi|116049220|ref|YP 791977.1|	62.78	2E-107
contig00037-orf00016	hypothetical protein plu2244 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37526157|ref|NP 929501.1|	46.9	7E-57
contig00038-orf00001	phosphoribosyltransferase [Trichodesmium erythraeum IMS101]	gi|113474287|ref|YP 720348.1|	48.15	1.2
contig00039-orf00001	surface protein [Yersinia pestis Nepal516]	gi|108813262|ref|YP 649029.1|	34.41	3E-14
contig00039-orf00004	hypothetical protein NMA2173 [Neisseria meningitidis Z2491]	gi|15795044|ref|NP 284866.1|	50.15	4E-96
contig00039-orf00007	hypothetical protein NGO1686 [Neisseria gonorrhoeae FA 1090]	gi|59802011|ref|YP 208723.1|	61.26	3E-146
contig00039-orf00010	hypothetical protein NMB0316 [Neisseria meningitidis MC58]	gi|15676233|ref|NP 273365.1|	95.92	7E-106
contig00039-orf00011	7-cyano-7-deazaguanine reductase [Neisseria meningitidis Z2491]	gi|15795041|ref|NP 284863.1|	98.73	4E-89
contig00039-orf00012	MarR family transcriptional regulator [Chromobacterium violaceum ATCC	gi|34496224|ref|NP 900439.1|	39.04	2E-25
contig00039-orf00013	outer membrane multidrug resistance lipoprotein [Chromobacterium violaceum ATCC 12472]	gi|34496223|ref|NP 900438.1|	37.84	1E-80
contig00039-orf00014	penicillin-binding protein 1 [Neisseria meningitidis Z2491]	gi|15793640|ref|NP 283462.1|	81.6	0
contig00039-orf00015	pilM protein [Neisseria meningitidis MC58]	gi|15677646|ref|NP 274805.1|	61.48	9E-117
contig00039-orf00016	pilus assembly protein [Neisseria meningitidis Z2491]	gi|15793638|ref|NP 283460.1|	55.93	8E-32
contig00039-orf00018	pilus assembly protein [Neisseria meningitidis Z2491]	gi|15793636|ref|NP 283458.1|	53.66	9E-20
contig00039-orf00019	hypothetical protein NGO0094 [Neisseria gonorrhoeae FA 1090]	gi|59800555|ref|YP 207267.1|	62.09	0
contig00039-orf00021	3-dehydroquinate synthase [Neisseria meningitidis MC58]	gi|15677650|ref|NP 274811.1|	81.62	7E-171
contig00039-orf00023	N-acetyl-gamma-glutamyl-phosphate reductase [Neisseria meningitidis MC58]	gi|15677627|ref|NP 274786.1|	77.52	1E-156
contig00039-orf00024	hypothetical protein NGO1484 [Neisseria gonorrhoeae FA 1090]	gi|59801822|ref|YP 208534.1|	69.93	4E-103
contig00039-orf00026	23S rRNA 5-methyluridine methyltransferase [Nitrosospira multiformis ATCC 25196]	gi|82703334|ref|YP 412900.1|	47.13	3E-104
contig00039-orf00028	hypothetical protein NMA2010 [Neisseria meningitidis Z2491]	gi|15794890|ref|NP 284712.1|	58.37	7E-142
contig00039-orf00029	hypothetical protein NMA2009 [Neisseria meningitidis Z2491]	gi|15794889|ref|NP 284711.1|	61.2	3E-123
contig00039-orf00030	hypothetical protein NMA2008 [Neisseria meningitidis Z2491]	gi|15794888|ref|NP 284710.1|	84.5	9E-59
contig00039-orf00031	hypothetical protein NMA2007 [Neisseria meningitidis Z2491]	gi|15794887|ref|NP 284709.1|	78.57	1E-12
contig00039-orf00032	hypothetical protein NMA2006 [Neisseria meningitidis Z2491]	gi|15794886|ref|NP 284708.1|	81.51	3E-48
contig00039-orf00034	HemK protein [Neisseria meningitidis Z2491]	gi|15793377|ref|NP 283199.1|	72.68	5E-77
contig00039-orf00036	hypothetical protein PEPE 1706 [Pediococcus pentosaceus ATCC 25745]	gi|116493434|ref|YP 805169.1|	51.85	2
contig00040-orf00001	Holliday junction DNA helicase B [Neisseria gonorrhoeae FA 1090]	gi|59801175|ref|YP 207887.1|	94.46	0
contig00040-orf00003	hypothetical protein NMA1411 [Neisseria meningitidis Z2491]	gi|15794323|ref|NP 284145.1|	95.1	4E-43

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contig00040-orf00005	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase [Neisseria meningitidis MC58]	gi|15677113|ref|NP 274265.1|	92.57	0
contig00040-orf00006	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794303|ref|NP 284125.1|	90.07	2E-150
contig00040-orf00008	hypothetical protein NMB1221 [Neisseria meningitidis MC58]	gi|15677094|ref|NP 274246.1|	53.79	1E-27
contig00040-orf00011	hypothetical protein Syncc9605 1067 [Synechococcus sp. CC9605]	gi|78212600|ref|YP 381379.1|	51.58	7E-127
contig00040-orf00012	SbmA protein [Mannheimia succiniciproducens MBEL55E]	gi|52425371|ref|YP 088508.1|	50.77	2E-169
contig00040-orf00014	TonB-dependent receptor protein [Neisseria meningitidis Z2491]	gi|15794451|ref|NP 284273.1|	79.92	0
contig00040-orf00015	ferredoxin--NADP reductase [Neisseria meningitidis Z2491]	gi|15794347|ref|NP 284169.1|	98.84	1E-147
contig00041-orf00001	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	84.85	4E-10
contig00041-orf00004	hypothetical protein NMB0350 [Neisseria meningitidis MC58]	gi|15676265|ref|NP 273399.1|	100	3E-22
contig00041-orf00006	adhesin HecA [Burkholderia xenovorans LB400]	gi|91779924|ref|YP 555132.1|	44.24	4E-25
contig00041-orf00007	hypothetical protein NMA0482 [Neisseria meningitidis Z2491]	gi|15793482|ref|NP 283304.1|	100	2E-20
contig00041-orf00010	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	80.5	0
contig00042-orf00001	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801511|ref|YP 208223.1|	95.52	3E-31
contig00042-orf00002	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801512|ref|YP 208224.1|	94.44	6E-43
contig00042-orf00004	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801513|ref|YP 208225.1|	90.85	6E-177
contig00042-orf00006	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	gi|59801514|ref|YP 208226.1|	81.08	1E-26
contig00042-orf00007	peptide transporter [Neisseria meningitidis MC58]	gi|15677949|ref|NP 275121.1|	77.11	0
contig00042-orf00009	hypothetical protein NMA0289 [Neisseria meningitidis Z2491]	gi|15793306|ref|NP 283128.1|	74.83	1E-51
contig00042-orf00013	prolyl endopeptidase [Neisseria meningitidis Z2491]	gi|15793570|ref|NP 283392.1|	94.63	0
contig00042-orf00014	hypothetical protein NMB1116 [Neisseria meningitidis MC58]	gi|15676995|ref|NP 274146.1|	55.81	0.0002
contig00042-orf00016	DNA ligase [Neisseria meningitidis Z2491]	gi|15793396|ref|NP 283218.1|	91.39	1E-142
contig00042-orf00017	hydrolase [Neisseria meningitidis Z2491]	gi|15793395|ref|NP 283217.1|	80	2E-98
contig00042-orf00020	lipoprotein [Neisseria meningitidis Z2491]	gi|15793551|ref|NP 283373.1|	71.13	2E-51
contig00042-orf00022	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793550|ref|NP 283372.1|	66.19	4E-48
contig00044-orf00001	transferrin-binding protein 2 precursor [Haemophilus influenzae Rd KW20]	gi|16272933|ref|NP 439158.1|	26.24	0.0000003
contig00044-orf00003	exodeoxyribonuclease small subunit [Neisseria meningitidis MC58]	gi|15676186|ref|NP 273318.1|	84.93	6E-26
contig00044-orf00006	geranyltranstransferase [Neisseria meningitidis Z2491]	gi|15795095|ref|NP 284917.1|	82.47	2E-119
contig00044-orf00008	hypothetical protein Bcen2424 5558 [Burkholderia cenocepacia HI2424]	gi|116693651|ref|YP 839184.1|	50.78	1E-30
contig00044-orf00010	phosphoglycerate kinase [Neisseria meningitidis Z2491]	gi|15793275|ref|NP 283097.1|	97.45	0
contig00044-orf00013	tRNA modification GTPase TrmE [Neisseria meningitidis MC58]	gi|15677815|ref|NP 274979.1|	79.07	0
contig00044-orf00016	Holliday junction DNA helicase motor protein [Neisseria gonorrhoeae FA 1090]	gi|59802051|ref|YP 208763.1|	86.6	1E-92
contig00044-orf00018	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794004|ref|NP 283826.1|	53.66	2E-13
contig00044-orf00020	ParA family protein [Neisseria meningitidis MC58]	gi|15676118|ref|NP 273249.1|	85.06	3E-105
contig00044-orf00021	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	87.5	2E-09
contig00044-orf00022	methionine aminopeptidase [Neisseria meningitidis Z2491]	gi|15793347|ref|NP 283169.1|	95.92	1E-139
contig00044-orf00024	TonB1 protein [Shewanella oneidensis MR-1]	gi|24375168|ref|NP 719211.1|	30.61	0.14

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contig00044-orf00026	lipoprotein [Neisseria meningitidis Z2491]	gi|15793349|ref|NP 283171.1|	83.54	1E-74
contig00044-orf00028	phosphoheptose isomerase [Neisseria gonorrhoeae FA 1090]	gi|59802294|ref|YP 209006.1|	95.94	3E-103
contig00044-orf00030	hypothetical protein NGO1987 [Neisseria gonorrhoeae FA 1090]	gi|59802295|ref|YP 209007.1|	88.7	1E-54
contig00044-orf00031	hypothetical protein NGO1988 [Neisseria gonorrhoeae FA 1090]	gi|59802296|ref|YP 209008.1|	85.12	5E-133
contig00044-orf00033	hypothetical protein MS1522 [Mannheimia succiniciproducens MBEL55E]	gi|52425577|ref|YP 088714.1|	53.72	9E-31
contig00044-orf00037	nuclease [Neisseria meningitidis Z2491]	gi|15793359|ref|NP 283181.1|	95.37	3E-148
contig00044-orf00038	hypothetical protein NGO1995 [Neisseria gonorrhoeae FA 1090]	gi|59802303|ref|YP 209015.1|	76.32	9E-51
contig00044-orf00040	hypothetical protein NGO1996 [Neisseria gonorrhoeae FA 1090]	gi|59802304|ref|YP 209016.1|	73.3	5E-73
contig00044-orf00042	zinc transporter ZupT [Neisseria meningitidis MC58]	gi|15676102|ref|NP 273233.1|	88.48	7E-115
contig00044-orf00044	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793107|ref|NP 282929.1|	49.69	5E-19
contig00044-orf00046	XRE family transcriptional regulator [Nitrosospira multiformis ATCC 25196]	gi|82703063|ref|YP 412629.1|	73.12	3E-35
contig00044-orf00048	valyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15676101|ref|NP 273232.1|	92.17	0
contig00044-orf00050	indole-3-glycerol-phosphate synthase [Neisseria meningitidis MC58]	gi|15676199|ref|NP 273331.1|	83.08	9E-107
contig00044-orf00051	membrane protein [Neisseria meningitidis Z2491]	gi|15794573|ref|NP 284395.1|	47.92	0.003
contig00044-orf00052	Phage integrase [Dechloromonas aromatica RCB]	gi|71906676|ref|YP 284263.1|	52.36	1E-59
contig00044-orf00053	excisionase/Xis, DNA-binding [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	gi|78357726|ref|YP 389175.1|	45.83	0.0005
contig00044-orf00054	hypothetical protein Cag 1180 [Chlorobium chlorochromatii CaD3]	gi|78189147|ref|YP 379485.1|	35.14	3.5
contig00045-orf00002	hypothetical protein NMA0245 [Neisseria meningitidis Z2491]	gi|15793263|ref|NP 283085.1|	92.79	4E-117
contig00045-orf00005	nicotinamidase [Neisseria meningitidis Z2491]	gi|15793262|ref|NP 283084.1|	96.21	4E-118
contig00045-orf00006	lipopolysaccharide heptosyltransferase I [Neisseria meningitidis Z2491]	gi|15793261|ref|NP 283083.1|	94.72	1E-178
contig00045-orf00008	electron transfer flavoprotein, beta subunit [Neisseria meningitidis MC58]	gi|15677968|ref|NP 275140.1|	97.07	2E-101
contig00045-orf00009	electron transfer flavoprotein subunit alpha [Neisseria meningitidis MC58]	gi|15677967|ref|NP 275139.1|	95.18	8E-161
contig00045-orf00010	hypothetical protein NMA0240 [Neisseria meningitidis Z2491]	gi|15793258|ref|NP 283080.1|	97.04	9E-105
contig00045-orf00011	hypothetical protein NMB2152 [Neisseria meningitidis MC58]	gi|15677965|ref|NP 275137.1|	93.27	2E-54
contig00045-orf00012	phosphoribosylamine--glycine ligase [Neisseria gonorrhoeae FA 1090]	gi|59802251|ref|YP 208963.1|	95.27	0
contig00045-orf00013	hypothetical protein NMA0237 [Neisseria meningitidis Z2491]	gi|15793255|ref|NP 283077.1|	81.22	3E-84
contig00045-orf00014	lipoprotein [Neisseria meningitidis Z2491]	gi|15793253|ref|NP 283075.1|	61.54	3E-40
contig00045-orf00017	ATP-dependent DNA helicase [Neisseria meningitidis MC58]	gi|15676198|ref|NP 273330.1|	78.1	0
contig00045-orf00018	site-specific DNA-methyltransferase (adenine-specific) [Nitrosococcus oceani ATCC 19707]	gi|77166378|ref|YP 344903.1|	65	8E-16
contig00045-orf00019	type III restriction system methylase [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	gi|78356789|ref|YP 388238.1|	51.11	0.0002
contig00045-orf00020	ribonuclease II-related protein [Neisseria meningitidis MC58]	gi|15676206|ref|NP 273338.1|	95.15	0
contig00045-orf00025	acyl-CoA dehydrogenase [Chromobacterium violaceum ATCC 12472]	gi|34499271|ref|NP 903486.1|	58.11	5E-138
contig00045-orf00028	ATP-dependent DNA helicase DinG [Neisseria meningitidis MC58]	gi|15676210|ref|NP 273342.1|	92.04	0
contig00045-orf00030	hypothetical protein Daro 3801 [Dechloromonas aromatica RCB]	gi|71909412|ref|YP 286999.1|	66.67	5E-18

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contig00045-orf00032	RNA polymerase sigma factor [Neisseria meningitidis MC58]	gi|15677957|ref|NP 275129.1|	74.6	3E-80
contig00045-orf00033	hypothetical protein NMB2145 [Neisseria meningitidis MC58]	gi|15677958|ref|NP 275130.1|	54.55	2E-08
contig00045-orf00036	cytochrome [Neisseria meningitidis Z2491]	gi|15794819|ref|NP 284641.1|	78.05	1E-34
contig00045-orf00038	phnA protein [Neisseria meningitidis MC58]	gi|15675977|ref|NP 273103.1|	84.55	9E-49
contig00045-orf00039	periplasmic protein [Neisseria meningitidis Z2491]	gi|15795088|ref|NP 284910.1|	79.61	3E-86
contig00045-orf00042	RNA methyltransferase [Neisseria meningitidis MC58]	gi|15676192|ref|NP 273324.1|	88.96	2E-76
contig00045-orf00044	hypothetical protein NGO1726 [Neisseria gonorrhoeae FA 1090]	gi|59802047|ref|YP 208759.1|	73.89	3E-85
contig00045-orf00046	hydrolase [Neisseria meningitidis Z2491]	gi|15795085|ref|NP 284907.1|	74.6	4E-92
contig00045-orf00048	anion transporter [Rhodoferax ferrireducens T118]	gi|89899730|ref|YP 522201.1|	68.47	0
contig00045-orf00051	hypothetical protein NGO1724 [Neisseria gonorrhoeae FA 1090]	gi|59802045|ref|YP 208757.1|	70.11	8E-95
contig00045-orf00054	trifunctional thioredoxin/methionine sulfoxide reductase A/B protein [Neisseria meningitidis Z2491]	gi|15793307|ref|NP 283129.1|	94.64	0
contig00045-orf00057	signal recognition particle protein [Neisseria meningitidis Z2491]	gi|15793308|ref|NP 283130.1|	98.68	3E-164
contig00045-orf00060	hypothetical protein NMA0229 [Neisseria meningitidis Z2491]	gi|15793251|ref|NP 283073.1|	68.58	3E-85
contig00045-orf00061	hypothetical protein NGO1946 [Neisseria gonorrhoeae FA 1090]	gi|59802258|ref|YP 208970.1|	96.79	2E-156
contig00045-orf00065	hypothetical protein NMB2140 [Neisseria meningitidis MC58]	gi|15677953|ref|NP 275125.1|	84.96	6E-35
contig00045-orf00066	ribosome-associated GTPase [Neisseria meningitidis Z2491]	gi|15795093|ref|NP 284915.1|	87.41	2E-120
contig00045-orf00068	hypothetical protein CV 0778 [Chromobacterium violaceum ATCC 12472]	gi|34496233|ref|NP 900448.1|	65.71	1E-74
contig00045-orf00069	tRNA pseudouridine synthase C [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602344|ref|NP 245416.1|	62.98	5E-79
contig00045-orf00075	adenylosuccinate lyase [Neisseria meningitidis MC58]	gi|15676208|ref|NP 273340.1|	93.86	0
contig00045-orf00076	hypothetical protein STH2030 [Symbiobacterium thermophilum IAM 14863]	gi|51893168|ref|YP 075859.1|	34.81	5E-14
contig00045-orf00077	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	55.56	0.0002
contig00045-orf00079	serine/threonine transporter SstT [Neisseria meningitidis MC58]	gi|15677946|ref|NP 275118.1|	74.32	7E-138
contig00045-orf00081	hypothetical protein NGO1956 [Neisseria gonorrhoeae FA 1090]	gi|59802267|ref|YP 208979.1|	76.33	0
contig00045-orf00083	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793305|ref|NP 283127.1|	73.23	1E-29
contig00045-orf00086	hypothetical protein RPC 1722 [Rhodopseudomonas palustris BisB18]	gi|90423230|ref|YP 531600.1|	57.24	6E-29
contig00045-orf00089	hypothetical protein NMB2135 [Neisseria meningitidis MC58]	gi|15677948|ref|NP 275120.1|	65.19	0
contig00045-orf00090	hypothetical protein NMA2201 [Neisseria meningitidis Z2491]	gi|15795070|ref|NP 284892.1|	67.49	3E-50
contig00045-orf00091	NADH dehydrogenase I chain A [Neisseria meningitidis Z2491]	gi|15793053|ref|NP 282875.1|	94.07	4E-60
contig00045-orf00092	NADH dehydrogenase subunit B [Neisseria meningitidis MC58]	gi|15676166|ref|NP 273298.1|	99.38	4E-78
contig00045-orf00093	NADH dehydrogenase subunit C [Neisseria meningitidis MC58]	gi|15676167|ref|NP 273299.1|	96.95	1E-109
contig00045-orf00095	NADH dehydrogenase subunit D [Neisseria meningitidis Z2491]	gi|15793050|ref|NP 282872.1|	99.04	0
contig00045-orf00096	NADH dehydrogenase subunit E [Neisseria meningitidis MC58]	gi|15676169|ref|NP 273301.1|	96.82	6E-84
contig00045-orf00097	NADH dehydrogenase I chain F [Neisseria meningitidis MC58]	gi|15676170|ref|NP 273302.1|	98.15	0
contig00045-orf00098	hypothetical protein SAV 3744 [Streptomyces avermitilis MA-4680]	gi|29830287|ref|NP 824921.1|	31.48	0.14
contig00045-orf00099	hypothetical protein NMA0012 [Neisseria meningitidis Z2491]	gi|15793046|ref|NP 282868.1|	81.08	6E-11

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contig00045-orf00101	hypothetical protein NMA0011 [Neisseria meningitidis Z2491]	gi|15793045|ref|NP 282867.1|	96.63	8E-48
contig00045-orf00104	NADH dehydrogenase subunit G [Neisseria meningitidis Z2491]	gi|15793044|ref|NP 282866.1|	96.15	0
contig00045-orf00105	NADH dehydrogenase I chain H [Neisseria meningitidis Z2491]	gi|15793043|ref|NP 282865.1|	98.88	0
contig00045-orf00108	NADH dehydrogenase subunit I [Neisseria meningitidis Z2491]	gi|15793042|ref|NP 282864.1|	98.74	6E-80
contig00045-orf00109	NADH dehydrogenase I chain J [Neisseria meningitidis MC58]	gi|15676177|ref|NP 273309.1|	95.07	4E-75
contig00045-orf00110	NADH dehydrogenase subunit K [Neisseria meningitidis Z2491]	gi|15793039|ref|NP 282861.1|	100	9E-41
contig00045-orf00113	hypothetical protein NMA0004 [Neisseria meningitidis Z2491]	gi|15793038|ref|NP 282860.1|	98.43	6E-92
contig00045-orf00117	NADH dehydrogenase subunit L [Neisseria meningitidis Z2491]	gi|15793036|ref|NP 282858.1|	97.63	0
contig00045-orf00120	hypothetical protein STER 1555 [Streptococcus thermophilus LMD-9]	gi|116628284|ref|YP 820903.1|	61.36	4E-22
contig00045-orf00121	hypothetical protein NMA0001 [Neisseria meningitidis Z2491]	gi|15793035|ref|NP 282857.1|	92.45	4E-53
contig00045-orf00123	NADH dehydrogenase subunit M [Neisseria meningitidis Z2491]	gi|15795098|ref|NP 284920.1|	93.17	0
contig00045-orf00125	NADH dehydrogenase subunit N [Neisseria meningitidis MC58]	gi|15676183|ref|NP 273315.1|	81.87	0
contig00045-orf00127	hypothetical protein NMB0260 [Neisseria meningitidis MC58]	gi|15676184|ref|NP 273316.1|	85.71	0.0001
contig00045-orf00128	hypothetical protein NMA2227 [Neisseria meningitidis Z2491]	gi|15795096|ref|NP 284918.1|	87.34	4E-37
contig00045-orf00130	gamma-glutamyl kinase [Methylobacillus flagellatus KT]	gi|91776568|ref|YP 546324.1|	62.74	5E-116
contig00045-orf00133	deoxyribodopyrimidine photolyase [Neisseria meningitidis Z2491]	gi|15795067|ref|NP 284889.1|	48	1E-100
contig00045-orf00137	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793108|ref|NP 282930.1|	86.33	7E-149
contig00045-orf00138	hypothetical protein NMB0013 [Neisseria meningitidis MC58]	gi|15675961|ref|NP 273079.1|	83.22	4E-58
contig00045-orf00140	hypothetical protein NMB0012 [Neisseria meningitidis MC58]	gi|15675960|ref|NP 273078.1|	75	2E-34
contig00045-orf00141	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793277|ref|NP 283099.1|	82.11	9E-101
contig00045-orf00145	Rrf [Neisseria gonorrhoeae FA 1090]	gi|59802114|ref|YP 208826.1|	97.3	5E-95
contig00045-orf00146	undecaprenyl pyrophosphate synthetase [Neisseria meningitidis MC58]	gi|15676113|ref|NP 273244.1|	95.95	4E-136
contig00045-orf00148	phosphatidate cytidylyltransferase [Neisseria meningitidis Z2491]	gi|15793111|ref|NP 282933.1|	84.79	3E-136
contig00045-orf00151	1-deoxy-D-xylulose 5-phosphate reductoisomerase [Neisseria meningitidis Z2491]	gi|15793112|ref|NP 282934.1|	93.91	0
contig00045-orf00154	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793113|ref|NP 282935.1|	76.85	0
contig00045-orf00157	outer membrane protein OMP85 [Neisseria meningitidis Z2491]	gi|15793114|ref|NP 282936.1|	83.25	0
contig00045-orf00159	hypothetical protein NMA0086 [Neisseria meningitidis Z2491]	gi|15793115|ref|NP 282937.1|	68.06	2E-50
contig00045-orf00160	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Neisseria meningitidis MC58]	gi|15676107|ref|NP 273238.1|	93.64	3E-172
contig00045-orf00162	(3R)-hydroxymyristoyl-ACP dehydratase [Neisseria meningitidis MC58]	gi|15676106|ref|NP 273237.1|	96.64	4E-77
contig00045-orf00164	hypothetical protein NMA0089 [Neisseria meningitidis Z2491]	gi|15793118|ref|NP 282940.1|	94.69	2E-114
contig00045-orf00165	UDP-N-acetylglucosamine acyltransferase [Neisseria meningitidis Z2491]	gi|15793119|ref|NP 282941.1|	96.12	4E-145
contig00045-orf00170	pyridoxal phosphate biosynthetic protein [Neisseria meningitidis MC58]	gi|15676122|ref|NP 273253.1|	76.22	1E-124
contig00045-orf00172	hypothetical protein NGO1925 [Neisseria gonorrhoeae FA 1090]	gi|59802238|ref|YP 208950.1|	74.05	4E-69
contig00045-orf00174	ArsC [Neisseria gonorrhoeae FA 1090]	gi|59802237|ref|YP 208949.1|	76.72	3E-44
contig00045-orf00178	putative thioredoxin [Neisseria gonorrhoeae FA 1090]	gi|59802236|ref|YP 208948.1|	80	2E-68

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contig00045-orf00180	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793272|ref|NP 283094.1|	96.3	3E-114
contig00045-orf00181	ABC transporter integral membrane protein [Neisseria meningitidis Z2491]	gi|15793273|ref|NP 283095.1|	89.51	6E-142
contig00045-orf00184	DNA mismatch repair protein [Neisseria gonorrhoeae FA 1090]	gi|59802243|ref|YP 208955.1|	85.25	0
contig00045-orf00185	hypothetical protein NMB0507 [Neisseria meningitidis MC58]	gi|15676416|ref|NP 273553.1|	98.44	2E-31
contig00045-orf00186	lipoprotein [Neisseria meningitidis Z2491]	gi|15794539|ref|NP 284361.1|	82.72	1E-73
contig00045-orf00189	hypothetical protein HD0279 [Haemophilus ducreyi 35000HP]	gi|33151516|ref|NP 872869.1|	33.97	9E-17
contig00045-orf00193	hypothetical protein NMA1494 [Neisseria meningitidis Z2491]	gi|15794394|ref|NP 284216.1|	50.37	7E-31
contig00045-orf00196	putative twitching motility - like protein [Neisseria gonorrhoeae FA 1090]	gi|59802223|ref|YP 208935.1|	68.69	2E-157
contig00045-orf00197	#N/A	#N/A	#N/A	#N/A
contig00045-orf00199	twitching motility protein PilT [Neisseria meningitidis MC58]	gi|15675990|ref|NP 273117.1|	89.06	5E-159
contig00045-orf00201	hypothetical protein NMA0217 [Neisseria meningitidis Z2491]	gi|15793240|ref|NP 283062.1|	80.62	5E-100
contig00045-orf00202	lipoprotein [Neisseria meningitidis Z2491]	gi|15793239|ref|NP 283061.1|	65.77	3E-35
contig00045-orf00203	pyrroline-5-carboxylate reductase [Neisseria meningitidis Z2491]	gi|15793238|ref|NP 283060.1|	81.75	9E-104
contig00045-orf00204	hypothetical protein Daro 3886 [Dechloromonas aromatica RCB]	gi|71909497|ref|YP 287084.1|	26.53	0.001
contig00045-orf00206	DnaK suppressor protein [Neisseria meningitidis MC58]	gi|15675994|ref|NP 273121.1|	93.48	7E-70
contig00046-orf00003	response regulator/TPR domain-containing protein [Pseudomonas entomophila L48]	gi|104780135|ref|YP 606633.1|	39.22	3.5
contig00046-orf00006	aldehyde dehydrogenase A [Neisseria meningitidis MC58]	gi|15677798|ref|NP 274962.1|	98.32	0
contig00046-orf00010	lysyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59801795|ref|YP 208507.1|	98.41	0
contig00046-orf00012	septum formation inhibitor [Neisseria gonorrhoeae FA 1090]	gi|59802133|ref|YP 208845.1|	66.06	1E-75
contig00046-orf00013	septum site-determining protein [Neisseria meningitidis Z2491]	gi|15793128|ref|NP 282950.1|	94.58	3E-123
contig00046-orf00015	hypothetical protein NGO1814 [Neisseria gonorrhoeae FA 1090]	gi|59802132|ref|YP 208844.1|	92.5	1E-34
contig00046-orf00017	hydrogen peroxide-inducible genes activator [Neisseria meningitidis Z2491]	gi|15793126|ref|NP 282948.1|	90.52	2E-155
contig00046-orf00021	dihydrodipicolinate reductase [Neisseria gonorrhoeae FA 1090]	gi|59802100|ref|YP 208812.1|	94.78	7E-142
contig00046-orf00022	lipoprotein [Neisseria meningitidis Z2491]	gi|15793094|ref|NP 282916.1|	78.45	1E-47
contig00046-orf00023	hypothetical protein NGO1779 [Neisseria gonorrhoeae FA 1090]	gi|59802098|ref|YP 208810.1|	96.53	5E-77
contig00046-orf00027	leucyl/phenylalanyl-tRNA--protein transferase [Neisseria gonorrhoeae FA 1090]	gi|59802097|ref|YP 208809.1|	73.73	4E-102
contig00046-orf00029	D-tyrosyl-tRNA deacylase [Neisseria meningitidis Z2491]	gi|15795011|ref|NP 284833.1|	75.17	4E-60
contig00046-orf00031	hypothetical protein NMA2142 [Neisseria meningitidis Z2491]	gi|15795013|ref|NP 284835.1|	59.14	9E-81
contig00046-orf00032	hypothetical protein NGO1657 [Neisseria gonorrhoeae FA 1090]	gi|59801984|ref|YP 208696.1|	66.27	5E-16
contig00046-orf00033	YciI-like protein [Neisseria gonorrhoeae FA 1090]	gi|59801985|ref|YP 208697.1|	81.25	3E-39
contig00046-orf00034	morphogene [Neisseria meningitidis Z2491]	gi|15795016|ref|NP 284838.1|	77.27	2E-76
contig00046-orf00037	antigen protein TspA [Neisseria meningitidis Z2491]	gi|15795017|ref|NP 284839.1|	43.08	3E-33
contig00046-orf00039	tRNA pseudouridine synthase A [Neisseria meningitidis MC58]	gi|15677859|ref|NP 275027.1|	77.12	6E-104
contig00046-orf00040	porin, major outer membrane protein P.I [Neisseria meningitidis Z2491]	gi|15793406|ref|NP 283228.1|	53.74	4E-95
contig00046-orf00042	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	46.34	0.001
contig00046-orf00043	ribose 5-phosphate isomerase [Mycobacterium sp. MCS]	gi|108799528|ref|YP 639725.1|	47.06	0.029

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contig00046-orf00052	DNA gyrase subunit B [Neisseria gonorrhoeae FA 1090]	gi|59802091|ref|YP 208803.1|	96.73	0
contig00046-orf00055	L-serine dehydratase [Neisseria meningitidis Z2491]	gi|15793088|ref|NP 282910.1|	95.42	7E-151
contig00046-orf00058	L-serine dehydratase [Neisseria meningitidis MC58]	gi|15676137|ref|NP 273268.1|	79.77	1E-74
contig00046-orf00060	putative site-specific recombinase [Neisseria gonorrhoeae FA 1090]	gi|59800504|ref|YP 207216.1|	68.75	4E-108
contig00046-orf00061	esterase [Alkalilimnicola ehrlichii MLHE-1]	gi|114320612|ref|YP 742295.1|	44.27	2E-28
contig00046-orf00063	fructose-1,6-bisphosphate aldolase [Neisseria meningitidis Z2491]	gi|15793578|ref|NP 283400.1|	96.89	0
contig00046-orf00067	two-component system, regulatory protein [Chromobacterium violaceum ATCC 12472]	gi|34495662|ref|NP 899877.1|	43.46	4E-40
contig00046-orf00068	glutamyl-Q tRNA(Asp) synthetase [Neisseria meningitidis Z2491]	gi|15795009|ref|NP 284831.1|	76.45	2E-123
contig00046-orf00069	protoheme IX farnesyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74316353|ref|YP 314093.1|	40.62	5.9
contig00046-orf00070	hypothetical protein NGO0032 [Neisseria gonorrhoeae FA 1090]	gi|59800501|ref|YP 207213.1|	72.77	1E-89
contig00046-orf00071	acetyltransferase [Neisseria meningitidis Z2491]	gi|15793575|ref|NP 283397.1|	59.18	2E-41
contig00046-orf00072	hypothetical protein NMA0583 [Neisseria meningitidis Z2491]	gi|15793574|ref|NP 283396.1|	43.01	1E-49
contig00046-orf00077	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein [Neisseria meningitidis Z2491]	gi|15793440|ref|NP 283262.1|	86.95	0
contig00046-orf00080	hypothetical protein NMB2003 [Neisseria meningitidis MC58]	gi|15677831|ref|NP 274995.1|	83.78	3E-42
contig00046-orf00081	hypothetical protein NMA0436 [Neisseria meningitidis Z2491]	gi|15793441|ref|NP 283263.1|	90.31	3E-81
contig00047-orf00001	hypothetical protein NMB1828 [Neisseria meningitidis MC58]	gi|15677664|ref|NP 274825.1|	55.3	5E-76
contig00047-orf00003	TonB-dependent receptor [Neisseria meningitidis MC58]	gi|15677665|ref|NP 274826.1|	81.7	0
contig00047-orf00005	sugar transporter [Xanthomonas axonopodis pv. citri str. 306]	gi|21244213|ref|NP 643795.1|	44.68	2E-97
contig00047-orf00007	LacI family transcriptional regulator [Rhizobium etli CFN 42]	gi|86360634|ref|YP 472522.1|	38.04	3E-52
contig00047-orf00008	glucose-6-phosphate isomerase 2 [Neisseria meningitidis Z2491]	gi|15795025|ref|NP 284847.1|	73	0
contig00047-orf00012	hypothetical protein NGO1195 [Neisseria gonorrhoeae FA 1090]	gi|59801555|ref|YP 208267.1|	79.54	2E-177
contig00047-orf00013	phosphoenolpyruvate carboxylase [Neisseria meningitidis Z2491]	gi|15793382|ref|NP 283204.1|	92.68	9E-28
contig00047-orf00015	phosphoenolpyruvate carboxylase [Neisseria meningitidis Z2491]	gi|15793382|ref|NP 283204.1|	89.29	0
contig00047-orf00019	molybdenum cofactor biosynthesis protein C [Campylobacter jejuni subsp. jejuni NCTC 11168]	gi|15791623|ref|NP 281446.1|	39.85	1E-20
contig00047-orf00021	hypothetical protein NGO1370 [Neisseria gonorrhoeae FA 1090]	gi|59801718|ref|YP 208430.1|	80.61	0
contig00047-orf00023	putative transferase [Neisseria gonorrhoeae FA 1090]	gi|59802308|ref|YP 209020.1|	88.41	5E-75
contig00047-orf00027	bifunctional biotin--[acetyl-CoA-carboxylase] ligase/pantothenate kinase [Neisseria meningitidis MC58]	gi|15677897|ref|NP 275065.1|	71.57	0
contig00047-orf00030	hypothetical protein NMB2074 [Neisseria meningitidis MC58]	gi|15677896|ref|NP 275064.1|	53.55	5E-40
contig00047-orf00032	hypothetical protein BPSL0300 [Burkholderia pseudomallei K96243]	gi|53717941|ref|YP 106927.1|	28.21	7E-13
contig00047-orf00033	TPR repeat-containing protein [Clostridium tetani E88]	gi|28211870|ref|NP 782814.1|	44.44	0.53
contig00047-orf00034	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793692|ref|NP 283514.1|	93.21	0
contig00047-orf00035	hypothetical protein NMB1796 [Neisseria meningitidis MC58]	gi|15677635|ref|NP 274794.1|	84.57	2E-88
contig00047-orf00037	PnuC protein [Mannheimia succiniciproducens MBEL55E]	gi|52424248|ref|YP 087385.1|	74.03	3E-93

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contig00047-orf00041	radical SAM family protein [Psychrobacter cryohalolentis K5]	gi|93005656|ref|YP 580093.1|	65.39	8E-155
contig00047-orf00042	hypothetical protein Pcryo 0825 [Psychrobacter cryohalolentis K5]	gi|93005655|ref|YP 580092.1|	42.47	4E-53
contig00048-orf00001	elongation factor G [Neisseria meningitidis Z2491]	gi|15793163|ref|NP 282985.1|	98.43	0
contig00048-orf00003	30S ribosomal protein S7 [Neisseria gonorrhoeae FA 1090]	gi|59802165|ref|YP 208877.1|	99.31	2E-75
contig00048-orf00004	30S ribosomal protein S12 [Neisseria meningitidis Z2491]	gi|15793165|ref|NP 282987.1|	100	4E-37
contig00048-orf00007	DNA-directed RNA polymerase subunit beta' [Neisseria meningitidis Z2491]	gi|15793169|ref|NP 282991.1|	98.49	0
contig00048-orf00010	DNA-directed RNA polymerase subunit beta [Neisseria meningitidis Z2491]	gi|15793170|ref|NP 282992.1|	97.63	0
contig00048-orf00011	50S ribosomal protein L7/L12 [Neisseria meningitidis Z2491]	gi|15793171|ref|NP 282993.1|	98.37	1E-46
contig00048-orf00012	50S ribosomal protein L10 [Neisseria meningitidis Z2491]	gi|15793172|ref|NP 282994.1|	98.68	2E-27
contig00048-orf00013	50S ribosomal protein L1 [Neisseria meningitidis Z2491]	gi|15793173|ref|NP 282995.1|	97.84	1E-110
contig00048-orf00014	50S ribosomal protein L11 [Neisseria meningitidis Z2491]	gi|15793174|ref|NP 282996.1|	99.31	6E-75
contig00048-orf00015	transcription antitermination protein NusG [Neisseria meningitidis Z2491]	gi|15793175|ref|NP 282997.1|	88.82	8E-83
contig00048-orf00016	preprotein translocase subunit SecE [Neisseria meningitidis Z2491]	gi|15793176|ref|NP 282998.1|	73.53	4E-09
contig00049-orf00001	integral membrane ion transporter [Neisseria meningitidis Z2491]	gi|15794844|ref|NP 284666.1|	86.52	0
contig00049-orf00003	NosX accesory protein [Sinorhizobium meliloti 1021]	gi|16263101|ref|NP 435894.1|	46.24	2E-57
contig00049-orf00005	peptide chain release factor 1 [Neisseria meningitidis MC58]	gi|15677534|ref|NP 274690.1|	98.88	2E-171
contig00049-orf00006	putative ABC transporter, permease protein [Neisseria gonorrhoeae FA 1090]	gi|59802435|ref|YP 209147.1|	95.18	9E-94
contig00049-orf00008	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677778|ref|NP 274942.1|	97.55	2E-122
contig00049-orf00009	hypothetical protein NMA0181 [Neisseria meningitidis Z2491]	gi|15793209|ref|NP 283031.1|	40.38	0.00002
contig00049-orf00010	coproporphyrinogen III oxidase [Neisseria meningitidis Z2491]	gi|15794982|ref|NP 284804.1|	93.7	0
contig00049-orf00011	coproporphyrinogen III oxidase [Neisseria meningitidis Z2491]	gi|15794982|ref|NP 284804.1|	84.09	8E-16
contig00049-orf00012	anaerobic transcriptional regulatory protein [Neisseria meningitidis Z2491]	gi|15794981|ref|NP 284803.1|	91.8	1E-116
contig00049-orf00014	cell division inhibitor SULA [Bdellovibrio bacteriovorus HD100]	gi|42523666|ref|NP 969046.1|	30.28	5E-09
contig00049-orf00016	hypothetical protein PSEEN3677 [Pseudomonas entomophila L48]	gi|104782694|ref|YP 609192.1|	27.8	6E-20
contig00049-orf00021	DNA ligase [Neisseria meningitidis Z2491]	gi|15793834|ref|NP 283656.1|	91.06	0
contig00049-orf00022	hypothetical protein NMB0667 [Neisseria meningitidis MC58]	gi|15676565|ref|NP 273709.1|	69.16	2E-162
contig00049-orf00023	N-acetyl-anhydromuranmyl-L-alanine amidase [Neisseria meningitidis Z2491]	gi|15793836|ref|NP 283658.1|	77.09	1E-79
contig00049-orf00024	hypothetical protein NMB0669 [Neisseria meningitidis MC58]	gi|15676567|ref|NP 273711.1|	79.76	2E-136
contig00049-orf00026	single-stranded-DNA-specific exonuclease RecJ [Neisseria meningitidis MC58]	gi|15676738|ref|NP 273883.1|	93.99	0
contig00049-orf00028	Fe-S protein [Photobacterium profundum SS9]	gi|54308726|ref|YP 129746.1|	52.33	1E-17
contig00049-orf00031	hypothetical protein NGO1981 [Neisseria gonorrhoeae FA 1090]	gi|59802289|ref|YP 209001.1|	30.65	1E-09
contig00049-orf00035	hypothetical protein NGO1455 [Neisseria gonorrhoeae FA 1090]	gi|59801796|ref|YP 208508.1|	89.5	0
contig00049-orf00036	hypothetical protein NMA1703 [Neisseria meningitidis Z2491]	gi|15794596|ref|NP 284418.1|	94.16	6E-76
contig00049-orf00039	hypothetical protein NGO0960 [Neisseria gonorrhoeae FA 1090]	gi|59801349|ref|YP 208061.1|	88.37	7E-122
contig00049-orf00041	ABC transporter, permease protein [Streptococcus pneumoniae TIGR4]	gi|15900033|ref|NP 344637.1|	26.53	0.053
contig00049-orf00043	segregation and condensation protein A [Neisseria meningitidis MC58]	gi|15677357|ref|NP 274512.1|	89.73	3E-122
contig00049-orf00046	branched-chain amino acid transporter [Oceanobacillus iheyensis HTE831]	gi|23097876|ref|NP 691342.1|	49.41	1E-110

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contig00049-orf00049	nicotinate phosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15794599|ref|NP 284421.1|	90.84	0
contig00050-orf00001	hypothetical protein SG1155 [Sodalis glossinidius str. 'morsitans']	gi|85059133|ref|YP 454835.1|	63.29	1E-23
contig00050-orf00002	excinuclease ABC subunit B [Neisseria gonorrhoeae FA 1090]	gi|59801006|ref|YP 207718.1|	98.07	0
contig00050-orf00003	putative thioredoxin I [Neisseria gonorrhoeae FA 1090]	gi|59801079|ref|YP 207791.1|	90.91	2E-52
contig00050-orf00006	ABC transporter related [Polaromonas sp. JS666]	gi|91788288|ref|YP 549240.1|	50.94	9E-141
contig00050-orf00008	acyl-CoA synthetase [Neisseria meningitidis Z2491]	gi|15794382|ref|NP 284204.1|	85.6	0
contig00050-orf00011	ABC peptide transporter, inner membrane subunit [Burkholderia xenovorans LB400]	gi|91784163|ref|YP 559369.1|	63.72	6E-94
contig00050-orf00013	#N/A	#N/A	#N/A	#N/A
contig00050-orf00014	binding-protein dependent transport system inner membrane protein [Ralstonia eutropha JMP134]	gi|73541816|ref|YP 296336.1|	69.94	9E-119
contig00050-orf00016	hypothetical protein Neut 1890 [Nitrosomonas eutropha C91]	gi|114331865|ref|YP 748087.1|	55.56	1E-47
contig00050-orf00017	hypothetical protein NGO1755 [Neisseria gonorrhoeae FA 1090]	gi|59802076|ref|YP 208788.1|	92.86	3.5
contig00050-orf00019	hypothetical protein Pcryo 0666 [Psychrobacter cryohalolentis K5]	gi|93005496|ref|YP 579933.1|	68.57	1E-19
contig00050-orf00022	hypothetical protein NGO0543 [Neisseria gonorrhoeae FA 1090]	gi|59800977|ref|YP 207689.1|	97.08	3E-173
contig00050-orf00023	cation uptake regulator [Neisseria meningitidis Z2491]	gi|15794372|ref|NP 284194.1|	94.3	3E-66
contig00050-orf00025	hypothetical protein BL1634 [Bifidobacterium longum NCC2705]	gi|23466183|ref|NP 696786.1|	44.44	2.1
contig00050-orf00028	hypothetical protein NMB1048 [Neisseria meningitidis MC58]	gi|15676934|ref|NP 274082.1|	80.41	0
contig00050-orf00031	hypothetical protein Psyc 0269 [Psychrobacter arcticus 273-4]	gi|71064846|ref|YP 263573.1|	65.63	2E-153
contig00050-orf00035	hypothetical protein Rmet 3395 [Ralstonia metallidurans CH34]	gi|94312326|ref|YP 585536.1|	46.69	1E-63
contig00050-orf00037	hypothetical protein MGA 1222 [Mycoplasma gallisepticum R]	gi|31544535|ref|NP 853113.1|	26.87	0.077
contig00050-orf00038	malate dehydrogenase [Burkholderia pseudomallei K96243]	gi|53722743|ref|YP 111728.1|	69.51	1E-103
contig00050-orf00041	hypothetical protein NGO0984 [Neisseria gonorrhoeae FA 1090]	gi|59801370|ref|YP 208082.1|	75.16	0
contig00050-orf00045	peptidyl-prolyl isomerase [Neisseria meningitidis Z2491]	gi|15794615|ref|NP 284437.1|	87.76	8E-71
contig00050-orf00049	glycogen branching enzyme [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602406|ref|NP 245478.1|	63.95	0
contig00051-orf00001	plasmid stability protein StbB [Pseudomonas syringae pv. tomato str. DC3000]	gi|29171560|ref|NP 808606.1|	57.41	4E-11
contig00051-orf00004	putative DNA relaxase/nickase, TraS/VirD2-like [Burkholderia xenovorans	gi|91780509|ref|YP 555716.1|	44.54	2E-43
contig00051-orf00005	hypothetical protein PSPTO 0530 [Pseudomonas syringae pv. tomato str. DC3000]	gi|28867759|ref|NP 790378.1|	33.62	5E-12
contig00051-orf00007	hypothetical protein LSL 1826 [Lactobacillus salivarius UCC118]	gi|90962799|ref|YP 536714.1|	34.78	0.00002
contig00051-orf00008	inner membrane protein [Burkholderia pseudomallei 1710b]	gi|76810763|ref|YP 331725.1|	36.96	1E-46
contig00051-orf00009	protein VirD4 [Vibrio fischeri ES114]	gi|59714400|ref|YP 207174.1|	38.29	1E-87
contig00051-orf00010	single-stranded binding protein [Neisseria meningitidis Z2491]	gi|15794566|ref|NP 284388.1|	39.77	1E-12
contig00051-orf00011	hypothetical protein Mhun 1899 [Methanospirillum hungatei JF-1]	gi|88603154|ref|YP 503332.1|	32.35	0.017
contig00051-orf00012	#N/A	#N/A	#N/A	#N/A
contig00051-orf00014	conjugal transfer protein [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71725291|ref|YP 272291.1|	38.94	7E-61
contig00051-orf00015	channel protein VirB10 [Vibrio fischeri ES114]	gi|59714398|ref|YP 207172.1|	41.98	3E-50

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contig00051-orf00017	type IV secretion system protein VirB9 [Brucella suis 1330]	gi|23499828|ref|NP 699268.1|	33.82	3E-30
contig00051-orf00018	trwG protein [Bartonella quintana str. Toulouse]	gi|49474750|ref|YP 032792.1|	35.21	7E-28
contig00051-orf00020	hypothetical protein CV 2642 [Chromobacterium violaceum ATCC 12472]	gi|34498097|ref|NP 902312.1|	35.71	4.5
contig00051-orf00021	putative periplasmic transport system [Pseudomonas aeruginosa UCBPP-PA14]	gi|116054182|ref|YP 788626.1|	36.11	0.032
contig00051-orf00022	#N/A	gi|10956722|ref|NP 061667.1|	26.41	7E-18
contig00051-orf00023	putative metalloproteinase [Candidatus Protochlamydia amoebophila UWE25]	gi|46447592|ref|YP 008957.1|	43.33	6
contig00051-orf00024	TraF protein [Xanthomonas oryzae pv. oryzae KACC10331]	gi|58580226|ref|YP 199242.1|	33.15	2E-16
contig00051-orf00026	conjugal transfer protein [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71725274|ref|YP 272283.1|	33.6	9E-110
contig00051-orf00028	cobalamin biosynthetic protein [Gloeobacter violaceus PCC 7421]	gi|37522017|ref|NP 925394.1|	48.65	4.5
contig00051-orf00034	pilus retraction protein [Neisseria meningitidis Z2491]	gi|15793936|ref|NP 283758.1|	84.55	0
contig00051-orf00038	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Neisseria meningitidis Z2491]	gi|15793935|ref|NP 283757.1|	88.84	6E-95
contig00051-orf00040	GTP-binding protein LepA [Neisseria meningitidis MC58]	gi|15676664|ref|NP 273808.1|	99.5	0
contig00051-orf00041	signal peptidase I [Neisseria meningitidis MC58]	gi|15676663|ref|NP 273807.1|	69.53	7E-140
contig00051-orf00044	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793932|ref|NP 283754.1|	72.28	2E-98
contig00051-orf00045	hypothetical protein NGO1432 [Neisseria gonorrhoeae FA 1090]	gi|59801775|ref|YP 208487.1|	95.08	2E-175
contig00051-orf00046	LacI family sugar-binding transcriptional regulator [Streptococcus pneumoniae TIGR4]	gi|15901650|ref|NP 346254.1|	28.12	4.2
contig00051-orf00049	putative ABC transporter, permease protein [Neisseria gonorrhoeae FA 1090]	gi|59801776|ref|YP 208488.1|	93.99	6E-106
contig00051-orf00051	putative ABC transporter, ATP-binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801777|ref|YP 208489.1|	94.55	1E-94
contig00051-orf00053	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793708|ref|NP 283530.1|	93.56	1E-152
contig00051-orf00054	putative acyl-CoA hydrolase [Neisseria gonorrhoeae FA 1090]	gi|59801445|ref|YP 208157.1|	86.9	9E-57
contig00051-orf00056	hypothetical protein NMB0706 [Neisseria meningitidis MC58]	gi|15676604|ref|NP 273748.1|	86.27	2E-127
contig00051-orf00060	ribosomal large subunit pseudouridine synthase D [Neisseria meningitidis MC58]	gi|15676602|ref|NP 273746.1|	90.65	2E-176
contig00051-orf00061	ComL [Neisseria gonorrhoeae FA 1090]	gi|59800727|ref|YP 207439.1|	85.83	8E-125
contig00051-orf00063	threonine dehydratase [Neisseria meningitidis Z2491]	gi|15794044|ref|NP 283866.1|	86.05	4E-156
contig00051-orf00064	threonine dehydratase [Neisseria gonorrhoeae FA 1090]	gi|59800885|ref|YP 207597.1|	88.11	5E-66
contig00051-orf00067	D-ala-D-ala-carboxypeptidase [Chromobacterium violaceum ATCC 12472]	gi|34498549|ref|NP 902764.1|	60.7	2E-106
contig00051-orf00068	hypothetical protein NMB1071 [Neisseria meningitidis MC58]	gi|15676955|ref|NP 274104.1|	70.87	6E-82
contig00051-orf00070	hypothetical protein NMB0932 [Neisseria meningitidis MC58]	gi|15676826|ref|NP 273971.1|	58.45	4E-34
contig00051-orf00071	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	82.22	7E-15
contig00051-orf00073	hypothetical protein NMB1023 [Neisseria meningitidis MC58]	gi|15676911|ref|NP 274057.1|	96.24	2E-177
contig00051-orf00075	cation transporter E1-E2 family ATPase [Neisseria meningitidis MC58]	gi|15677191|ref|NP 274344.1|	94.59	0
contig00051-orf00078	putative mercury transport periplasmic protein [Neisseria meningitidis MC58]	gi|15677139|ref|NP 274292.1|	72.46	2E-21
contig00051-orf00079	MerR family transcriptional regulator [Haemophilus influenzae Rd KW20]	gi|16272248|ref|NP 438460.1|	66.67	4E-35
contig00051-orf00080	OsmC family protein [Burkholderia ambifaria AMMD]	gi|115361194|ref|YP 778331.1|	34.26	2E-10
contig00051-orf00081	YdfQ [Bacillus licheniformis ATCC 14580]	gi|52786524|ref|YP 092353.1|	50	0.0005

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contig00051-orf00083	ArsR family transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59801545|ref|YP 208257.1|	96.12	2E-51
contig00051-orf00084	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	92.65	1E-104
contig00051-orf00085	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	92.41	3E-37
contig00051-orf00087	malate dehydrogenase [Propionibacterium acnes KPA171202]	gi|50841800|ref|YP 055027.1|	71.06	0
contig00051-orf00088	LysR protein [Mannheimia succiniciproducens MBEL55E]	gi|52425265|ref|YP 088402.1|	49.37	3E-63
contig00051-orf00090	ARA1 protein [Mannheimia succiniciproducens MBEL55E]	gi|52425264|ref|YP 088401.1|	71.59	6E-41
contig00051-orf00091	aldo/keto reductase family oxidoreductase [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116873958|ref|YP 850739.1|	61.83	1E-41
contig00051-orf00092	hypothetical protein MS0141 [Mannheimia succiniciproducens MBEL55E]	gi|52424196|ref|YP 087333.1|	62.55	2E-95
contig00051-orf00093	dihydroorotate dehydrogenase 1A [Streptococcus pneumoniae TIGR4]	gi|15900658|ref|NP 345262.1|	81.94	1E-150
contig00051-orf00095	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.59	2E-14
contig00051-orf00096	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein [Neisseria meningitidis MC58]	gi|15677236|ref|NP 274389.1|	82.95	0
contig00051-orf00099	hypothetical protein NGO0448 [Neisseria gonorrhoeae FA 1090]	gi|59800888|ref|YP 207600.1|	75.76	1E-24
contig00051-orf00100	hypothetical protein bll4008 [Bradyrhizobium japonicum USDA 110]	gi|27379119|ref|NP 770648.1|	35.85	3.5
contig00051-orf00102	phosphatidylserine decarboxylase [Neisseria gonorrhoeae FA 1090]	gi|59801565|ref|YP 208277.1|	78.28	4E-107
contig00051-orf00106	excinuclease ABC subunit A [Neisseria meningitidis MC58]	gi|15676855|ref|NP 274000.1|	97.18	0
contig00051-orf00107	SMC family chromosome segregation protein [Candidatus Pelagibacter ubique HTCC1062]	gi|71082822|ref|YP 265541.1|	27.27	0.051
contig00052-orf00001	glyceraldehyde 3-phosphate dehydrogenase C [Neisseria meningitidis Z2491]	gi|15793264|ref|NP 283086.1|	97.31	0
contig00052-orf00005	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Neisseria meningitidis Z2491]	gi|15793281|ref|NP 283103.1|	96.68	6E-158
contig00052-orf00008	hypothetical protein BSU12680 [Bacillus subtilis subsp. subtilis str. 168]	gi|16078333|ref|NP 389150.1|	30.61	3.4
contig00052-orf00010	gamma-glutamyltranspeptidase [Neisseria meningitidis Z2491]	gi|15794189|ref|NP 284011.1|	65.47	0
contig00052-orf00013	6-phosphogluconate dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59802227|ref|YP 208939.1|	90.46	0
contig00052-orf00018	glycerate dehydrogenase [Neisseria meningitidis Z2491]	gi|15793292|ref|NP 283114.1|	76.27	3E-137
contig00052-orf00019	hypothetical protein NMB0028 [Neisseria meningitidis MC58]	gi|15675968|ref|NP 273094.1|	71.83	1E-23
contig00052-orf00022	#N/A	#N/A	#N/A	#N/A
contig00052-orf00023	peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58]	gi|15675967|ref|NP 273093.1|	92.66	3E-54
contig00052-orf00025	periplasmic type I secretion system protein [Neisseria meningitidis Z2491]	gi|15794874|ref|NP 284696.1|	43.36	8E-92
contig00052-orf00026	SLT domain-containing protein [Lactococcus lactis subsp. cremoris SK11]	gi|116512775|ref|YP 811682.1|	33.33	1.9
contig00052-orf00027	hypothetical protein all5192 [Nostoc sp. PCC 7120]	gi|17232684|ref|NP 489232.1|	22.73	0.93
contig00052-orf00028	protein AraJ [Escherichia coli UTI89]	gi|91209462|ref|YP 539448.1|	31.91	0.7
contig00052-orf00030	hypothetical protein CPS 4814 [Colwellia psychrerythraea 34H]	gi|71278508|ref|YP 271453.1|	35.29	4.6
contig00052-orf00031	VirB6 family type IV secretion system protein [Ehrlichia chaffeensis str. Arkansas]	gi|88658162|ref|YP 507314.1|	30.36	3.5
contig00052-orf00036	putative secretion protein [Neisseria gonorrhoeae FA 1090]	gi|59800583|ref|YP 207295.1|	51.18	4E-117

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contig00052-orf00037	hypothetical protein plu0852 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37524849|ref|NP 928193.1|	54.63	2E-37
contig00052-orf00039	colicin V-processing peptidase [Burkholderia pseudomallei K96243]	gi|53720702|ref|YP 109688.1|	53.63	1E-152
contig00052-orf00041	glutamyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59802239|ref|YP 208951.1|	100	8E-32
contig00052-orf00043	putative periplasmic iron/siderophore binding protein [Yersinia pseudotuberculosis IP 32953]	gi|51595709|ref|YP 069900.1|	38.1	2E-69
contig00052-orf00046	glutamyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793268|ref|NP 283090.1|	96.12	0
contig00052-orf00047	peptidase M16-like [Nitrosospira multiformis ATCC 25196]	gi|82703849|ref|YP 413415.1|	48.68	4E-43
contig00052-orf00049	putative zinc protease [Aromatoleum aromaticum EbN1]	gi|56476191|ref|YP 157780.1|	37.18	8E-34
contig00052-orf00053	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676188|ref|NP 273320.1|	89	0
contig00052-orf00057	hypothetical protein NMA0169 [Neisseria meningitidis Z2491]	gi|15793196|ref|NP 283018.1|	83.93	4E-129
contig00052-orf00058	enolase [Bradyrhizobium japonicum USDA 110]	gi|27379905|ref|NP 771434.1|	41.67	0.53
contig00052-orf00062	hypothetical protein NGO2032 [Neisseria gonorrhoeae FA 1090]	gi|59802340|ref|YP 209052.1|	74.09	1E-165
contig00052-orf00070	ABC transporter ATP-binding protein [Neisseria meningitidis MC58]	gi|15677865|ref|NP 275033.1|	63.46	6E-106
contig00052-orf00074	hypothetical protein NMA0394 [Neisseria meningitidis Z2491]	gi|15793402|ref|NP 283224.1|	64.21	1E-106
contig00052-orf00076	putative carbonic anhydrase [Neisseria gonorrhoeae FA 1090]	gi|59802380|ref|YP 209092.1|	84.86	3E-86
contig00052-orf00078	hypothetical protein NMB2024 [Neisseria meningitidis MC58]	gi|15677849|ref|NP 275016.1|	79	6E-91
contig00052-orf00080	hypothetical protein NGO2081 [Neisseria gonorrhoeae FA 1090]	gi|59802382|ref|YP 209094.1|	93.75	3E-63
contig00052-orf00082	SPOUT methyltransferase superfamily protein [Neisseria meningitidis Z2491]	gi|15793423|ref|NP 283245.1|	97.44	7E-83
contig00052-orf00085	hypothetical protein NMA2176 [Neisseria meningitidis Z2491]	gi|15795047|ref|NP 284869.1|	40.51	2E-15
contig00052-orf00088	hypothetical protein NMA2177 [Neisseria meningitidis Z2491]	gi|15795048|ref|NP 284870.1|	68.18	2E-37
contig00052-orf00090	hypothetical protein NGO1693 [Neisseria gonorrhoeae FA 1090]	gi|59802017|ref|YP 208729.1|	70.13	1E-61
contig00052-orf00092	CoA enzyme activase [Sulfurimonas denitrificans DSM 1251]	gi|78776473|ref|YP 392788.1|	46.15	6
contig00052-orf00094	GNA33) [Neisseria gonorrhoeae FA 1090]	gi|59802356|ref|YP 209068.1|	92.47	2E-46
contig00052-orf00095	putative membrane-bound lytic murein transglycosylase A [Neisseria meningitidis MC58]	gi|15675973|ref|NP 273099.1|	76.6	1E-130
contig00052-orf00096	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793297|ref|NP 283119.1|	89.96	3E-130
contig00052-orf00097	hypothetical protein NMA0281 [Neisseria meningitidis Z2491]	gi|15793298|ref|NP 283120.1|	83.76	4E-177
contig00052-orf00101	hypothetical protein NMA0282 [Neisseria meningitidis Z2491]	gi|15793299|ref|NP 283121.1|	84.34	0
contig00053-orf00002	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit [Neisseria meningitidis Z2491]	gi|15793587|ref|NP 283409.1|	91.3	4E-14
contig00053-orf00006	hypothetical protein NMA1806 [Neisseria meningitidis Z2491]	gi|15794696|ref|NP 284518.1|	64.74	2E-71
contig00053-orf00010	formate--tetrahydrofolate ligase [Neisseria gonorrhoeae FA 1090]	gi|59800526|ref|YP 207238.1|	98.16	0
contig00053-orf00011	polyphosphate kinase [Neisseria meningitidis Z2491]	gi|15793549|ref|NP 283371.1|	86.11	0
contig00053-orf00016	magnesium transporter [Neisseria meningitidis MC58]	gi|15677827|ref|NP 274991.1|	93.39	0
contig00053-orf00021	putative sugar transporter [Neisseria meningitidis MC58]	gi|15676302|ref|NP 273437.1|	96	0
contig00053-orf00025	maltose phosphorylase [Neisseria meningitidis Z2491]	gi|15794973|ref|NP 284795.1|	97.46	0

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contig00053-orf00028	beta-phosphoglucomutase [Neisseria meningitidis Z2491]	gi|15794972|ref|NP 284794.1|	96.83	1E-96
contig00053-orf00030	hypothetical protein NMB1840 [Neisseria meningitidis MC58]	gi|15677676|ref|NP 274837.1|	96.06	6E-58
contig00053-orf00032	fimbrial assembly protein [Neisseria meningitidis Z2491]	gi|15794588|ref|NP 284410.1|	66.8	3E-85
contig00053-orf00034	hypothetical protein NMB0436 [Neisseria meningitidis MC58]	gi|15676348|ref|NP 273484.1|	89.05	2E-99
contig00053-orf00036	membrane protein [Neisseria meningitidis Z2491]	gi|15793729|ref|NP 283551.1|	75.63	1E-49
contig00053-orf00038	hypothetical protein NMB0572 [Neisseria meningitidis MC58]	gi|15676477|ref|NP 273616.1|	85.19	5E-91
contig00053-orf00039	#N/A	#N/A	#N/A	#N/A
contig00053-orf00040	polyamine permease substrate-binding protein [Neisseria meningitidis Z2491]	gi|15793802|ref|NP 283624.1|	78.63	2E-170
contig00053-orf00041	insertion element IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15794668|ref|NP 284490.1|	100	1E-22
contig00055-orf00001	hypothetical protein NMA0028 [Neisseria meningitidis Z2491]	gi|15793061|ref|NP 282883.1|	98.14	2E-119
contig00055-orf00003	hypothetical protein NMA0029 [Neisseria meningitidis Z2491]	gi|15793062|ref|NP 282884.1|	98.71	3E-162
contig00055-orf00005	hypothetical protein NMA0030 [Neisseria meningitidis Z2491]	gi|15793063|ref|NP 282885.1|	98.78	5E-118
contig00055-orf00007	hypothetical protein NMB0227 [Neisseria meningitidis MC58]	gi|15676153|ref|NP 273284.1|	99.75	0
contig00055-orf00008	hypothetical protein NMB0226 [Neisseria meningitidis MC58]	gi|15676152|ref|NP 273283.1|	96.52	1E-131
contig00055-orf00010	hypothetical protein RS00868 [Ralstonia solanacearum GMI1000]	gi|17548632|ref|NP 521972.1|	42.59	4E-50
contig00055-orf00013	integral membrane efflux protein [Neisseria meningitidis Z2491]	gi|15794920|ref|NP 284742.1|	78.96	2E-149
contig00055-orf00014	hypothetical protein ELI 07200 [Erythrobacter litoralis HTCC2594]	gi|85374267|ref|YP 458329.1|	40.91	1E-10
contig00055-orf00016	D,D-heptose 1,7-bisphosphate phosphatase [Neisseria meningitidis Z2491]	gi|15793412|ref|NP 283234.1|	81.82	7E-85
contig00055-orf00018	NlaB [Neisseria gonorrhoeae FA 1090]	gi|59802370|ref|YP 209082.1|	81.74	3E-109
contig00055-orf00021	chaperonin GroEL [Neisseria meningitidis Z2491]	gi|15793474|ref|NP 283296.1|	98.5	0
contig00055-orf00023	co-chaperonin GroES [Neisseria meningitidis MC58]	gi|15677803|ref|NP 274967.1|	98.95	2E-46
contig00055-orf00026	FetA [Neisseria gonorrhoeae FA 1090]	gi|59802394|ref|YP 209106.1|	45.9	4E-133
contig00055-orf00028	membrane transport solute-binding protein [Neisseria meningitidis Z2491]	gi|15793455|ref|NP 283277.1|	94.33	2E-141
contig00055-orf00029	phosphoglyceromutase [Neisseria meningitidis MC58]	gi|15677454|ref|NP 274610.1|	95.15	4E-106
contig00055-orf00032	aromatic acid decarboxylase [Neisseria gonorrhoeae FA 1090]	gi|59802437|ref|YP 209149.1|	78.49	5E-80
contig00055-orf00033	valine--pyruvate transaminase [Neisseria meningitidis MC58]	gi|15677659|ref|NP 274820.1|	91.36	0
contig00055-orf00035	KatA [Neisseria gonorrhoeae FA 1090]	gi|59802086|ref|YP 208798.1|	94.11	0
contig00055-orf00037	D-fructose-6-phosphate amidotransferase [Neisseria meningitidis Z2491]	gi|15793294|ref|NP 283116.1|	89.54	0
contig00055-orf00039	diaminohydroxyphosphoribosylaminopyrimidine deaminase/phosphoribosylamino)uracil reductase [Neisseria meningitidis Z2491]	gi|15793630|ref|NP 283452.1|	74.73	1E-149
contig00055-orf00040	asparaginase [Pyrobaculum aerophilum str. IM2]	gi|18313808|ref|NP 560475.1|	42.22	1.2
contig00055-orf00042	transcriptional regulator NrdR [Chromobacterium violaceum ATCC 12472]	gi|34496742|ref|NP 900957.1|	57.6	2E-32
contig00055-orf00044	2-dehydro-3-deoxyphosphooctonate aldolase [Neisseria meningitidis MC58]	gi|15677150|ref|NP 274303.1|	82.42	3E-123
contig00055-orf00045	aspartate alpha-decarboxylase [Neisseria meningitidis MC58]	gi|15677149|ref|NP 274302.1|	92.13	2E-61
contig00055-orf00047	hypothetical protein WS1043 [Wolinella succinogenes DSM 1740]	gi|34557428|ref|NP 907243.1|	42.42	8E-12
contig00055-orf00049	TonB [Neisseria gonorrhoeae FA 1090]	gi|59801727|ref|YP 208439.1|	32.93	0.004
contig00055-orf00052	hypothetical protein NMB1075 [Neisseria meningitidis MC58]	gi|15676959|ref|NP 274108.1|	94.14	2E-122

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contig00055-orf00053	hypothetical protein NGO0841 [Neisseria gonorrhoeae FA 1090]	gi|59801246|ref|YP 207958.1|	89.19	2E-112
contig00055-orf00055	hypothetical protein NGO0869 [Neisseria gonorrhoeae FA 1090]	gi|59801270|ref|YP 207982.1|	77.25	5E-87
contig00055-orf00058	hypothetical protein VCA0414 [Vibrio cholerae O1 biovar eltor str. N16961]	gi|15601177|ref|NP 232808.1|	68.81	2E-41
contig00055-orf00060	hypothetical protein NMB1610 [Neisseria meningitidis MC58]	gi|15677460|ref|NP 274616.1|	53.08	1E-65
contig00055-orf00061	hypothetical protein NMA1810 [Neisseria meningitidis Z2491]	gi|15794700|ref|NP 284522.1|	89.02	1E-34
contig00055-orf00062	histidine-binding periplasmic protein [Neisseria meningitidis Z2491]	gi|15794701|ref|NP 284523.1|	86.49	9E-108
contig00055-orf00065	respiratory nitrate reductase alpha chain [Chromobacterium violaceum ATCC 12472]	gi|34497998|ref|NP 902213.1|	78.15	0
contig00055-orf00066	molybdenum cofactor biosynthesis protein [Aromatoleum aromaticum EbN1]	gi|56475974|ref|YP 157563.1|	63.83	9E-61
contig00055-orf00068	transposase (fragment) [Neisseria meningitidis Z2491]	gi|15795054|ref|NP 284876.1|	89.66	9E-15
contig00055-orf00069	hypothetical protein NGO0253 [Neisseria gonorrhoeae FA 1090]	gi|59800705|ref|YP 207417.1|	70.59	0.00004
contig00055-orf00070	hypothetical protein NMA2056 [Neisseria meningitidis Z2491]	gi|15794934|ref|NP 284756.1|	87.5	4E-10
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	25.41	9E-128
contig00056-orf00008	N-terminal part of IF-2 [Synechococcus sp. WH 8102]	gi|33865132|ref|NP 896691.1|	27.53	0.002
contig00056-orf00009	hypothetical protein NGO1598 [Neisseria gonorrhoeae FA 1090]	gi|59801926|ref|YP 208638.1|	67.86	4E-28
contig00056-orf00011	putative transcriptional regulator [Pseudomonas aeruginosa UCBPP-PA14]	gi|116053844|ref|YP 788281.1|	37.75	2E-43
contig00056-orf00012	NAD-dependent epimerase/dehydratase [Polaromonas sp. JS666]	gi|91790410|ref|YP 551362.1|	49.54	3E-39
contig00056-orf00013	hypothetical protein MS2001 [Mannheimia succiniciproducens MBEL55E]	gi|52426056|ref|YP 089193.1|	57.14	2E-17
contig00056-orf00014	#N/A	#N/A	#N/A	#N/A
contig00056-orf00015	WblA protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37528609|ref|NP 931954.1|	74.83	0
contig00056-orf00018	hypothetical protein NGO0088 [Neisseria gonorrhoeae FA 1090]	gi|59800549|ref|YP 207261.1|	47.83	9E-92
contig00056-orf00020	hypothetical protein MS1493 [Mannheimia succiniciproducens MBEL55E]	gi|52425548|ref|YP 088685.1|	34.34	3E-35
contig00056-orf00023	hypothetical protein NGO0087 [Neisseria gonorrhoeae FA 1090]	gi|59800548|ref|YP 207260.1|	78.31	1E-165
contig00056-orf00025	hypothetical protein NGO0086 [Neisseria gonorrhoeae FA 1090]	gi|59800547|ref|YP 207259.1|	88.97	0
contig00056-orf00026	pilin glycosylation protein PglB [Neisseria meningitidis MC58]	gi|15677656|ref|NP 274817.1|	87.88	1E-98
contig00056-orf00028	putative carbamoyl phosphate synthase large subunit [Vibrio parahaemolyticus RIMD 2210633]	gi|28897006|ref|NP 796611.1|	51.79	5E-89
contig00056-orf00029	hypothetical protein VP0233 [Vibrio parahaemolyticus RIMD 2210633]	gi|28897007|ref|NP 796612.1|	41.86	4E-38
contig00056-orf00030	methionyl-tRNA formyltransferase [Chlorobium tepidum TLS]	gi|21674274|ref|NP 662339.1|	37.7	2E-12
contig00056-orf00031	pilin glycosylation protein [Neisseria meningitidis Z2491]	gi|15793626|ref|NP 283448.1|	94.86	0
contig00056-orf00034	pilin glycosylation protein [Neisseria meningitidis MC58]	gi|15677658|ref|NP 274819.1|	74.33	0
contig00056-orf00037	putative polysaccharide export protein [Pectobacterium atrosepticum SCRI1043]	gi|50120356|ref|YP 049523.1|	46.77	5E-92
contig00056-orf00039	putative tyrosine-phosphatase [Sodalis glossinidius str. 'morsitans']	gi|85058957|ref|YP 454659.1|	54.55	4E-37
contig00056-orf00040	tyrosine kinase [Pectobacterium atrosepticum SCRI1043]	gi|50120358|ref|YP 049525.1|	42.17	6E-157
contig00056-orf00041	hypothetical protein ACIAD1673 [Acinetobacter sp. ADP1]	gi|50084830|ref|YP 046340.1|	53.04	2E-58
contig00056-orf00042	murein hydrolase exporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619114|ref|YP 858228.1|	38.52	6E-19

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contig00056-orf00043	LysR family transcriptional regulator [Acinetobacter sp. ADP1]	gi|50084832|ref|YP 046342.1|	52.24	3E-11
contig00056-orf00045	WblB protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37528610|ref|NP 931955.1|	73.28	2E-151
contig00056-orf00046	putative NAD(P)H nitroreductase [Haemophilus influenzae 86-028NP]	gi|68250198|ref|YP 249310.1|	58.6	1E-69
contig00056-orf00048	phospho-N-acetylmuramoyl-pentapeptide-transferase [Neisseria meningitidis Z2491]	gi|15794944|ref|NP 284766.1|	94.17	5E-167
contig00056-orf00049	hypothetical protein NMB0417 [Neisseria meningitidis MC58]	gi|15676329|ref|NP 273465.1|	85.19	0.0000003
contig00056-orf00050	UDP-MurNAc-pentapeptide synthetase [Neisseria meningitidis MC58]	gi|15676328|ref|NP 273464.1|	91.43	0
contig00056-orf00052	hypothetical protein TTHA1287 [Thermus thermophilus HB8]	gi|55981256|ref|YP 144553.1|	22.84	4E-11
contig00056-orf00054	peptidase M23B [Deinococcus geothermalis DSM 11300]	gi|94986326|ref|YP 605690.1|	56.74	4E-41
contig00056-orf00057	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase [Neisseria gonorrhoeae FA 1090]	gi|59801877|ref|YP 208589.1|	93.28	0
contig00056-orf00059	penicillin-binding protein 2 [Neisseria meningitidis Z2491]	gi|15794948|ref|NP 284770.1|	79.04	0
contig00056-orf00061	small periplasmic protein [Neisseria meningitidis Z2491]	gi|15794949|ref|NP 284771.1|	65.52	2E-17
contig00056-orf00062	S-adenosyl-methyltransferase MraW [Neisseria meningitidis Z2491]	gi|15794950|ref|NP 284772.1|	85.22	3E-149
contig00056-orf00063	cell division protein MraZ [Neisseria meningitidis Z2491]	gi|15794951|ref|NP 284773.1|	78.47	4E-61
contig00056-orf00064	hypothetical protein NGO1546 [Neisseria gonorrhoeae FA 1090]	gi|59801882|ref|YP 208594.1|	71.76	3E-142
contig00056-orf00067	dihydroorotate dehydrogenase 2 [Neisseria meningitidis MC58]	gi|15676147|ref|NP 273278.1|	90.39	4E-163
contig00056-orf00068	putative phosphoglycolate phosphatase [Neisseria meningitidis MC58]	gi|15677666|ref|NP 274827.1|	63.38	1E-72
contig00056-orf00070	hypothetical protein Sala 2257 [Sphingopyxis alaskensis RB2256]	gi|103487738|ref|YP 617299.1|	36.58	2E-31
contig00056-orf00071	putative periplasmic iron/siderophore binding protein [Yersinia pseudotuberculosis IP 32953]	gi|51595709|ref|YP 069900.1|	39.71	9E-72
contig00056-orf00074	Fe(III) dicitrate ABC transporter, permease [Methanosarcina barkeri str. Fusaro]	gi|73668013|ref|YP 304028.1|	48.96	5E-62
contig00056-orf00077	Fe(III) dicitrate ABC transporter, ATP-binding protein [Propionibacterium acnes KPA171202]	gi|50843238|ref|YP 056465.1|	41.27	5E-44
contig00056-orf00078	pseudoazurin [Bdellovibrio bacteriovorus HD100]	gi|42523990|ref|NP 969370.1|	46.22	8E-23
contig00056-orf00080	putative transcriptional regulator [Neisseria meningitidis MC58]	gi|15676212|ref|NP 273344.1|	74.92	6E-124
contig00056-orf00082	hypothetical protein NMA2196 [Neisseria meningitidis Z2491]	gi|15795065|ref|NP 284887.1|	76.69	6E-45
contig00056-orf00083	hypothetical protein NMA2195 [Neisseria meningitidis Z2491]	gi|15795064|ref|NP 284886.1|	85.57	3E-97
contig00056-orf00085	hypothetical protein NMA0419 [Neisseria meningitidis Z2491]	gi|15793424|ref|NP 283246.1|	95.4	6E-43
contig00056-orf00086	putative secreted peptidase [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]	gi|29142255|ref|NP 805597.1|	38.89	2.1
contig00056-orf00087	hypothetical protein plu3515 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527388|ref|NP 930732.1|	41.92	2E-31
contig00056-orf00088	hypothetical protein plu3514 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527387|ref|NP 930731.1|	34.45	1E-75
contig00056-orf00091	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793314|ref|NP 283136.1|	91.55	2E-31
contig00056-orf00092	hypothetical protein NMA0301 [Neisseria meningitidis Z2491]	gi|15793315|ref|NP 283137.1|	83.1	7E-27

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contig00056-orf00093	argininosuccinate synthase [Neisseria meningitidis Z2491]	gi|15793316|ref|NP 283138.1|	98.21	0
contig00056-orf00094	hypothetical protein Mbar A1323 [Methanosarcina barkeri str. Fusaro]	gi|73668850|ref|YP 304865.1|	27.27	2
contig00056-orf00096	CinA-related protein [Neisseria meningitidis MC58]	gi|15677941|ref|NP 275113.1|	85.77	2E-130
contig00057-orf00001	hypothetical protein NMB1853 [Neisseria meningitidis MC58]	gi|15677688|ref|NP 274849.1|	76.32	0.01
contig00057-orf00004	unknown transmembrane protein [Mesoplasma florum L1]	gi|50365013|ref|YP 053438.1|	35	3.5
contig00057-orf00008	carbamoyl phosphate synthase large subunit [Neisseria meningitidis Z2491]	gi|15793592|ref|NP 283414.1|	96.36	0
contig00057-orf00009	hypothetical protein NMB1486 [Neisseria meningitidis MC58]	gi|15677339|ref|NP 274494.1|	75	0.19
contig00057-orf00010	hypothetical protein NMB1485 [Neisseria meningitidis MC58]	gi|15677338|ref|NP 274493.1|	91.51	0
contig00057-orf00011	beta-hexosaminidase [Neisseria meningitidis Z2491]	gi|15793686|ref|NP 283508.1|	81.44	1E-161
contig00057-orf00015	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793687|ref|NP 283509.1|	89.44	0
contig00057-orf00018	protease DO [Neisseria meningitidis MC58]	gi|15677994|ref|NP 273577.1|	73.95	0
contig00057-orf00021	endonuclease III [Neisseria meningitidis MC58]	gi|15676439|ref|NP 273578.1|	94.71	3E-112
contig00057-orf00026	primosome assembly protein PriA [Neisseria meningitidis MC58]	gi|15676457|ref|NP 273596.1|	95.2	0
contig00057-orf00027	thiol:disulphide interchange protein [Neisseria meningitidis Z2491]	gi|15793706|ref|NP 283528.1|	78.6	9E-107
contig00057-orf00029	hypothetical protein NMA0716 [Neisseria meningitidis Z2491]	gi|15793693|ref|NP 283515.1|	91.97	1E-139
contig00057-orf00031	hypothetical protein NMB0538 [Neisseria meningitidis MC58]	gi|15676444|ref|NP 273583.1|	86.39	3E-72
contig00057-orf00034	phenylalanyl-tRNA synthetase subunit beta [Vibrio parahaemolyticus RIMD 2210633]	gi|28898065|ref|NP 797670.1|	36.54	2.7
contig00057-orf00035	porphobilinogen deaminase [Neisseria gonorrhoeae FA 1090]	gi|59800604|ref|YP 207316.1|	91.29	3E-142
contig00057-orf00037	O-succinylhomoserine sulfhydrolase [Neisseria meningitidis Z2491]	gi|15794698|ref|NP 284520.1|	97.43	0
contig00057-orf00038	hypothetical protein NMA1807 [Neisseria meningitidis Z2491]	gi|15794697|ref|NP 284519.1|	86.57	2E-15
contig00057-orf00040	deoxyguanosinetriphosphate triphosphohydrolase-like protein [Chromobacterium violaceum ATCC 12472]	gi|34498665|ref|NP 902880.1|	62.08	2E-149
contig00057-orf00041	ribonuclease HI [Neisseria meningitidis Z2491]	gi|15794707|ref|NP 284529.1|	84.03	6E-72
contig00057-orf00044	tellurite resistance protein TehB [Neisseria gonorrhoeae FA 1090]	gi|59801527|ref|YP 208239.1|	71.68	1E-104
contig00057-orf00045	Irg1 [Neisseria gonorrhoeae FA 1090]	gi|59801187|ref|YP 207899.1|	64.38	3E-114
contig00058-orf00002	homoserine kinase [Neisseria meningitidis MC58]	gi|15678023|ref|NP 275021.1|	74.67	3E-132
contig00058-orf00003	GTP-binding protein Era [Neisseria meningitidis Z2491]	gi|15793858|ref|NP 283680.1|	83.55	3E-127
contig00058-orf00005	ribonuclease III [Neisseria meningitidis Z2491]	gi|15793857|ref|NP 283679.1|	85.77	1E-105
contig00058-orf00006	hypothetical protein NGO0258 [Neisseria gonorrhoeae FA 1090]	gi|59800709|ref|YP 207421.1|	81.31	2E-48
contig00058-orf00008	riboflavin synthase subunit beta [Neisseria meningitidis Z2491]	gi|15793855|ref|NP 283677.1|	84.81	5E-62
contig00058-orf00011	transcription antitermination protein NusB [Neisseria meningitidis Z2491]	gi|15793854|ref|NP 283676.1|	87.86	5E-66
contig00058-orf00012	leucine-responsive regulatory protein [Neisseria meningitidis MC58]	gi|15677499|ref|NP 274655.1|	86.33	3E-64
contig00058-orf00013	D-amino acid dehydrogenase small subunit [Neisseria meningitidis MC58]	gi|15676103|ref|NP 273234.1|	78.12	0
contig00058-orf00016	hypothetical protein NMB1644 [Neisseria meningitidis MC58]	gi|15677493|ref|NP 274649.1|	86.97	0
contig00058-orf00019	hypothetical protein NMB1645 [Neisseria meningitidis MC58]	gi|15677494|ref|NP 274650.1|	87.44	0
contig00058-orf00020	#N/A	#N/A	#N/A	#N/A

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contig00058-orf00023	isocitrate dehydrogenase, NADP-dependent, monomeric type [Neisseria meningitidis MC58]	gi|15676815|ref|NP 273960.1|	96.12	0
contig00058-orf00024	isocitrate dehydrogenase, NADP-dependent, monomeric type [Neisseria meningitidis MC58]	gi|15676815|ref|NP 273960.1|	86.44	7E-79
contig00058-orf00026	helix-turn-helix, Fis-type [Ralstonia eutropha JMP134]	gi|73539493|ref|YP 299860.1|	46.7	4E-116
contig00058-orf00027	#N/A	#N/A	#N/A	#N/A
contig00058-orf00028	phenol hydroxylase P1 protein [Ralstonia eutropha H16]	gi|116694491|ref|YP 728702.1|	50.15	6E-89
contig00058-orf00029	monooxygenase component MmoB/DmpM [Ralstonia eutropha JMP134]	gi|73539504|ref|YP 299871.1|	49.43	2E-21
contig00058-orf00031	phenol hydroxylase P3 protein [Ralstonia eutropha H16]	gi|116694493|ref|YP 728704.1|	66.33	0
contig00058-orf00032	phenol hydroxylase region [Ralstonia eutropha JMP134]	gi|73541392|ref|YP 295912.1|	48.31	1E-25
contig00058-orf00033	ferredoxin:oxidoreductase FAD/NAD(P)-binding:oxidoreductase FAD-binding region [Dechloromonas aromatica RCB]	gi|71909404|ref|YP 286991.1|	59.53	2E-108
contig00058-orf00034	acetaldehyde dehydrogenase [Dechloromonas aromatica RCB]	gi|71909395|ref|YP 286982.1|	78.26	7E-130
contig00058-orf00035	4-hydroxy-2-ketovalerate aldolase [Pseudoalteromonas haloplanktis TAC125]	gi|77361066|ref|YP 340641.1|	78.64	7E-153
contig00058-orf00036	hydratase/decarboxylase [Dechloromonas aromatica RCB]	gi|71908386|ref|YP 285973.1|	65.64	3E-93
contig00058-orf00038	4-oxalocrotonate tautomerase [Ralstonia metallidurans CH34]	gi|94310259|ref|YP 583469.1|	62.5	5E-13
contig00058-orf00039	ferredoxin [Ralstonia metallidurans CH34]	gi|94310267|ref|YP 583477.1|	50.7	0.0002
contig00058-orf00040	catechol 2,3-dioxygenase [Ralstonia eutropha H16]	gi|116694497|ref|YP 728708.1|	58.16	2E-91
contig00058-orf00041	aldehyde dehydrogenase [Dechloromonas aromatica RCB]	gi|71909399|ref|YP 286986.1|	72.22	0
contig00058-orf00042	hydratase/decarboxylase [Ralstonia metallidurans CH34]	gi|94310263|ref|YP 583473.1|	63.46	1E-90
contig00058-orf00043	cell division initiation protein [Thermoanaerobacter tengcongensis MB4]	gi|20808025|ref|NP 623196.1|	32.63	0.022
contig00058-orf00044	amidophosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15793861|ref|NP 283683.1|	96.32	0
contig00058-orf00045	spermidine synthase [Ralstonia eutropha JMP134]	gi|73542987|ref|YP 297507.1|	63.07	9E-156
contig00058-orf00047	sulfite reductase subunit beta [Escherichia coli CFT073]	gi|26249161|ref|NP 755201.1|	70.25	0
contig00058-orf00050	hypothetical protein NGO1063 [Neisseria gonorrhoeae FA 1090]	gi|59801433|ref|YP 208145.1|	66.22	5E-22
contig00058-orf00051	50S ribosomal protein L31 type B [Neisseria meningitidis MC58]	gi|15676835|ref|NP 273980.1|	94.51	1E-46
contig00058-orf00052	hypothetical protein NGO1299 [Neisseria gonorrhoeae FA 1090]	gi|59801653|ref|YP 208365.1|	71.33	6E-61
contig00058-orf00053	hypothetical protein NGO1299 [Neisseria gonorrhoeae FA 1090]	gi|59801653|ref|YP 208365.1|	65.31	4E-31
contig00058-orf00055	hypothetical protein NGO0306 [Neisseria gonorrhoeae FA 1090]	gi|59800753|ref|YP 207465.1|	58.65	7E-28
contig00058-orf00056	IfhA [Neisseria gonorrhoeae FA 1090]	gi|59800752|ref|YP 207464.1|	99	4E-50
contig00058-orf00058	phenylalanyl-tRNA synthetase subunit beta [Neisseria meningitidis MC58]	gi|15676626|ref|NP 273770.1|	93.9	0
contig00058-orf00059	type II restriction enzyme HpaII (endonuclease HpaII) [Bacillus thuringiensis serovar konkukian str. 97-27]	gi|49476999|ref|YP 035185.1|	32.59	1E-53
contig00058-orf00061	DNA (cytosine-5-)-methyltransferase [Sulfurimonas denitrificans DSM 1251]	gi|78777762|ref|YP 394077.1|	47.03	1E-49
contig00058-orf00062	C-5 cytosine-specific DNA-methylase [Bacteroides fragilis YCH46]	gi|53714966|ref|YP 100958.1|	62.39	5E-34
contig00058-orf00063	putative very-short-patch-repair endonuclease [Neisseria gonorrhoeae FA 1090]	gi|59800748|ref|YP 207460.1|	94.16	1E-72
contig00058-orf00065	phenylalanyl-tRNA synthetase alpha subunit [Neisseria gonorrhoeae FA 1090]	gi|59800747|ref|YP 207459.1|	97.87	2E-149

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contig00058-orf00067	50S ribosomal protein L20 [Neisseria meningitidis Z2491]	gi|15793891|ref|NP 283713.1|	99.1	1E-47
contig00058-orf00068	50S ribosomal protein L35 [Neisseria meningitidis Z2491]	gi|15793890|ref|NP 283712.1|	100	4E-30
contig00058-orf00069	translation initiation factor IF-3 [Neisseria meningitidis Z2491]	gi|15793889|ref|NP 283711.1|	99.25	1E-70
contig00058-orf00070	threonyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15676618|ref|NP 273762.1|	97.33	0
contig00058-orf00073	queuine tRNA-ribosyltransferase [Neisseria meningitidis Z2491]	gi|15793887|ref|NP 283709.1|	95.96	0
contig00058-orf00074	ferrochelatase [Neisseria meningitidis Z2491]	gi|15793886|ref|NP 283708.1|	78.92	8E-147
contig00058-orf00075	putative cytochrome [Neisseria meningitidis MC58]	gi|15676615|ref|NP 273759.1|	71.97	4E-52
contig00058-orf00078	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase [Neisseria meningitidis MC58]	gi|15677504|ref|NP 274660.1|	90.27	8E-156
contig00058-orf00079	hypothetical protein NMA1699 [Neisseria meningitidis Z2491]	gi|15794592|ref|NP 284414.1|	90	5E-21
contig00058-orf00081	carbon starvation protein A [Neisseria meningitidis MC58]	gi|15677346|ref|NP 274501.1|	96.68	0
contig00058-orf00085	alcohol dehydrogenase, zinc-containing [Neisseria meningitidis MC58]	gi|15677256|ref|NP 274409.1|	97.4	0
contig00058-orf00086	adenine glycosylase [Neisseria meningitidis Z2491]	gi|15794508|ref|NP 284330.1|	84.62	2E-173
contig00058-orf00089	hypothetical protein Bxe A2276 [Burkholderia xenovorans LB400]	gi|91783539|ref|YP 558745.1|	51.52	8E-130
contig00058-orf00090	binding-protein-dependent transport systems inner membrane protein [Neisseria meningitidis Z2491]	gi|15794602|ref|NP 284424.1|	91.53	8E-104
contig00058-orf00093	putative protease [Neisseria meningitidis MC58]	gi|15677513|ref|NP 274669.1|	96.88	0
contig00058-orf00096	CsbD-like [Mesorhizobium sp. BNC1]	gi|110636332|ref|YP 676540.1|	63.08	1E-19
contig00058-orf00102	glycine dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801676|ref|YP 208388.1|	93.47	0
contig00058-orf00105	DNA-3-methyladenine glycosylase I [Neisseria meningitidis MC58]	gi|15677522|ref|NP 274678.1|	79.78	4E-84
contig00058-orf00107	glycine cleavage system protein H [Neisseria gonorrhoeae FA 1090]	gi|59801749|ref|YP 208461.1|	96.88	3E-67
contig00058-orf00109	glycine cleavage system aminomethyltransferase T [Neisseria meningitidis	gi|15676479|ref|NP 273618.1|	98.91	0
contig00058-orf00111	transcription regulator AsnC [Neisseria meningitidis Z2491]	gi|15793731|ref|NP 283553.1|	87.97	1E-74
contig00058-orf00112	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	76.47	2.7
contig00058-orf00114	putative ATP-dependent RNA helicase [Neisseria gonorrhoeae FA 1090]	gi|59800607|ref|YP 207319.1|	80.64	0
contig00058-orf00115	beta-ketoacyl synthase [Frankia sp. CcI3]	gi|86741618|ref|YP 482018.1|	31.71	9.9
contig00058-orf00117	hypothetical protein MS0012 [Mannheimia succiniciproducens MBEL55E]	gi|52424067|ref|YP 087204.1|	35.38	0.00001
contig00058-orf00119	glutaredoxin 2 [Neisseria meningitidis Z2491]	gi|15794872|ref|NP 284694.1|	79.81	2E-98
contig00058-orf00123	GTP pyrophosphokinase [Neisseria meningitidis MC58]	gi|15677581|ref|NP 274738.1|	97.56	0
contig00058-orf00124	alcohol dehydrogenase [Neisseria meningitidis MC58]	gi|15676452|ref|NP 273591.1|	95.29	6E-166
contig00058-orf00127	PutA protein [Mannheimia succiniciproducens MBEL55E]	gi|52425606|ref|YP 088743.1|	83.2	0
contig00058-orf00129	sugar ABC transporter, sugar-binding protein [Leifsonia xyli subsp. xyli str. CTCB07]	gi|50955812|ref|YP 063100.1|	41.38	3.5
contig00058-orf00131	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	51.61	0.41
contig00058-orf00133	hypothetical protein NMA1952 [Neisseria meningitidis Z2491]	gi|15794835|ref|NP 284657.1|	97.56	0
contig00058-orf00135	putative DNA polymerase III, alpha subunit [Neisseria gonorrhoeae FA 1090]	gi|59800539|ref|YP 207251.1|	95.98	0
contig00058-orf00136	acetate kinase [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	gi|78358282|ref|YP 389731.1|	27	0.91

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contig00058-orf00137	ribokinase [Chromobacterium violaceum ATCC 12472]	gi|34498475|ref|NP 902690.1|	50	3E-63
contig00058-orf00138	regulator [Neisseria meningitidis Z2491]	gi|15794772|ref|NP 284594.1|	72.07	3E-71
contig00058-orf00141	phage transposase [Neisseria meningitidis Z2491]	gi|15794213|ref|NP 284035.1|	93.84	0
contig00058-orf00142	hypothetical protein NMB1082 [Neisseria meningitidis MC58]	gi|15676963|ref|NP 274114.1|	91.3	6E-16
contig00058-orf00143	phage transposase [Neisseria meningitidis Z2491]	gi|15794215|ref|NP 284037.1|	88.49	1E-147
contig00058-orf00144	hypothetical protein NMA1287 [Neisseria meningitidis Z2491]	gi|15794216|ref|NP 284038.1|	85.37	8E-15
contig00058-orf00145	hypothetical protein NMA1287 [Neisseria meningitidis Z2491]	gi|15794216|ref|NP 284038.1|	69.64	3E-15
contig00058-orf00147	hypothetical protein SAV 6609 [Streptomyces avermitilis MA-4680]	gi|29833151|ref|NP 827785.1|	39.22	1.2
contig00058-orf00151	stringent starvation protein A [Methylococcus capsulatus str. Bath]	gi|53803979|ref|YP 114392.1|	46.67	2.7
contig00058-orf00152	hypothetical protein Mlg 1933 [Alkalilimnicola ehrlichii MLHE-1]	gi|114321082|ref|YP 742765.1|	41.18	1.6
contig00058-orf00154	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800902|ref|YP 207614.1|	65.18	9E-75
contig00058-orf00155	hypothetical protein NMA1290 [Neisseria meningitidis Z2491]	gi|15794219|ref|NP 284041.1|	76.36	3E-19
contig00058-orf00157	hypothetical protein HD1520 [Haemophilus ducreyi 35000HP]	gi|33152568|ref|NP 873921.1|	50.91	6E-23
contig00058-orf00158	hypothetical protein amb2120 [Magnetospirillum magneticum AMB-1]	gi|83311219|ref|YP 421483.1|	45.16	2.1
contig00058-orf00159	host-nuclease inhibitor protein [Neisseria meningitidis Z2491]	gi|15794220|ref|NP 284042.1|	80.23	2E-73
contig00058-orf00162	E16-related protein [Neisseria meningitidis MC58]	gi|15676876|ref|NP 274021.1|	61.31	1E-38
contig00058-orf00165	putative bacteriophage DNA transposition protein B [Neisseria meningitidis MC58]	gi|15676964|ref|NP 274115.1|	50	5E-22
contig00058-orf00168	hypothetical protein ACIAD2145 [Acinetobacter sp. ADP1]	gi|50085260|ref|YP 046770.1|	53.18	1E-37
contig00058-orf00169	hypothetical protein NMB0988 [Neisseria meningitidis MC58]	gi|15676879|ref|NP 274024.1|	70.97	0.0003
contig00058-orf00171	hypothetical protein NMA1862 [Neisseria meningitidis Z2491]	gi|15794750|ref|NP 284572.1|	92.5	8E-35
contig00058-orf00172	hypothetical protein NMA1191 [Neisseria meningitidis Z2491]	gi|15794135|ref|NP 283957.1|	85.29	5E-60
contig00058-orf00174	hypothetical protein NMA1307 [Neisseria meningitidis Z2491]	gi|15794236|ref|NP 284058.1|	96.88	1E-30
contig00058-orf00175	hypothetical protein NMA1195 [Neisseria meningitidis Z2491]	gi|15794139|ref|NP 283961.1|	67.57	7E-35
contig00058-orf00176	hypothetical protein NMA1310 [Neisseria meningitidis Z2491]	gi|15794239|ref|NP 284061.1|	100	1E-44
contig00058-orf00177	hypothetical protein NMA1311 [Neisseria meningitidis Z2491]	gi|15794240|ref|NP 284062.1|	100	3E-30
contig00058-orf00179	DNA-binding protein [Neisseria meningitidis Z2491]	gi|15794241|ref|NP 284063.1|	74.25	3E-63
contig00058-orf00180	hypothetical protein NMA1852 [Neisseria meningitidis Z2491]	gi|15794740|ref|NP 284562.1|	50.19	1E-142
contig00058-orf00182	Mu-like prophage protein [Psychrobacter arcticus 273-4]	gi|71065562|ref|YP 264289.1|	23.08	3E-14
contig00058-orf00184	prophage MuSo2, F protein, putative [Shewanella oneidensis MR-1]	gi|24374222|ref|NP 718265.1|	42.02	6E-50
contig00058-orf00185	putative multidrug resistance protein [Vibrio vulnificus YJ016]	gi|37678221|ref|NP 932830.1|	29.27	2.1
contig00058-orf00186	hypothetical protein PMT1010 [Prochlorococcus marinus str. MIT 9313]	gi|33863281|ref|NP 894841.1|	31.65	1.8
contig00058-orf00187	hypothetical protein Ta0272 [Thermoplasma acidophilum DSM 1728]	gi|16081414|ref|NP 393752.1|	28.57	0.24
contig00058-orf00189	hypothetical protein MCA2923 [Methylococcus capsulatus str. Bath]	gi|53802937|ref|YP 115315.1|	34.59	3E-46
contig00058-orf00191	hypothetical protein SO 0677 [Shewanella oneidensis MR-1]	gi|24372268|ref|NP 716310.1|	36.63	0.0001
contig00058-orf00193	mu-like prophage Flumu G protein [Syntrophus aciditrophicus SB]	gi|85858391|ref|YP 460593.1|	35.81	3E-11
contig00058-orf00194	DNA translocase FtsK [Ralstonia eutropha JMP134]	gi|73541139|ref|YP 295659.1|	27.87	0.46

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contig00058-orf00195	hypothetical protein SO 0679 [Shewanella oneidensis MR-1]	gi|24372270|ref|NP 716312.1|	27.98	7E-16
contig00058-orf00198	hypothetical protein BCE 4074 [Bacillus cereus ATCC 10987]	gi|42783121|ref|NP 980368.1|	34.88	2.1
contig00058-orf00200	prophage P2W3, tail tape measure protein [Wolbachia endosymbiont of Drosophila melanogaster]	gi|42520427|ref|NP 966342.1|	36.06	5E-58
contig00058-orf00202	hypothetical protein RSc0874 [Ralstonia solanacearum GMI1000]	gi|17545593|ref|NP 518995.1|	37.21	2E-15
contig00058-orf00204	putative transmembrane protein [Ralstonia solanacearum GMI1000]	gi|17545594|ref|NP 518996.1|	32.28	2E-54
contig00058-orf00206	hypothetical protein MCA2672 [Methylococcus capsulatus str. Bath]	gi|53803122|ref|YP 115076.1|	36.16	7E-64
contig00058-orf00208	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative [Treponema denticola ATCC 35405]	gi|42525817|ref|NP 970915.1|	29.17	0.33
contig00058-orf00209	hypothetical protein Sfri 1687 [Shewanella frigidimarina NCIMB 400]	gi|114562863|ref|YP 750376.1|	33.33	8E-11
contig00058-orf00210	hypothetical protein RSc0877 [Ralstonia solanacearum GMI1000]	gi|17545596|ref|NP 518998.1|	40.28	1E-09
contig00058-orf00212	hypothetical protein RSc0879 [Ralstonia solanacearum GMI1000]	gi|17545598|ref|NP 519000.1|	28	3E-25
contig00058-orf00215	hypothetical protein DP1597 [Desulfotalea psychrophila LSv54]	gi|51245449|ref|YP 065333.1|	31.82	1.5
contig00058-orf00218	Cro/CI family transcriptional regulator [Shewanella oneidensis MR-1]	gi|24372296|ref|NP 716338.1|	37.5	1.5
contig00058-orf00221	hypothetical protein RSc0854 [Ralstonia solanacearum GMI1000]	gi|17545573|ref|NP 518975.1|	38.15	2E-23
contig00058-orf00222	hypothetical protein Saci 1794 [Sulfolobus acidocaldarius DSM 639]	gi|70607523|ref|YP 256393.1|	44.44	0.082
contig00058-orf00225	translational regulator [Escherichia coli O157:H7 str. Sakai]	gi|15834251|ref|NP 313024.1|	45.71	0.001
contig00058-orf00227	DNA adenine methylase [Methylobacillus flagellatus KT]	gi|91777030|ref|YP 546786.1|	73.48	1E-50
contig00058-orf00228	prophage PSPPH02, putative adenine modification methytransferase [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71736103|ref|YP 274122.1|	49.09	8E-08
contig00058-orf00229	putative ABC transporter ATP-binding protein [Neisseria meningitidis MC58]	gi|15676301|ref|NP 273436.1|	99.28	0
contig00058-orf00231	putative type I restriction-modification system (HsdR) [Acinetobacter sp. ADP1]	gi|50086398|ref|YP 047908.1|	63.14	0
contig00058-orf00233	type I restriction-modification system specificity determinant [Geobacillus kaustophilus HTA426]	gi|56421440|ref|YP 148758.1|	62.07	5E-69
contig00058-orf00235	HsdM protein [Mannheimia succiniciproducens MBEL55E]	gi|52426220|ref|YP 089357.1|	69.29	0
contig00058-orf00237	L-aspartate oxidase [Neisseria meningitidis Z2491]	gi|15794967|ref|NP 284789.1|	94.41	0
contig00058-orf00240	quinolinate synthetase [Neisseria gonorrhoeae FA 1090]	gi|59801900|ref|YP 208612.1|	98.11	0
contig00058-orf00242	hypothetical protein NMB0395 [Neisseria meningitidis MC58]	gi|15676309|ref|NP 273444.1|	98.08	8E-177
contig00058-orf00244	putative Rhs family protein [Pseudomonas aeruginosa UCBPP-PA14]	gi|116049601|ref|YP 791594.1|	51.61	0.14
contig00058-orf00245	hypothetical protein Acid 1654 [Solibacter usitatus Ellin6076]	gi|116620773|ref|YP 822929.1|	38.64	1.9
contig00058-orf00247	putative nicotinate-nucleotide pyrophosphorylase [Neisseria gonorrhoeae FA 1090]	gi|59801898|ref|YP 208610.1|	95.52	5E-137
contig00058-orf00253	monofunctional biosynthetic peptidoglycan transglycosylase [Neisseria meningitidis Z2491]	gi|15795001|ref|NP 284823.1|	87.12	7E-116
contig00058-orf00254	putative shikimate dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801930|ref|YP 208642.1|	78.07	1E-102
contig00058-orf00256	glutamine synthetase [Neisseria meningitidis Z2491]	gi|15794999|ref|NP 284821.1|	97.46	0
contig00058-orf00258	putative transposase [Neisseria meningitidis Z2491]	gi|15794960|ref|NP 284782.1|	94.44	0.017

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contig00058-orf00260	putative zinc-binding alcohol dehydrogenas [Neisseria gonorrhoeae FA 1090]	gi|59800641|ref|YP 207353.1|	96.61	1E-175
contig00058-orf00261	outer membrane ferripyoverdine receptor [Pseudomonas fluorescens Pf-5]	gi|70729895|ref|YP 259634.1|	35.04	2E-48
contig00058-orf00264	outer membrane ferripyoverdine receptor [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71737812|ref|YP 274101.1|	37.63	2E-44
contig00058-orf00267	hypothetical protein NMB0529 [Neisseria meningitidis MC58]	gi|15676436|ref|NP 273574.1|	91.51	1E-112
contig00058-orf00268	membrane protein [Neisseria meningitidis Z2491]	gi|15793684|ref|NP 283506.1|	95.51	9E-44
contig00058-orf00270	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	58.33	0.003
contig00058-orf00272	hypothetical protein NMA0704 [Neisseria meningitidis Z2491]	gi|15793683|ref|NP 283505.1|	91.34	8E-66
contig00058-orf00273	hypothetical protein NMB0526 [Neisseria meningitidis MC58]	gi|15676433|ref|NP 273571.1|	94.19	2E-82
contig00058-orf00276	putative aluminum resistance protein [Neisseria meningitidis MC58]	gi|15676432|ref|NP 273570.1|	97.72	1E-121
contig00058-orf00278	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase [Neisseria meningitidis Z2491]	gi|15794505|ref|NP 284327.1|	97.17	5E-114
contig00058-orf00281	phosphogluconate dehydratase [Neisseria gonorrhoeae FA 1090]	gi|59801134|ref|YP 207846.1|	98.04	0
contig00058-orf00284	glucose-6-phosphate 1-dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801135|ref|YP 207847.1|	91.68	0
contig00058-orf00288	hypothetical protein NGO0716 [Neisseria gonorrhoeae FA 1090]	gi|59801136|ref|YP 207848.1|	76.96	4E-91
contig00058-orf00289	glucokinase [Neisseria meningitidis Z2491]	gi|15794501|ref|NP 284323.1|	90.57	3E-166
contig00058-orf00290	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15794500|ref|NP 284322.1|	97.52	1E-149
contig00058-orf00293	glucose-6-phosphate isomerase [Neisseria meningitidis MC58]	gi|15677249|ref|NP 274402.1|	94.33	0
contig00058-orf00296	hypothetical protein NMA0903 [Neisseria meningitidis Z2491]	gi|15793869|ref|NP 283691.1|	89.95	3E-99
contig00058-orf00297	hypothetical protein Daro 0097 [Dechloromonas aromatica RCB]	gi|71905739|ref|YP 283326.1|	38.89	3E-50
contig00058-orf00298	N-(5'-phosphoribosyl)anthranilate isomerase [Neisseria gonorrhoeae FA 1090]	gi|59800712|ref|YP 207424.1|	72.68	2E-71
contig00058-orf00299	hypothetical protein NMB1480 [Neisseria meningitidis MC58]	gi|15677333|ref|NP 274488.1|	85.42	8E-16
contig00058-orf00301	hypothetical protein Rfer 1322 [Rhodoferax ferrireducens T118]	gi|89900116|ref|YP 522587.1|	28.44	0.00003
contig00058-orf00303	transcription termination factor Rho [Neisseria meningitidis MC58]	gi|15676520|ref|NP 273661.1|	95.47	0
contig00058-orf00305	hypothetical protein NMB1619 [Neisseria meningitidis MC58]	gi|15677469|ref|NP 274625.1|	85.27	8E-63
contig00058-orf00307	hypothetical protein NGO1274 [Neisseria gonorrhoeae FA 1090]	gi|59801631|ref|YP 208343.1|	74.52	1E-144
contig00058-orf00309	peptide chain release factor 3 [Neisseria meningitidis Z2491]	gi|15793806|ref|NP 283628.1|	98.68	0
contig00058-orf00312	hypothetical protein NMA0944 [Neisseria meningitidis Z2491]	gi|15793902|ref|NP 283724.1|	45.18	8E-27
contig00058-orf00313	dithiobiotin synthetase [Neisseria meningitidis MC58]	gi|15676631|ref|NP 273775.1|	91.55	2E-97
contig00058-orf00315	putative adenosylmethionine-8-amino-7-oxononanoate aminotranferase [Neisseria gonorrhoeae FA 1090]	gi|59800755|ref|YP 207467.1|	95.76	0
contig00058-orf00317	putative murein transglycosylase / nitrite reductase transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59801036|ref|YP 207748.1|	56.49	0
contig00058-orf00318	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	94.74	9E-15
contig00058-orf00319	multidrug efflux pump channel protein [Neisseria meningitidis MC58]	gi|15677561|ref|NP 274717.1|	78.33	5E-171
contig00058-orf00321	drug efflux protein [Neisseria meningitidis Z2491]	gi|15794852|ref|NP 284674.1|	89.66	0
contig00058-orf00323	antibiotic resistance efflux pump component [Neisseria gonorrhoeae FA 1090]	gi|59801713|ref|YP 208425.1|	85.01	3E-160

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contig00059-orf00003	hypothetical protein NMA0459 [Neisseria meningitidis Z2491]	gi|15793462|ref|NP 283284.1|	76.68	1E-94
contig00059-orf00004	resolvase [Ralstonia eutropha JMP134]	gi|72384321|ref|YP 293674.1|	57.14	2E-40
contig00059-orf00007	modification methyltransferase, cytosine-specific [Methanothermobacter thermautotrophicus str. Delta H]	gi|15678523|ref|NP 275638.1|	43.81	7E-93
contig00059-orf00008	putative sensor histidine kinase [Myxococcus xanthus DK 1622]	gi|108762891|ref|YP 631794.1|	28.88	9E-68
contig00059-orf00009	DNA helicase/exodeoxyribonuclease V, gamma subunit [Prochlorococcus marinus str. MIT 9312]	gi|78779499|ref|YP 397611.1|	19.47	0.14
contig00059-orf00010	DNA polymerase V subunit UmuD [Salmonella enterica subsp. enterica serovar Typhi str. Ty2]	gi|29141368|ref|NP 804710.1|	39.02	2E-09
contig00059-orf00011	DNA repair protein [Azoarcus sp. EbN1]	gi|58616540|ref|YP 195670.1|	44.08	6E-88
contig00059-orf00013	hypothetical protein NMB0909 [Neisseria meningitidis MC58]	gi|15676804|ref|NP 273949.1|	45.45	6E-11
contig00060-orf00001	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	93.71	0
contig00060-orf00004	cytidine and deoxycytidylate deaminase family protein [Neisseria meningitidis MC58]	gi|15676827|ref|NP 273972.1|	69.33	2E-86
contig00060-orf00005	tRNA delta(2)-isopentenylpyrophosphate transferase [Neisseria meningitidis Z2491]	gi|15794076|ref|NP 283898.1|	70.61	6E-122
contig00060-orf00008	3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis MC58]	gi|15677291|ref|NP 274444.1|	96.51	0
contig00060-orf00012	anthranilate synthase component I [Neisseria meningitidis Z2491]	gi|15794182|ref|NP 284004.1|	97.76	0
contig00060-orf00014	hypothetical protein NMB0047 [Neisseria meningitidis MC58]	gi|15675987|ref|NP 273113.1|	82.98	6E-42
contig00060-orf00015	phosphoribosylaminoimidazole carboxylase ATPase subunit [Neisseria meningitidis MC58]	gi|15676907|ref|NP 274053.1|	91.27	0
contig00060-orf00017	hypothetical protein NGO0876 [Neisseria gonorrhoeae FA 1090]	gi|59801277|ref|YP 207989.1|	76.23	1E-49
contig00060-orf00019	hypothetical protein NMA1237 [Neisseria meningitidis Z2491]	gi|15794177|ref|NP 283999.1|	71.5	3E-67
contig00060-orf00022	pyruvate dehydrogenase subunit E1 [Neisseria gonorrhoeae FA 1090]	gi|59800998|ref|YP 207710.1|	96.17	0
contig00060-orf00023	#N/A	#N/A	#N/A	#N/A
contig00060-orf00024	dihydrolipoamide acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59800997|ref|YP 207709.1|	93.03	0
contig00060-orf00027	dihydrolipoamide dehydrogenase (E3 component of pyruvate and 2-oxoglutarate dehydrogenase complexes) [Neisseria meningitidis Z2491]	gi|15794449|ref|NP 284271.1|	95.29	0
contig00060-orf00029	tRNA (guanine-N(7))-methyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801008|ref|YP 207720.1|	81.2	3E-110
contig00060-orf00031	riboflavin synthase subunit alpha [Neisseria gonorrhoeae FA 1090]	gi|59801170|ref|YP 207882.1|	74.75	5E-82
contig00060-orf00032	hypothetical protein NMA1415 [Neisseria meningitidis Z2491]	gi|15794327|ref|NP 284149.1|	83.62	8E-133
contig00060-orf00035	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794326|ref|NP 284148.1|	57.36	5E-38
contig00060-orf00036	ribulose-phosphate 3-epimerase [Neisseria meningitidis MC58]	gi|15677116|ref|NP 274268.1|	89.69	4E-101
contig00060-orf00038	hypothetical protein NGO1083 [Neisseria gonorrhoeae FA 1090]	gi|59801450|ref|YP 208162.1|	78.57	4E-27
contig00060-orf00040	ATP phosphoribosyltransferase regulatory subunit [Neisseria meningitidis MC58]	gi|15676712|ref|NP 273856.1|	91.1	0
contig00060-orf00041	adenylosuccinate synthetase [Neisseria meningitidis Z2491]	gi|15793980|ref|NP 283802.1|	95.83	0

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contig00060-orf00042	hypothetical protein NGO0549 [Neisseria gonorrhoeae FA 1090]	gi|59800983|ref|YP 207695.1|	71.05	7E-43
contig00060-orf00044	hypothetical protein NMA1462 [Neisseria meningitidis Z2491]	gi|15794364|ref|NP 284186.1|	72.5	3E-62
contig00060-orf00046	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	94.44	1E-13
contig00060-orf00047	dnaJ-family protein [Neisseria meningitidis Z2491]	gi|15794363|ref|NP 284185.1|	37.82	2E-38
contig00060-orf00049	integral membrane protein [Neisseria meningitidis Z2491]	gi|15794362|ref|NP 284184.1|	75.28	2E-108
contig00060-orf00051	aspartate ammonia-lyase [Neisseria meningitidis MC58]	gi|15676916|ref|NP 274063.1|	94.41	0
contig00061-orf00001	extracellular solute-binding protein [Ralstonia eutropha JMP134]	gi|73541817|ref|YP 296337.1|	45.09	1E-133
contig00061-orf00002	lipoprotein [Neisseria meningitidis Z2491]	gi|15793295|ref|NP 283117.1|	48.26	1E-41
contig00061-orf00004	fused ribonuclease BN/uncharacterized domain-containing protein [Neisseria meningitidis Z2491]	gi|15793680|ref|NP 283502.1|	81.36	2E-135
contig00061-orf00006	trp repressor binding protein [Chromobacterium violaceum ATCC 12472]	gi|34496264|ref|NP 900479.1|	68.21	3E-64
contig00061-orf00009	hypothetical protein PP 0487 [Pseudomonas putida KT2440]	gi|26987228|ref|NP 742653.1|	47.31	2E-65
contig00061-orf00010	putative clavaminate synthase-like (oxidase) [Frankia alni ACN14a]	gi|111224079|ref|YP 714873.1|	31.8	3E-19
contig00061-orf00014	hypothetical protein Pcryo 0802 [Psychrobacter cryohalolentis K5]	gi|93005632|ref|YP 580069.1|	44.75	1E-42
contig00061-orf00015	transmembrane hexose transporter [Neisseria meningitidis Z2491]	gi|15793691|ref|NP 283513.1|	89.43	0
contig00061-orf00016	membrane protein [Neisseria meningitidis Z2491]	gi|15793690|ref|NP 283512.1|	72.09	2E-48
contig00061-orf00018	aromatic amino acid aminotransferase [Neisseria meningitidis Z2491]	gi|15793696|ref|NP 283518.1|	96.47	0
contig00062-orf00002	hypothetical protein Bamb 3214 [Burkholderia ambifaria AMMD]	gi|115353265|ref|YP 775104.1|	53.66	6E-16
contig00062-orf00004	ATP-dependent protease ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793996|ref|NP 283818.1|	92.51	0
contig00062-orf00005	hypothetical protein NMA1046 [Neisseria meningitidis Z2491]	gi|15793997|ref|NP 283819.1|	84.47	2E-46
contig00062-orf00006	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15793998|ref|NP 283820.1|	98.51	2E-32
contig00062-orf00009	hypothetical protein CV 1536 [Chromobacterium violaceum ATCC 12472]	gi|34496991|ref|NP 901206.1|	55.36	8E-31
contig00062-orf00010	hypothetical protein NGO1252 [Neisseria gonorrhoeae FA 1090]	gi|59801611|ref|YP 208323.1|	73.36	5E-104
contig00062-orf00011	hemolysin III [Chromobacterium violaceum ATCC 12472]	gi|34498797|ref|NP 903012.1|	65.22	9E-76
contig00062-orf00014	protein-PII uridylyltransferase [Neisseria meningitidis MC58]	gi|15677076|ref|NP 274228.1|	93.54	0
contig00062-orf00015	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15794296|ref|NP 284118.1|	87.62	6E-39
contig00062-orf00017	50S ribosomal protein L25/general stress protein Ctc [Neisseria meningitidis Z2491]	gi|15794042|ref|NP 283864.1|	95.26	2E-97
contig00062-orf00018	ribose-phosphate pyrophosphokinase [Neisseria meningitidis Z2491]	gi|15794041|ref|NP 283863.1|	97.86	2E-175
contig00062-orf00019	putative isopentenyl monophosphate kinase [Neisseria gonorrhoeae FA 1090]	gi|59800881|ref|YP 207593.1|	74.64	3E-110
contig00062-orf00022	outer membrane lipoprotein LolB [Neisseria meningitidis MC58]	gi|15676769|ref|NP 273914.1|	58.52	1E-57
contig00062-orf00023	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794038|ref|NP 283860.1|	53.2	8E-173
contig00062-orf00027	hypothetical protein ebA5123 [Aromatoleum aromaticum EbN1]	gi|56478345|ref|YP 159934.1|	43.37	5E-28
contig00062-orf00028	UTP--glucose-1-phosphate uridylyltransferase [Neisseria meningitidis MC58]	gi|15676538|ref|NP 273681.1|	88.46	6E-145
contig00062-orf00029	RNA-binding protein [Neisseria meningitidis Z2491]	gi|15793972|ref|NP 283794.1|	88.07	7E-111
contig00062-orf00033	4-hydroxybenzoate octaprenyltransferase [Neisseria meningitidis MC58]	gi|15676633|ref|NP 273777.1|	74.05	1E-54
contig00062-orf00034	4-hydroxybenzoate octaprenyltransferase [Neisseria meningitidis Z2491]	gi|15793903|ref|NP 283725.1|	66.09	3E-39

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contig00062-orf00035	PTS system, nitrogen regulatory IIA protein [Neisseria meningitidis MC58]	gi|15676634|ref|NP 273778.1|	85.23	6E-59
contig00062-orf00037	HPr kinase/phosphorylase [Neisseria gonorrhoeae FA 1090]	gi|59800761|ref|YP 207473.1|	93.12	5E-166
contig00062-orf00039	hypothetical protein NGO0315 [Neisseria gonorrhoeae FA 1090]	gi|59800762|ref|YP 207474.1|	83.45	9E-132
contig00062-orf00044	ribosomal biogenesis GTPase [Neisseria gonorrhoeae FA 1090]	gi|59800763|ref|YP 207475.1|	97.76	4E-170
contig00062-orf00045	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	62.07	0.14
contig00062-orf00046	succinyl-diaminopimelate desuccinylase [Neisseria gonorrhoeae FA 1090]	gi|59801375|ref|YP 208087.1|	96.59	0
contig00062-orf00047	putative methylated-DNA--protein-cysteine methyltransferase [Neisseria meningitidis MC58]	gi|15677380|ref|NP 274535.1|	86.45	4E-118
contig00063-orf00002	putative transcriptional accessory protein Tex [Neisseria meningitidis MC58]	gi|15676011|ref|NP 273139.1|	95.65	0
contig00063-orf00005	TLDD protein [Neisseria meningitidis Z2491]	gi|15793375|ref|NP 283197.1|	90	0
contig00063-orf00007	hypothetical protein mlr0977 [Mesorhizobium loti MAFF303099]	gi|13471093|ref|NP 102662.1|	29.55	1.3
contig00063-orf00008	sugar permease [Thermoplasma volcanium GSS1]	gi|13541976|ref|NP 111664.1|	32.26	0.91
contig00063-orf00009	hypothetical protein RHE CH03136 [Rhizobium etli CFN 42]	gi|86358737|ref|YP 470629.1|	36.03	2E-19
contig00063-orf00011	phage shock protein A, PspA [Arthrobacter sp. FB24]	gi|116671291|ref|YP 832224.1|	45	5.9
contig00063-orf00013	TonB-dependent receptor [Myxococcus xanthus DK 1622]	gi|108757959|ref|YP 632908.1|	33.33	1.2
contig00063-orf00015	hypothetical protein NMA2018 [Neisseria meningitidis Z2491]	gi|15794898|ref|NP 284720.1|	61.43	6E-21
contig00063-orf00017	hypothetical protein NMA2018 [Neisseria meningitidis Z2491]	gi|15794898|ref|NP 284720.1|	50.68	2E-15
contig00063-orf00018	hypothetical protein RSc2685 [Ralstonia solanacearum GMI1000]	gi|17547404|ref|NP 520806.1|	31.48	0.24
contig00063-orf00020	hypothetical protein Tbd 2219 [Thiobacillus denitrificans ATCC 25259]	gi|74318237|ref|YP 315977.1|	36.41	2E-26
contig00063-orf00023	phosphatidylglycerophosphatase B [Pectobacterium atrosepticum SCRI1043]	gi|50120874|ref|YP 050041.1|	40.62	0.64
contig00063-orf00029	band 7 protein [Shewanella sp. MR-7]	gi|114048390|ref|YP 738940.1|	50.72	3E-129
contig00063-orf00031	hypothetical protein NMB0545 [Neisseria meningitidis MC58]	gi|15676451|ref|NP 273590.1|	97.67	0
contig00063-orf00033	gamma-glutamyltransferase [Burkholderia cenocepacia HI2424]	gi|116692848|ref|YP 838381.1|	32.08	3.4
contig00063-orf00036	putative sodium-dependent transporter [Neisseria gonorrhoeae FA 1090]	gi|59802397|ref|YP 209109.1|	87.62	0
contig00063-orf00039	putative amidase [Neisseria gonorrhoeae FA 1090]	gi|59801840|ref|YP 208552.1|	75.54	2E-164
contig00063-orf00040	hypothetical protein NMB0457 [Neisseria meningitidis MC58]	gi|15676368|ref|NP 273504.1|	73.51	7E-61
contig00063-orf00041	aspartate-semialdehyde dehydrogenase [Neisseria meningitidis Z2491]	gi|15793362|ref|NP 283184.1|	98.11	0
contig00063-orf00044	hypothetical protein NGO0117 [Neisseria gonorrhoeae FA 1090]	gi|59800577|ref|YP 207289.1|	94.41	0
contig00067-orf00001	carboxy-terminal protease [Shigella sonnei Ss046]	gi|74311859|ref|YP 310278.1|	98.55	2E-31
contig00069-orf00002	TrbM [Ralstonia eutropha JMP134]	gi|72384315|ref|YP 293668.1|	49.09	1E-34
contig00069-orf00003	putative pyruvate oxidoreductase [Photobacterium profundum SS9]	gi|54309173|ref|YP 130193.1|	32	7.7
contig00069-orf00004	transfer origin protein, TraL [Ralstonia eutropha JMP134]	gi|72384331|ref|YP 293684.1|	37.85	5E-32
contig00069-orf00005	aldehyde dehydrogenase [Bacillus cereus ATCC 10987]	gi|42781220|ref|NP 978467.1|	38	0.41
contig00070-orf00002	glycine betaine/carnitine/choline ABC transporter, glycine betaine/carnitine/choline-binding protein [Enterococcus faecalis V583]	gi|29375273|ref|NP 814426.1|	56.77	1E-121
contig00070-orf00003	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	92.72	1E-79
contig00070-orf00004	putative mercury transport periplasmic protein [Neisseria meningitidis MC58]	gi|15677139|ref|NP 274292.1|	72.46	3E-22

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contig00070-orf00006	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	65.73	1E-120
contig00070-orf00008	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	78.63	6E-49
contig00070-orf00009	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	66.67	2E-17
contig00070-orf00010	CRISPR-associated helicase Cas3 [Methylococcus capsulatus str. Bath]	gi|53804974|ref|YP 113170.1|	46.04	1E-142
contig00070-orf00011	hypothetical protein LA0688 [Leptospira interrogans serovar Lai str. 56601]	gi|24213388|ref|NP 710869.1|	46.09	2E-22
contig00070-orf00013	CRISPR-associated Csd1 family protein [Methylococcus capsulatus str. Bath]	gi|53804984|ref|YP 113168.1|	46.59	2E-129
contig00070-orf00014	hypothetical protein CT1132 [Chlorobium tepidum TLS]	gi|21673958|ref|NP 662023.1|	60.19	6E-97
contig00070-orf00015	hypothetical protein MS0985 [Mannheimia succiniciproducens MBEL55E]	gi|52425040|ref|YP 088177.1|	74.87	4E-83
contig00071-orf00001	DNA transport competence protein [Neisseria meningitidis Z2491]	gi|15795057|ref|NP 284879.1|	70	2E-16
contig00071-orf00003	glucan phosphorylase [Clostridium acetobutylicum ATCC 824]	gi|15894144|ref|NP 347493.1|	47.06	7.8
contig00072-orf00002	very long chain acyl-CoA dehydrogenase-related protein [Neisseria meningitidis MC58]	gi|15677147|ref|NP 274300.1|	93.43	0
contig00072-orf00003	hypothetical protein Psyc 2082 [Psychrobacter arcticus 273-4]	gi|71066636|ref|YP 265363.1|	60.7	2E-55
contig00073-orf00002	pilin gene inverting protein PivNM-1B [Neisseria meningitidis MC58]	gi|15677475|ref|NP 274631.1|	58.86	1E-95
contig00073-orf00004	truncated FmtB protein [Staphylococcus aureus subsp. aureus USA300 FPR3757]	gi|87161033|ref|YP 494756.1|	32.88	0.13
contig00074-orf00001	elongation factor Tu [Neisseria meningitidis Z2491]	gi|15793177|ref|NP 282999.1|	99.47	0
contig00075-orf00002	glycine betaine transporter [Roseobacter denitrificans OCh 114]	gi|115345534|ref|YP 771716.1|	32.75	9E-49
contig00075-orf00004	carnitine O-acetyltransferase [Mycoplasma pulmonis UAB CTIP]	gi|15829246|ref|NP 326606.1|	23.51	1E-27
contig00075-orf00006	sugar kinase [Thermoanaerobacter tengcongensis MB4]	gi|20808554|ref|NP 623725.1|	39.45	9E-28
contig00075-orf00007	hypothetical protein MS1159 [Mannheimia succiniciproducens MBEL55E]	gi|52425214|ref|YP 088351.1|	69.51	3E-26
contig00075-orf00008	recombination associated protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527784|ref|NP 931129.1|	52.94	0.53
contig00075-orf00011	FeoB protein [Mannheimia succiniciproducens MBEL55E]	gi|52425212|ref|YP 088349.1|	72.21	0
contig00075-orf00012	hypothetical protein MS1156 [Mannheimia succiniciproducens MBEL55E]	gi|52425211|ref|YP 088348.1|	66.67	0.007
contig00075-orf00014	hypothetical protein NMA1791 [Neisseria meningitidis Z2491]	gi|15794682|ref|NP 284504.1|	88.78	0
contig00075-orf00017	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase [Neisseria meningitidis Z2491]	gi|15794277|ref|NP 284099.1|	93.89	0
contig00075-orf00018	hypothetical protein glr0328 [Gloeobacter violaceus PCC 7421]	gi|37519897|ref|NP 923274.1|	46.76	3E-48
contig00075-orf00022	permease [Neisseria meningitidis Z2491]	gi|15793419|ref|NP 283241.1|	75.26	8E-169
contig00075-orf00024	membrane protein [Neisseria meningitidis Z2491]	gi|15794077|ref|NP 283899.1|	81.36	5E-22
contig00075-orf00027	hypothetical protein FN0016 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	gi|19703368|ref|NP 602930.1|	33.33	2E-14
contig00075-orf00028	hypothetical protein NMB1197 [Neisseria meningitidis MC58]	gi|15677071|ref|NP 274223.1|	75.19	2E-75
contig00075-orf00029	nickel-dependent hydrogenase, b-type cytochrome subunit [Neisseria meningitidis MC58]	gi|15677070|ref|NP 274222.1|	68.42	6E-66
contig00075-orf00032	hypothetical protein NMB1963 [Neisseria meningitidis MC58]	gi|15677793|ref|NP 274957.1|	39.88	1E-26

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contig00075-orf00033	hypothetical protein NMA1720 [Neisseria meningitidis Z2491]	gi|15794613|ref|NP 284435.1|	75.8	3E-66
contig00075-orf00035	DNA repair protein RadC [Neisseria meningitidis MC58]	gi|15676925|ref|NP 274072.1|	82.59	4E-98
contig00075-orf00036	spermidine/putrescine ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676514|ref|NP 273654.1|	92.16	0
contig00075-orf00038	polyamine permease inner membrane protein [Neisseria meningitidis Z2491]	gi|15793790|ref|NP 283612.1|	95.81	1E-152
contig00075-orf00039	spermidine/putrescine ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15676516|ref|NP 273656.1|	97.29	8E-126
contig00075-orf00041	oxidoreductase [Neisseria meningitidis Z2491]	gi|15793792|ref|NP 283614.1|	83.99	0
contig00075-orf00043	hypothetical protein NMB0938 [Neisseria meningitidis MC58]	gi|15676831|ref|NP 273976.1|	44.4	2E-54
contig00075-orf00045	iron-sulphur binding protein [Neisseria meningitidis Z2491]	gi|15794397|ref|NP 284219.1|	58.73	3E-16
contig00075-orf00047	ribonucleotide-diphosphate reductase beta subunit [Neisseria gonorrhoeae FA 1090]	gi|59801042|ref|YP 207754.1|	95.76	0
contig00075-orf00048	abortive infection bacteriophage resistance protein [Nitrosococcus oceani ATCC 19707]	gi|77165281|ref|YP 343806.1|	46.86	9E-75
contig00075-orf00050	ribonucleotide-diphosphate reductase subunit alpha [Neisseria meningitidis Z2491]	gi|15794401|ref|NP 284223.1|	94.86	0
contig00075-orf00051	chaperone protein HscB [Neisseria meningitidis MC58]	gi|15677246|ref|NP 274399.1|	77.71	6E-68
contig00075-orf00053	HesB/YadR/YfhF family protein [Neisseria meningitidis MC58]	gi|15677244|ref|NP 274397.1|	90.74	1E-53
contig00075-orf00056	hypothetical protein PM1196 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603061|ref|NP 246133.1|	61.73	1E-17
contig00075-orf00058	scaffold protein [Neisseria meningitidis Z2491]	gi|15794489|ref|NP 284311.1|	99.22	5E-68
contig00075-orf00060	hypothetical protein NMA1595 [Neisseria meningitidis Z2491]	gi|15794488|ref|NP 284310.1|	100	0.0000008
contig00075-orf00063	NifS-like aminotranfserase [Neisseria meningitidis Z2491]	gi|15794487|ref|NP 284309.1|	98.27	0
contig00075-orf00064	hypothetical protein NMA1593 [Neisseria meningitidis Z2491]	gi|15794486|ref|NP 284308.1|	91.22	5E-63
contig00075-orf00066	L-lactate dehydrogenase [Neisseria meningitidis Z2491]	gi|15794485|ref|NP 284307.1|	97.66	0
contig00075-orf00067	putative RNA methyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801230|ref|YP 207942.1|	60.38	4E-76
contig00075-orf00068	sigma-E factor negative regulatory protein RseA [Vibrio cholerae O1 biovar El Tor str. N16961]	gi|15642462|ref|NP 232095.1|	32.69	0.049
contig00075-orf00069	RNA polymerase sigma factor RpoE [Chromobacterium violaceum ATCC	gi|34497513|ref|NP 901728.1|	65.08	2E-69
contig00075-orf00070	hypothetical protein NGO0820 [Neisseria gonorrhoeae FA 1090]	gi|59801231|ref|YP 207943.1|	47.46	4E-100
contig00075-orf00072	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Neisseria meningitidis Z2491]	gi|15794271|ref|NP 284093.1|	89.34	4E-159
contig00075-orf00075	hypothetical protein NMA1348 [Neisseria meningitidis Z2491]	gi|15794270|ref|NP 284092.1|	80.45	5E-57
contig00075-orf00077	#N/A	#N/A	#N/A	#N/A
contig00075-orf00078	proline/alanine-rich repetetive membrane anchored protein [Tropheryma whipplei TW08/27]	gi|28572767|ref|NP 789547.1|	27.37	0.06
contig00076-orf00001	hypothetical protein NGO0015 [Neisseria gonorrhoeae FA 1090]	gi|59800484|ref|YP 207196.1|	81.25	1.6
contig00076-orf00003	sulphate-binding protein [Neisseria meningitidis Z2491]	gi|15794178|ref|NP 284000.1|	70.66	4E-145

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contig00076-orf00005	hypothetical protein Reut B4623 [Ralstonia eutropha JMP134]	gi|73538450|ref|YP 298817.1|	54.14	9E-88
contig00076-orf00010	biotin synthetase [Neisseria meningitidis MC58]	gi|15677058|ref|NP 274210.1|	95.17	0
contig00076-orf00011	hypothetical protein NGO0814 [Neisseria gonorrhoeae FA 1090]	gi|59801226|ref|YP 207938.1|	50	0.049
contig00076-orf00014	fructose-1,6-bisphosphatase [Neisseria meningitidis Z2491]	gi|15794192|ref|NP 284014.1|	78.88	6E-143
contig00076-orf00016	streptococcal hemagglutinin protein [Staphylococcus epidermidis ATCC 12228]	gi|27469167|ref|NP 765804.1|	30.43	0.049
contig00076-orf00019	poly(A) polymerase [Neisseria meningitidis Z2491]	gi|15794003|ref|NP 283825.1|	71.3	5E-168
contig00076-orf00020	putative tRNA pseudouridine synthase B [Neisseria gonorrhoeae FA 1090]	gi|59801069|ref|YP 207781.1|	86.75	2E-147
contig00076-orf00022	ribosome-binding factor A [Neisseria meningitidis MC58]	gi|15677238|ref|NP 274391.1|	89.43	7E-59
contig00076-orf00023	hypothetical protein PM0652 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602517|ref|NP 245589.1|	56.3	2E-106
contig00076-orf00024	recombinase A [Neisseria meningitidis MC58]	gi|15677302|ref|NP 274457.1|	90.23	4E-157
contig00076-orf00025	pyruvate formate lyase-activating enzyme 1 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15601942|ref|NP 245014.1|	63.93	2E-86
contig00076-orf00026	hypothetical protein NMB0513 [Neisseria meningitidis MC58]	gi|15676422|ref|NP 273559.1|	97	2E-54
contig00076-orf00028	formate acetyltransferase [Haemophilus influenzae Rd KW20]	gi|16272145|ref|NP 438348.1|	80.55	0
contig00076-orf00031	bacterioferritin B [Neisseria meningitidis Z2491]	gi|15794297|ref|NP 284119.1|	94.27	1E-79
contig00076-orf00032	bacterioferritin A [Neisseria meningitidis MC58]	gi|15677080|ref|NP 274232.1|	94.81	2E-82
contig00076-orf00035	GTP-binding protein [Neisseria meningitidis Z2491]	gi|15794291|ref|NP 284113.1|	99.17	0
contig00076-orf00037	hypothetical protein Pcar 0125 [Pelobacter carbinolicus DSM 2380]	gi|77917742|ref|YP 355557.1|	48.65	4E-176
contig00076-orf00038	putative NTP-binding protein TniB [Pelobacter carbinolicus DSM 2380]	gi|77917741|ref|YP 355556.1|	60.43	1E-90
contig00076-orf00039	hypothetical protein Tcr 1645 [Thiomicrospira crunogena XCL-2]	gi|78485986|ref|YP 391911.1|	43.58	1E-81
contig00076-orf00040	hypothetical protein NGO0253 [Neisseria gonorrhoeae FA 1090]	gi|59800705|ref|YP 207417.1|	81.22	2E-83
contig00076-orf00042	hypothetical protein Tcr 1640 [Thiomicrospira crunogena XCL-2]	gi|78485981|ref|YP 391906.1|	33.22	1E-70
contig00076-orf00043	lipoyl synthase [Neisseria meningitidis Z2491]	gi|15794299|ref|NP 284121.1|	97.81	0
contig00076-orf00044	lipoate-protein ligase B [Neisseria meningitidis MC58]	gi|77358711|ref|NP 274242.2|	91.71	2E-106
contig00076-orf00045	hypothetical protein NGO0791 [Neisseria gonorrhoeae FA 1090]	gi|59801205|ref|YP 207917.1|	74.44	4E-32
contig00076-orf00049	ATP-dependent protease La [Neisseria meningitidis MC58]	gi|15677103|ref|NP 274255.1|	89.76	0
contig00076-orf00051	DNA-binding protein [Neisseria meningitidis Z2491]	gi|15794310|ref|NP 284132.1|	96.43	7E-38
contig00076-orf00053	hypothetical protein SFV 2498 [Shigella flexneri 5 str. 8401]	gi|110806387|ref|YP 689907.1|	39.22	0.55
contig00076-orf00054	peptidyl-tRNA hydrolase [Neisseria meningitidis MC58]	gi|15676693|ref|NP 273837.1|	83.33	4E-86
contig00076-orf00058	hypothetical protein NMA1005 [Neisseria meningitidis Z2491]	gi|15793961|ref|NP 283783.1|	74.14	4E-17
contig00076-orf00059	hypothetical protein NMA1006 [Neisseria meningitidis Z2491]	gi|15793962|ref|NP 283784.1|	83.92	8E-66
contig00076-orf00060	hypothetical protein NMB1327 [Neisseria meningitidis MC58]	gi|15677193|ref|NP 274346.1|	51.75	3E-108
contig00076-orf00061	transferase [Neisseria meningitidis Z2491]	gi|15794614|ref|NP 284436.1|	75.19	9E-116
contig00076-orf00063	hypothetical protein Mfla 1025 [Methylobacillus flagellatus KT]	gi|91775378|ref|YP 545134.1|	39.56	3E-32
contig00076-orf00064	hypothetical protein NGO0853 [Neisseria gonorrhoeae FA 1090]	gi|59801257|ref|YP 207969.1|	56.47	0.0000006
contig00076-orf00065	hypothetical protein NGO0972 [Neisseria gonorrhoeae FA 1090]	gi|59801358|ref|YP 208070.1|	65.79	7E-81
contig00076-orf00066	DNA polymerase III, epsilon subunit [Neisseria meningitidis MC58]	gi|15677367|ref|NP 274522.1|	81.03	2E-102

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contig00076-orf00067	hypothetical protein NGO0322 [Neisseria gonorrhoeae FA 1090]	gi|59800769|ref|YP 207481.1|	48.7	5E-38
contig00076-orf00068	hypothetical protein NGO0666 [Neisseria gonorrhoeae FA 1090]	gi|59801093|ref|YP 207805.1|	48.36	3E-15
contig00077-orf00003	beta-glucosidase [Lactobacillus plantarum WCFS1]	gi|28379931|ref|NP 786823.1|	38.64	3.5
contig00077-orf00005	hypothetical protein Rmet 6243 [Ralstonia metallidurans CH34]	gi|94152650|ref|YP 582052.1|	35.89	4E-32
contig00077-orf00006	hypothetical protein Pfl01 3559 [Pseudomonas fluorescens Pf0-1]	gi|77459781|ref|YP 349288.1|	26.97	1.7
contig00078-orf00001	hypothetical protein NGO1559 [Neisseria gonorrhoeae FA 1090]	gi|59801892|ref|YP 208604.1|	74.44	2E-90
contig00078-orf00002	hypothetical protein CV 0489 [Chromobacterium violaceum ATCC 12472]	gi|34495944|ref|NP 900159.1|	47.64	5E-51
contig00078-orf00004	branched-chain amino acid aminotransferase [Neisseria meningitidis MC58]	gi|15676252|ref|NP 273386.1|	93.07	1E-171
contig00078-orf00006	hypothetical protein NMA2149 [Neisseria meningitidis Z2491]	gi|15795020|ref|NP 284842.1|	83.15	3E-25
contig00078-orf00008	hypothetical protein NGO1662 [Neisseria gonorrhoeae FA 1090]	gi|59801987|ref|YP 208699.1|	89.46	0
contig00078-orf00011	flagellar protein, putative [Borrelia garinii PBi]	gi|51598441|ref|YP 072629.1|	44.44	2.1
contig00078-orf00012	cell surface protein [Methanosarcina acetivorans C2A]	gi|20091708|ref|NP 617783.1|	21.49	0.01
contig00078-orf00014	thymidylate synthase [Neisseria gonorrhoeae FA 1090]	gi|59801705|ref|YP 208417.1|	94.7	3E-148
contig00078-orf00016	glutamate dehydrogenase [Neisseria meningitidis Z2491]	gi|15794847|ref|NP 284669.1|	92.1	0
contig00078-orf00018	peptidase M16-like [Nitrosospira multiformis ATCC 25196]	gi|82703850|ref|YP 413416.1|	42.23	4E-91
contig00078-orf00019	lipoprotein [Neisseria meningitidis Z2491]	gi|15793247|ref|NP 283069.1|	75.84	9E-107
contig00078-orf00021	putative cytochrome synthesis protein [Neisseria gonorrhoeae FA 1090]	gi|59800564|ref|YP 207276.1|	83.04	0
contig00078-orf00022	membrane protein [Neisseria meningitidis Z2491]	gi|15793643|ref|NP 283465.1|	81.54	0
contig00078-orf00026	cytochrome C [Neisseria meningitidis Z2491]	gi|15793642|ref|NP 283464.1|	80.19	3E-80
contig00078-orf00027	GTPase EngB [Neisseria meningitidis Z2491]	gi|15793641|ref|NP 283463.1|	88.78	1E-97
contig00078-orf00029	biopolymer transport protein [Neisseria meningitidis Z2491]	gi|15794865|ref|NP 284687.1|	78.57	3E-48
contig00078-orf00030	biopolymer transport protein [Neisseria meningitidis Z2491]	gi|15794866|ref|NP 284688.1|	76.26	5E-91
contig00078-orf00031	TonB protein [Neisseria meningitidis Z2491]	gi|15794867|ref|NP 284689.1|	68.18	0.0000005
contig00078-orf00033	hypothetical protein NMA2048 [Neisseria meningitidis Z2491]	gi|15794926|ref|NP 284748.1|	82.99	2E-67
contig00078-orf00034	hypothetical protein NMA2047 [Neisseria meningitidis Z2491]	gi|15794925|ref|NP 284747.1|	69.88	1E-28
contig00078-orf00037	hypothetical protein NGO1516 [Neisseria gonorrhoeae FA 1090]	gi|59801854|ref|YP 208566.1|	88.48	0
contig00078-orf00038	pilus-associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800520|ref|YP 207232.1|	37.97	2E-99
contig00078-orf00041	carbamoyl phosphate synthase small subunit [Neisseria meningitidis Z2491]	gi|15793598|ref|NP 283420.1|	96.53	0
contig00078-orf00044	hypothetical protein ACIAD0111 [Acinetobacter sp. ADP1]	gi|50083401|ref|YP 044911.1|	62.2	6E-23
contig00078-orf00045	hypothetical protein NGO0050 [Neisseria gonorrhoeae FA 1090]	gi|59800517|ref|YP 207229.1|	94.57	4E-67
contig00079-orf00003	membrane peptidase [Neisseria meningitidis Z2491]	gi|15794585|ref|NP 284407.1|	53.73	2E-61
contig00079-orf00004	3-oxoacid CoA-transferase subunit A [Myxococcus xanthus DK 1622]	gi|108764087|ref|YP 631972.1|	50	4.6
contig00079-orf00005	SurE protein [Neisseria meningitidis Z2491]	gi|15794586|ref|NP 284408.1|	76.73	3E-111
contig00079-orf00006	heat shock protein HtpX [Neisseria meningitidis MC58]	gi|15676720|ref|NP 273864.1|	86.74	4E-124
contig00079-orf00008	hypothetical protein Pcryo 0464 [Psychrobacter cryohalolentis K5]	gi|93005294|ref|YP 579731.1|	41.71	2E-35
contig00079-orf00010	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein [Neisseria meningitidis Z2491]	gi|15794338|ref|NP 284160.1|	95.3	0

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contig00079-orf00014	DNA mismatch repair protein [Neisseria meningitidis MC58]	gi|15677300|ref|NP 274454.1|	87.78	0
contig00079-orf00016	NAD-dependent deacetylase [Haemophilus influenzae 86-028NP]	gi|68249977|ref|YP 249089.1|	60.81	2E-62
contig00079-orf00019	hypothetical protein NGO0895 [Neisseria gonorrhoeae FA 1090]	gi|59801294|ref|YP 208006.1|	83.67	3E-19
contig00080-orf00001	hypothetical protein NMA2003 [Neisseria meningitidis Z2491]	gi|15794883|ref|NP 284705.1|	66.67	0.063
contig00080-orf00002	hypothetical protein CRP 180 [Candidatus Carsonella ruddii PV]	gi|116335082|ref|YP 802577.1|	32.81	0.93
contig00080-orf00003	putative tspB protein [Neisseria meningitidis MC58]	gi|15677591|ref|NP 274748.1|	41.27	0.0003
contig00080-orf00005	putative tspB protein [Neisseria meningitidis MC58]	gi|15677591|ref|NP 274748.1|	44.96	2E-49
contig00080-orf00009	hypothetical protein NMB1749 [Neisseria meningitidis MC58]	gi|15677593|ref|NP 274750.1|	71.7	6E-151
contig00080-orf00011	DNA-invertase [Neisseria meningitidis Z2491]	gi|15793747|ref|NP 283569.1|	50.78	9E-89
contig00080-orf00012	nicotinamidase [Neisseria meningitidis Z2491]	gi|15793262|ref|NP 283084.1|	38.12	7E-25
contig00080-orf00016	hypothetical protein Bpro 3822 [Polaromonas sp. JS666]	gi|91789666|ref|YP 550618.1|	32.08	1E-38
contig00080-orf00017	hypothetical protein NGO1488 [Neisseria gonorrhoeae FA 1090]	gi|59801826|ref|YP 208538.1|	73.97	5E-26
contig00080-orf00018	sec-independent protein translocase component [Neisseria meningitidis Z2491]	gi|15793777|ref|NP 283599.1|	85.66	1E-109
contig00080-orf00019	hypothetical protein NMB0600 [Neisseria meningitidis MC58]	gi|15676505|ref|NP 273644.1|	70.93	8E-63
contig00080-orf00020	sec-independent protein translocase component [Neisseria meningitidis Z2491]	gi|15793779|ref|NP 283601.1|	90.62	3E-20
contig00080-orf00022	nucleotide-binding protein [Neisseria meningitidis Z2491]	gi|15793780|ref|NP 283602.1|	93.4	1E-53
contig00080-orf00023	phosphoribosyl-ATP cyclohydrolase [Neisseria meningitidis Z2491]	gi|15793781|ref|NP 283603.1|	77.57	2E-40
contig00080-orf00025	phosphoribosyl-AMP cyclohydrolase [Neisseria meningitidis Z2491]	gi|15793807|ref|NP 283629.1|	87.02	6E-64
contig00080-orf00027	imidazole glycerol phosphate synthase subunit HisF [Neisseria gonorrhoeae FA 1090]	gi|59800664|ref|YP 207376.1|	90.2	1E-128
contig00080-orf00028	V-type ATP synthase subunit I [Pyrococcus furiosus DSM 3638]	gi|18976549|ref|NP 577906.1|	26.85	0.01
contig00080-orf00030	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase [Neisseria meningitidis MC58]	gi|15676531|ref|NP 273672.1|	93.85	7E-127
contig00080-orf00031	imidazole glycerol phosphate synthase subunit HisH [Neisseria meningitidis MC58]	gi|15676532|ref|NP 273673.1|	74.53	4E-93
contig00080-orf00035	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793699|ref|NP 283521.1|	91.8	0
contig00080-orf00037	bifunctional GMP synthase/glutamine amidotransferase protein [Neisseria meningitidis Z2491]	gi|15793529|ref|NP 283351.1|	98.08	0
contig00080-orf00038	hypothetical protein Mmcs 0501 [Mycobacterium sp. MCS]	gi|108797481|ref|YP 637678.1|	36.84	0.69
contig00080-orf00040	SsrA-binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801371|ref|YP 208083.1|	92.57	2E-76
contig00080-orf00042	DNA repair protein RadA [Neisseria meningitidis Z2491]	gi|15793949|ref|NP 283771.1|	97.59	0
contig00080-orf00044	carboxy-terminal peptidase [Neisseria meningitidis MC58]	gi|15677198|ref|NP 274351.1|	83.4	0
contig00080-orf00048	hypothetical protein NMB1333 [Neisseria meningitidis MC58]	gi|15677199|ref|NP 274352.1|	66.17	1E-62
contig00080-orf00049	lipoprotein [Neisseria meningitidis Z2491]	gi|15794442|ref|NP 284264.1|	69.61	5E-66
contig00080-orf00050	hypothetical protein NMB1336 [Neisseria meningitidis MC58]	gi|15677202|ref|NP 274355.1|	80.22	2E-84
contig00080-orf00051	Holliday junction resolvase-like protein [Neisseria meningitidis Z2491]	gi|15794444|ref|NP 284266.1|	81.88	5E-68
contig00080-orf00054	hypothetical protein ACIAD0324 [Acinetobacter sp. ADP1]	gi|50083594|ref|YP 045104.1|	43.1	1E-74

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contig00080-orf00056	hypothetical protein BURPS1710b A0579 [Burkholderia pseudomallei 1710b]	gi|76818274|ref|YP 335738.1|	28.91	0.0005
contig00080-orf00057	hypothetical protein Bcep18194 A5147 [Burkholderia sp. 383]	gi|78066616|ref|YP 369385.1|	47.9	6E-22
contig00080-orf00058	hypothetical protein NMB1064 [Neisseria meningitidis MC58]	gi|15676948|ref|NP 274097.1|	82.58	1E-79
contig00080-orf00060	dihydroneopterin aldolase [Neisseria meningitidis MC58]	gi|15676947|ref|NP 274096.1|	72.17	1E-41
contig00080-orf00061	hypothetical protein NMB1062 [Neisseria meningitidis MC58]	gi|15676946|ref|NP 274095.1|	82.74	6E-66
contig00080-orf00063	hypothetical protein MS2191 [Mannheimia succiniciproducens MBEL55E]	gi|52426246|ref|YP 089383.1|	49.44	8E-114
contig00080-orf00066	hypothetical protein NMB1039 [Neisseria meningitidis MC58]	gi|15676926|ref|NP 274073.1|	93.64	2E-134
contig00080-orf00067	chorismate mutase [Neisseria meningitidis Z2491]	gi|15794919|ref|NP 284741.1|	85.91	4E-175
contig00080-orf00069	hypothetical protein BURPS1710b 1598 [Burkholderia pseudomallei 1710b]	gi|76810028|ref|YP 333002.1|	37.5	4.6
contig00080-orf00071	two-component system regulator [Neisseria meningitidis Z2491]	gi|15793772|ref|NP 283594.1|	94.47	3E-101
contig00080-orf00072	putative two-component system sensor kinase [Neisseria gonorrhoeae FA 1090]	gi|59800631|ref|YP 207343.1|	86.88	0
contig00080-orf00074	hypothetical protein NMB0593 [Neisseria meningitidis MC58]	gi|15676498|ref|NP 273637.1|	63	0
contig00080-orf00075	30S ribosomal protein S16 [Neisseria meningitidis Z2491]	gi|15793769|ref|NP 283591.1|	90.12	5E-36
contig00080-orf00076	16S rRNA-processing protein [Neisseria gonorrhoeae FA 1090]	gi|59800629|ref|YP 207341.1|	90	4E-81
contig00080-orf00077	tRNA (guanine-N1)-methyltransferase [Neisseria meningitidis MC58]	gi|15676495|ref|NP 273634.1|	88.09	1E-106
contig00080-orf00078	50S ribosomal protein L19 [Neisseria meningitidis Z2491]	gi|15793766|ref|NP 283588.1|	99.17	2E-52
contig00080-orf00079	putative bacteriocin production protein [Neisseria gonorrhoeae FA 1090]	gi|59800715|ref|YP 207427.1|	54.88	4E-45
contig00080-orf00081	tetrapac protein [Neisseria meningitidis Z2491]	gi|15793863|ref|NP 283685.1|	93.51	1E-32
contig00080-orf00082	bifunctional folylpolyglutamate synthase/dihydrofolate synthase [Neisseria meningitidis Z2491]	gi|15793864|ref|NP 283686.1|	93.4	0
contig00080-orf00083	FolI [Neisseria gonorrhoeae FA 1090]	gi|59800718|ref|YP 207430.1|	57.45	1E-33
contig00080-orf00084	hypothetical protein NMA0899 [Neisseria meningitidis Z2491]	gi|15793866|ref|NP 283688.1|	90.24	6E-63
contig00080-orf00085	amino acid ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676594|ref|NP 273738.1|	93.8	1E-128
contig00080-orf00089	dimethyladenosine transferase [Neisseria meningitidis MC58]	gi|15676595|ref|NP 273739.1|	95.75	4E-138
contig00080-orf00091	NemA protein [Mannheimia succiniciproducens MBEL55E]	gi|52426351|ref|YP 089488.1|	67.28	2E-147
contig00080-orf00094	ornithine-acyl[acyl carrier protein] N-acyltransferase [Methylobacillus flagellatus KT]	gi|91774824|ref|YP 544580.1|	48.48	2E-58
contig00080-orf00095	lyso-ornithine lipid acyltransferase [Methylobacillus flagellatus KT]	gi|91774823|ref|YP 544579.1|	37.9	4E-37
contig00080-orf00098	RNA polymerase sigma factor RpoD [Neisseria meningitidis Z2491]	gi|15794630|ref|NP 284452.1|	86.31	0
contig00080-orf00102	DNA primase [Neisseria meningitidis MC58]	gi|15677389|ref|NP 274544.1|	95.59	0
contig00080-orf00105	transporter [Salmonella typhimurium LT2]	gi|16765725|ref|NP 461340.1|	51.78	5E-129
contig00080-orf00109	hypothetical protein plu3514 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527387|ref|NP 930731.1|	28.25	3E-50
contig00080-orf00110	#N/A	#N/A	#N/A	#N/A
contig00080-orf00113	hypothetical protein plu3515 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527388|ref|NP 930732.1|	45.88	2E-22

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contig00080-orf00114	hypothetical protein plu3513 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527386|ref|NP 930730.1|	36.99	0
contig00080-orf00116	hypothetical protein NMA0970 [Neisseria meningitidis Z2491]	gi|15793927|ref|NP 283749.1|	74	2E-64
contig00080-orf00119	hypothetical protein Nmul A0030 [Nitrosospira multiformis ATCC 25196]	gi|82701165|ref|YP 410731.1|	33.08	3E-50
contig00080-orf00122	succinate semialdehyde dehydrogenase [Neisseria meningitidis MC58]	gi|15677341|ref|NP 274496.1|	92.77	0
contig00080-orf00125	hypothetical protein Rru A1985 [Rhodospirillum rubrum ATCC 11170]	gi|83593320|ref|YP 427072.1|	29.46	0.0000004
contig00080-orf00127	hypothetical protein MA2018 [Methanosarcina acetivorans C2A]	gi|20090866|ref|NP 616941.1|	35.29	4.5
contig00080-orf00128	preprotein translocase subunit SecF [Neisseria gonorrhoeae FA 1090]	gi|59800645|ref|YP 207357.1|	95.67	2E-158
contig00080-orf00130	preprotein translocase subunit SecD [Neisseria gonorrhoeae FA 1090]	gi|59800644|ref|YP 207356.1|	91.25	0
contig00080-orf00131	hypothetical protein NMB0606 [Neisseria meningitidis MC58]	gi|15676510|ref|NP 273650.1|	92.86	8E-37
contig00080-orf00132	histone deacetylase family protein [Neisseria meningitidis MC58]	gi|15676509|ref|NP 273649.1|	74.02	2E-135
contig00080-orf00134	transferrin-binding protein-related protein [Neisseria meningitidis MC58]	gi|15677945|ref|NP 275117.1|	36.65	8E-24
contig00080-orf00136	heme utilisation protein [Neisseria meningitidis MC58]	gi|15677518|ref|NP 274674.1|	88.35	5E-106
contig00080-orf00137	#N/A	#N/A	#N/A	#N/A
contig00080-orf00139	hypothetical protein NGO0208 [Neisseria gonorrhoeae FA 1090]	gi|59800661|ref|YP 207373.1|	79.31	7E-78
contig00080-orf00140	hypothetical protein NGO0180 [Neisseria gonorrhoeae FA 1090]	gi|59800635|ref|YP 207347.1|	55.61	1E-59
contig00080-orf00141	hypothetical protein NMB0841 [Neisseria meningitidis MC58]	gi|15676737|ref|NP 273882.1|	25.27	0.0007
contig00080-orf00142	glutamate dehydrogenase [Neisseria meningitidis Z2491]	gi|15794580|ref|NP 284402.1|	95.96	0
contig00080-orf00145	phosphoglycolate phosphatase [Neisseria meningitidis Z2491]	gi|15794581|ref|NP 284403.1|	87.66	1E-106
contig00080-orf00146	recombination regulator RecX [Neisseria gonorrhoeae FA 1090]	gi|59801424|ref|YP 208136.1|	78.95	2E-53
contig00080-orf00149	hypothetical protein NMB0783 [Neisseria meningitidis MC58]	gi|15676681|ref|NP 273825.1|	72.46	1E-49
contig00080-orf00150	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793951|ref|NP 283773.1|	76.83	1E-31
contig00080-orf00152	hypothetical protein NMA1782 [Neisseria meningitidis Z2491]	gi|15794675|ref|NP 284497.1|	90.99	8E-31
contig00080-orf00154	AraC family transcription regulator [Neisseria meningitidis Z2491]	gi|15794676|ref|NP 284498.1|	54.97	6E-87
contig00080-orf00156	dihydrolipoamide dehydrogenase [Neisseria meningitidis Z2491]	gi|15794088|ref|NP 283910.1|	97.85	0
contig00080-orf00158	redoxin [Neisseria meningitidis Z2491]	gi|15794087|ref|NP 283909.1|	97.55	1E-138
contig00080-orf00159	1-acyl-SN-glycerol-3-phosphate acyltransferase [Neisseria meningitidis Z2491]	gi|15794403|ref|NP 284225.1|	57.14	7.7
contig00080-orf00160	1-acyl-SN-glycerol-3-phosphate acyltransferase [Neisseria gonorrhoeae FA	gi|59801039|ref|YP 207751.1|	74.15	2E-80
contig00080-orf00161	formamidopyrimidine-DNA glycosylase [Neisseria meningitidis MC58]	gi|15677162|ref|NP 274315.1|	82.91	7E-134
contig00080-orf00163	hypothetical protein NMA1506 [Neisseria meningitidis Z2491]	gi|15794405|ref|NP 284227.1|	60.36	7E-74
contig00080-orf00166	tryptophan synthase subunit beta [Neisseria meningitidis MC58]	gi|15676597|ref|NP 273741.1|	95.25	0
contig00080-orf00169	fumarate hydratase [Neisseria meningitidis Z2491]	gi|15794702|ref|NP 284524.1|	98.22	0
contig00080-orf00172	ferredoxin:4Fe-4S ferredoxin, iron-sulfur binding [Ralstonia eutropha JMP134]	gi|73538417|ref|YP 298784.1|	56.37	4E-68
contig00080-orf00173	L-aspartate oxidase [Ralstonia eutropha JMP134]	gi|73538416|ref|YP 298783.1|	64.6	1E-170
contig00080-orf00175	respiratory-chain NADH dehydrogenase domain-containing protein [Ralstonia metallidurans CH34]	gi|94313226|ref|YP 586435.1|	64.5	8E-132
contig00080-orf00180	anion transporter [Rhodoferax ferrireducens T118]	gi|89899730|ref|YP 522201.1|	65.56	6E-170

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contig00080-orf00182	potassium transporter peripheral membrane component [Neisseria gonorrhoeae FA 1090]	gi|59801520|ref|YP 208232.1|	80.29	2E-49
contig00080-orf00186	potassium transporter peripheral membrane component [Neisseria gonorrhoeae FA 1090]	gi|59801520|ref|YP 208232.1|	81.06	0
contig00080-orf00187	hypothetical protein NGO0420 [Neisseria gonorrhoeae FA 1090]	gi|59800863|ref|YP 207575.1|	50	2E-51
contig00080-orf00188	major outer membrane protein PIB [Neisseria meningitidis MC58]	gi|15677862|ref|NP 275030.1|	36.34	2E-48
contig00080-orf00191	CTP synthetase [Neisseria meningitidis Z2491]	gi|15794635|ref|NP 284457.1|	98.34	0
contig00080-orf00195	putative transport protein, potassium [Neisseria gonorrhoeae FA 1090]	gi|59800683|ref|YP 207395.1|	72.94	5E-180
contig00080-orf00197	nuclear export factor GLE1 [Deinococcus geothermalis DSM 11300]	gi|94985233|ref|YP 604597.1|	31.25	2E-13
contig00081-orf00003	prolyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677205|ref|NP 274358.1|	96.13	0
contig00081-orf00006	putative esterase [Streptococcus mutans UA159]	gi|24378638|ref|NP 720593.1|	51.46	1E-77
contig00081-orf00010	iron/sulphur-binding oxidoreductase [Neisseria meningitidis Z2491]	gi|15794464|ref|NP 284286.1|	85.63	2E-152
contig00081-orf00011	2-isopropylmalate synthase [Neisseria meningitidis Z2491]	gi|15794202|ref|NP 284024.1|	87.81	0
contig00081-orf00013	regulator protein pecM [Chromobacterium violaceum ATCC 12472]	gi|34497232|ref|NP 901447.1|	56.98	1E-60
contig00081-orf00017	putative outer membrane lipoprotein (lipocalin) [Acinetobacter sp. ADP1]	gi|50084784|ref|YP 046294.1|	48.77	4E-42
contig00081-orf00020	hypothetical protein NMB1586 [Neisseria meningitidis MC58]	gi|15677436|ref|NP 274592.1|	84.85	7E-09
contig00081-orf00022	hypothetical protein ZMO0800 [Zymomonas mobilis subsp. mobilis ZM4]	gi|56551696|ref|YP 162535.1|	52.8	0
contig00081-orf00024	ring-cleaving dioxygenase [Pseudomonas aeruginosa UCBPP-PA14]	gi|116048804|ref|YP 792396.1|	60.16	2E-35
contig00082-orf00001	hypothetical protein NMB0372 [Neisseria meningitidis MC58]	gi|15676286|ref|NP 273421.1|	88.32	2E-69
contig00085-orf00001	hypothetical protein NMA1799 [Neisseria meningitidis Z2491]	gi|15794690|ref|NP 284512.1|	34.29	1E-31
contig00085-orf00002	hypothetical protein NMB1627 [Neisseria meningitidis MC58]	gi|15677477|ref|NP 274633.1|	48.05	5E-12
contig00085-orf00004	TspB3 [Neisseria gonorrhoeae FA 1090]	gi|59801624|ref|YP 208336.1|	38.46	0.0000001
contig00086-orf00001	transposase [Neisseria meningitidis Z2491]	gi|15794129|ref|NP 283951.1|	92.96	2E-138
contig00088-orf00001	serine acetyltransferase [Neisseria meningitidis Z2491]	gi|15793718|ref|NP 283540.1|	90.07	3E-136
contig00088-orf00003	putative heat shock protein [Neisseria gonorrhoeae FA 1090]	gi|59801766|ref|YP 208478.1|	86.08	7E-72
contig00088-orf00007	molecular chaperone DnaK [Neisseria meningitidis Z2491]	gi|15793712|ref|NP 283534.1|	97.68	0
contig00088-orf00008	putative flippase [Bacteroides thetaiotaomicron VPI-5482]	gi|29346764|ref|NP 810267.1|	28.79	6
contig00088-orf00013	hypothetical protein PM1435 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603300|ref|NP 246374.1|	74.2	2E-174
contig00088-orf00016	acetolactate synthase isozyme III large subunit [Neisseria meningitidis MC58]	gi|15677427|ref|NP 274583.1|	92.35	0
contig00088-orf00018	acetolactate synthase 3 regulatory subunit [Neisseria meningitidis Z2491]	gi|15794658|ref|NP 284480.1|	98.71	2E-78
contig00088-orf00021	hypothetical protein NMA1764 [Neisseria meningitidis Z2491]	gi|15794657|ref|NP 284479.1|	82.29	5E-39
contig00088-orf00023	ketol-acid reductoisomerase [Chromobacterium violaceum ATCC 12472]	gi|34496043|ref|NP 900258.1|	86.69	4E-167
contig00088-orf00025	hypothetical protein FTH 1064 [Francisella tularensis subsp. holarctica OSU18]	gi|115314860|ref|YP 763583.1|	74.55	6E-26
contig00088-orf00027	putative transmembrane two-component sensor histidine kinase/response regulator hybrid [Rhizobium leguminosarum bv. viciae 3841]	gi|116250178|ref|YP 766016.1|	27.03	5.9
contig00088-orf00028	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793086|ref|NP 282908.1|	78.21	2E-123
contig00088-orf00029	hypothetical protein bll5851 [Bradyrhizobium japonicum USDA 110]	gi|27380962|ref|NP 772491.1|	34.15	7E-34

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contig00088-orf00033	PrlC [Neisseria gonorrhoeae FA 1090]	gi|59802089|ref|YP 208801.1|	94.54	0
contig00089-orf00001	amino acid permease substrate-binding protein [Neisseria meningitidis Z2491]	gi|15793954|ref|NP 283776.1|	91.61	7E-131
contig00089-orf00003	amino acid permease integral membrane protein [Neisseria meningitidis Z2491]	gi|15793955|ref|NP 283777.1|	94.54	1E-122
contig00089-orf00004	amino acid permease ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793956|ref|NP 283778.1|	95.14	3E-130
contig00089-orf00006	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677098|ref|NP 274250.1|	96.08	0
contig00089-orf00007	hypothetical protein NGO0782 [Neisseria gonorrhoeae FA 1090]	gi|59801196|ref|YP 207908.1|	64.58	3E-12
contig00089-orf00009	hypothetical protein NMB1225 [Neisseria meningitidis MC58]	gi|15677097|ref|NP 274249.1|	53.98	4E-37
contig00089-orf00010	putative GTP cyclohydrolase [Neisseria gonorrhoeae FA 1090]	gi|59800831|ref|YP 207543.1|	87.55	2E-127
contig00089-orf00014	cystathionine gamma-synthase [Neisseria meningitidis MC58]	gi|15676700|ref|NP 273844.1|	93.25	0
contig00089-orf00015	hypothetical protein DR 1940 [Deinococcus radiodurans R1]	gi|15806938|ref|NP 295663.1|	35.21	0.004
contig00089-orf00017	ferredoxin NADP+ reductase [Neisseria meningitidis Z2491]	gi|15794558|ref|NP 284380.1|	77.22	3E-114
contig00089-orf00019	GTP-binding protein [Neisseria meningitidis MC58]	gi|15678003|ref|NP 274075.1|	69.59	2E-123
contig00089-orf00026	cation transporter E1-E2 family ATPase [Neisseria meningitidis MC58]	gi|15676928|ref|NP 274076.1|	75.34	0
contig00089-orf00028	IS1106 transposase [Neisseria meningitidis Z2491]	gi|15793244|ref|NP 283066.1|	91.49	9E-17
contig00089-orf00029	putative IS1106 transposase [Neisseria meningitidis MC58]	gi|15676814|ref|NP 273959.1|	96.88	4E-09
contig00092-orf00001	hypothetical protein PM0591 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602456|ref|NP 245528.1|	43.1	4E-45
contig00092-orf00003	pyridine nucleotide transhydrogenase [Neisseria meningitidis MC58]	gi|15676870|ref|NP 274015.1|	93.06	0
contig00092-orf00005	amino acid transporter LysE [Colwellia psychrerythraea 34H]	gi|71282556|ref|YP 269839.1|	51.53	4E-45
contig00092-orf00007	GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961]	gi|15601603|ref|NP 233234.1|	43.59	1.5
contig00092-orf00010	NAD(P) transhydrogenase subunit alpha [Neisseria meningitidis Z2491]	gi|15794122|ref|NP 283944.1|	97.27	0
contig00092-orf00011	lactoylglutathione lyase [Neisseria meningitidis Z2491]	gi|15795018|ref|NP 284840.1|	88.89	2E-66
contig00092-orf00013	hypothetical protein NMA2030 [Neisseria meningitidis Z2491]	gi|15794910|ref|NP 284732.1|	74.6	2E-159
contig00092-orf00016	fumarate hydratase [Neisseria meningitidis Z2491]	gi|15794564|ref|NP 284386.1|	98.05	0
contig00092-orf00018	hypothetical protein NMB0711 [Neisseria meningitidis MC58]	gi|15676609|ref|NP 273753.1|	76.55	2E-124
contig00092-orf00019	ribonuclease PH [Neisseria meningitidis Z2491]	gi|15794595|ref|NP 284417.1|	90.79	1E-112
contig00092-orf00020	molybdenum transport protein ModG, putative [Methylococcus capsulatus str. Bath]	gi|53804320|ref|YP 113839.1|	52.11	5E-26
contig00092-orf00022	aspartate kinase [Neisseria gonorrhoeae FA 1090]	gi|59801345|ref|YP 208057.1|	96.54	0
contig00092-orf00028	hypothetical protein NMA1928 [Neisseria meningitidis Z2491]	gi|15794811|ref|NP 284633.1|	75.62	5E-169
contig00092-orf00030	hypothetical protein NMA1929 [Neisseria meningitidis Z2491]	gi|15794812|ref|NP 284634.1|	91.33	0
contig00092-orf00032	hypothetical protein NGO1321 [Neisseria gonorrhoeae FA 1090]	gi|59801672|ref|YP 208384.1|	66.47	1E-51
contig00092-orf00034	glutathione transferase [Xanthomonas campestris pv. vesicatoria str. 85-10]	gi|78046904|ref|YP 363079.1|	38.65	9E-33
contig00092-orf00035	two-component system sensor protein [Chromobacterium violaceum ATCC 12472]	gi|34495558|ref|NP 899773.1|	46.95	7E-43
contig00092-orf00036	argininosuccinate lyase [Neisseria meningitidis MC58]	gi|15676537|ref|NP 273680.1|	92.97	0
contig00092-orf00037	putative cytidylate kinase [Neisseria gonorrhoeae FA 1090]	gi|59801033|ref|YP 207745.1|	78.37	5E-79
contig00092-orf00039	LysR family transcriptional regulator [Burkholderia xenovorans LB400]	gi|91780930|ref|YP 556137.1|	39.47	3.4

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00092-orf00041	30S ribosomal protein S1 [Neisseria meningitidis MC58]	gi|15677167|ref|NP 274320.1|	97.33	0
contig00092-orf00042	integration host factor beta-subunit [Neisseria meningitidis Z2491]	gi|15794410|ref|NP 284232.1|	95.92	1E-47
contig00092-orf00046	nucleotide-binding protein [Neisseria meningitidis Z2491]	gi|15794414|ref|NP 284236.1|	90.69	0
contig00092-orf00048	nucleoside diphosphate kinase [Neisseria meningitidis Z2491]	gi|15794415|ref|NP 284237.1|	85.82	7E-65
contig00092-orf00049	hypothetical protein NMB1308 [Neisseria meningitidis MC58]	gi|15677174|ref|NP 274327.1|	93.11	0
contig00092-orf00050	putative fimbrial biogenesis and twitching motility protein [Neisseria meningitidis MC58]	gi|15677175|ref|NP 274328.1|	76.54	4E-108
contig00092-orf00051	XRE family transcriptional regulator [Burkholderia cenocepacia HI2424]	gi|116689834|ref|YP 835457.1|	40.3	2E-10
contig00092-orf00053	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Neisseria meningitidis Z2491]	gi|15794418|ref|NP 284240.1|	92.38	0
contig00092-orf00056	hypothetical protein NGO1277 [Neisseria gonorrhoeae FA 1090]	gi|59801634|ref|YP 208346.1|	82.87	1E-118
contig00092-orf00060	AniA [Neisseria gonorrhoeae FA 1090]	gi|59801633|ref|YP 208345.1|	89.16	4E-180
contig00092-orf00062	nitric oxide reductase [Neisseria meningitidis Z2491]	gi|15794774|ref|NP 284596.1|	94.22	0
contig00092-orf00064	hypothetical protein PBPRB0577 [Photobacterium profundum SS9]	gi|54302257|ref|YP 132250.1|	32.46	1E-23
contig00092-orf00067	haemoglobin-haptoglobin-utilization protein [Neisseria meningitidis Z2491]	gi|15793475|ref|NP 283297.1|	85.31	6E-147
contig00092-orf00068	haemoglobin-haptoglobin-utilization protein [Neisseria meningitidis Z2491]	gi|15793475|ref|NP 283297.1|	74.09	0
contig00092-orf00070	haemoglobin-haptoglobin-utilization protein [Neisseria meningitidis Z2491]	gi|15793476|ref|NP 283298.1|	47.49	4E-83
contig00092-orf00071	hypothetical protein NMB1971 [Neisseria meningitidis MC58]	gi|15677801|ref|NP 274965.1|	59.26	0.13
contig00092-orf00072	hypothetical protein NGO2111 [Neisseria gonorrhoeae FA 1090]	gi|59802411|ref|YP 209123.1|	60.41	2E-127
contig00092-orf00073	transcription elongation factor GreB [Neisseria gonorrhoeae FA 1090]	gi|59800713|ref|YP 207425.1|	98.16	2E-79
contig00092-orf00074	30S ribosomal protein S15 [Neisseria meningitidis Z2491]	gi|15793788|ref|NP 283610.1|	97.75	1E-36
contig00092-orf00075	#N/A	#N/A	#N/A	#N/A
contig00092-orf00076	disulfide bond formation protein B [Neisseria meningitidis MC58]	gi|15677498|ref|NP 274654.1|	65.82	7E-52
contig00092-orf00077	putative amino acid symporter [Neisseria meningitidis MC58]	gi|15677496|ref|NP 274652.1|	93.63	0
contig00092-orf00078	hypothetical protein SAV 1872 [Streptomyces avermitilis MA-4680]	gi|29828414|ref|NP 823048.1|	46.67	7.8
contig00094-orf00001	filamentation induced by cAMP protein Fic [Rhodoferax ferrireducens T118]	gi|89902795|ref|YP 525266.1|	74.6	5E-17
contig00094-orf00003	filamentation induced by cAMP protein Fic [Rhodoferax ferrireducens T118]	gi|89902795|ref|YP 525266.1|	62.64	2E-89
contig00094-orf00004	hypothetical protein SO 2079 [Shewanella oneidensis MR-1]	gi|24373639|ref|NP 717682.1|	24.49	0.021
contig00094-orf00007	hypothetical protein NMB1815 [Neisseria meningitidis MC58]	gi|15677651|ref|NP 274812.1|	86.04	7E-126
contig00094-orf00009	hypothetical protein NMA0740 [Neisseria meningitidis Z2491]	gi|15793716|ref|NP 283538.1|	44.12	5E-09
contig00094-orf00010	iron-sulfur cluster insertion protein ErpA [Neisseria meningitidis Z2491]	gi|15793715|ref|NP 283537.1|	97.85	2E-48
contig00094-orf00011	putative transcriptional regulator, repressor [Neisseria gonorrhoeae FA 1090]	gi|59801770|ref|YP 208482.1|	82.61	2E-109
contig00094-orf00012	hypothetical protein NMA0737 [Neisseria meningitidis Z2491]	gi|15793713|ref|NP 283535.1|	44.44	6E-13
contig00094-orf00013	DNA topoisomerase IV subunit A [Neisseria meningitidis Z2491]	gi|15794693|ref|NP 284515.1|	92.28	0
contig00094-orf00016	two component sensor kinase [Neisseria meningitidis Z2491]	gi|15794694|ref|NP 284516.1|	48.88	2E-128
contig00094-orf00017	helix-turn-helix, Fis-type [Dechloromonas aromatica RCB]	gi|71906301|ref|YP 283888.1|	46.48	2E-110
contig00094-orf00018	hypothetical protein Pcryo 1979 [Psychrobacter cryohalolentis K5]	gi|93006803|ref|YP 581240.1|	57.5	0.000001

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contig00094-orf00020	dTDP-D-glucose 4,6-dehydratase [Neisseria meningitidis MC58]	gi|15676012|ref|NP 273142.1|	93.24	0
contig00094-orf00021	glucose-1-phosphate thymidylyltransferase [Neisseria meningitidis MC58]	gi|15676013|ref|NP 273143.1|	90.28	4E-150
contig00095-orf00001	hypothetical protein Suden 1624 [Sulfurimonas denitrificans DSM 1251]	gi|78777821|ref|YP 394136.1|	31.25	0.01
contig00095-orf00003	hypothetical protein RL3477 [Rhizobium leguminosarum bv. viciae 3841]	gi|116253219|ref|YP 769057.1|	37.7	3E-10
contig00095-orf00004	hypothetical protein RL3478 [Rhizobium leguminosarum bv. viciae 3841]	gi|116253220|ref|YP 769058.1|	45.95	3E-11
contig00095-orf00007	putative dipeptide binding periplasmic protein [Sinorhizobium meliloti 1021]	gi|15966166|ref|NP 386519.1|	44	2
contig00095-orf00009	hypothetical protein Ava B0327 [Anabaena variabilis ATCC 29413]	gi|75812607|ref|YP 320226.1|	33.33	0.0001
contig00095-orf00011	oxidoreductase [Xanthomonas campestris pv. campestris str. ATCC 33913]	gi|21230250|ref|NP 636167.1|	38.24	2.7
contig00095-orf00013	recombinational DNA repair protein [Magnetospirillum magneticum AMB-1]	gi|83311360|ref|YP 421624.1|	32.73	0.54
contig00096-orf00001	hypothetical protein H16 B1328 [Ralstonia eutropha H16]	gi|116695272|ref|YP 840848.1|	35	0.0000003
contig00096-orf00002	cyclic nucleotide-binding protein [Brucella suis 1330]	gi|23502853|ref|NP 698980.1|	30.19	1.6
contig00096-orf00003	hypothetical protein NMB1543 [Neisseria meningitidis MC58]	gi|15677395|ref|NP 274550.1|	36.66	2E-61
contig00096-orf00006	hypothetical protein NMA2000 [Neisseria meningitidis Z2491]	gi|15794880|ref|NP 284702.1|	34.88	0.048
contig00096-orf00007	#N/A	#N/A	#N/A	#N/A
contig00096-orf00008	hypothetical protein NMA1796 [Neisseria meningitidis Z2491]	gi|15794687|ref|NP 284509.1|	44.74	1E-13
contig00096-orf00010	RNA polymerase sigma factor [Candidatus Protochlamydia amoebophila	gi|46445811|ref|YP 007176.1|	44.9	0.004
contig00096-orf00013	hypothetical protein Neut 0102 [Nitrosomonas eutropha C91]	gi|114330133|ref|YP 746355.1|	30.91	2.3
contig00097-orf00001	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794704|ref|NP 284526.1|	90.7	1E-17
contig00099-orf00001	#N/A	#N/A	#N/A	#N/A
contig00099-orf00002	putative lipoprotein [Enterococcus faecalis V583]	gi|29377947|ref|NP 817073.1|	34.26	2E-14
contig00099-orf00003	low molecular weight protein tyrosine-phosphatase [Neisseria meningitidis MC58]	gi|15677135|ref|NP 274288.1|	68.21	7E-56
contig00099-orf00005	hypothetical protein NMB1269 [Neisseria meningitidis MC58]	gi|15677137|ref|NP 274290.1|	69.81	3E-150
contig00099-orf00007	GTP cyclohydrolase II [Neisseria meningitidis MC58]	gi|15677125|ref|NP 274277.1|	83.59	3E-92
contig00099-orf00008	hypothetical protein NMA1424 [Neisseria meningitidis Z2491]	gi|15794335|ref|NP 284157.1|	59.09	1E-59
contig00099-orf00009	prophage CP4-like integrase [Chromobacterium violaceum ATCC 12472]	gi|34496106|ref|NP 900321.1|	47.18	4E-97
contig00099-orf00010	hypothetical protein c2416 [Escherichia coli CFT073]	gi|26248268|ref|NP 754308.1|	23.23	0.28
contig00099-orf00011	prophage CP4-57 regulatory protein [Haemophilus somnus 129PT]	gi|113461478|ref|YP 719547.1|	41.94	7E-09
contig00099-orf00013	methylthioribose-1-phosphate isomerase [Dechloromonas aromatica RCB]	gi|71908947|ref|YP 286534.1|	48.28	1.2
contig00099-orf00014	ABC transporter substrate binding protein [Xanthomonas oryzae pv. oryzae MAFF 311018]	gi|84621727|ref|YP 449099.1|	33.78	0.91
contig00099-orf00015	hypothetical protein PM1777 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603642|ref|NP 246716.1|	47.41	3E-19
contig00099-orf00016	hypothetical protein SAV 4435 [Streptomyces avermitilis MA-4680]	gi|29830978|ref|NP 825612.1|	42.86	2
contig00099-orf00017	PTS system, IID component [Enterococcus faecalis V583]	gi|29376372|ref|NP 815526.1|	38.89	3.5
contig00099-orf00019	hypothetical protein Daro 2694 [Dechloromonas aromatica RCB]	gi|71908307|ref|YP 285894.1|	33.33	5E-35
contig00099-orf00023	putative prophage primase [Pectobacterium atrosepticum SCRI1043]	gi|50121678|ref|YP 050845.1|	35.71	3E-69

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contig00099-orf00025	phosphoenolpyruvate-protein phosphotransferase [Shewanella denitrificans OS217]	gi|91794132|ref|YP 563783.1|	38.1	7.8
contig00099-orf00027	putative integrase prophage protein [Ralstonia solanacearum GMI1000]	gi|17546590|ref|NP 519992.1|	55.95	2E-16
contig00099-orf00028	TolC protein [Mannheimia succiniciproducens MBEL55E]	gi|52425186|ref|YP 088323.1|	44.67	2E-29
contig00099-orf00029	TolC protein [Mannheimia succiniciproducens MBEL55E]	gi|52425186|ref|YP 088323.1|	54.48	1E-61
contig00099-orf00030	putative mitomycin resistance protein [Shewanella sp. ANA-3]	gi|117918933|ref|YP 868125.1|	58.06	7E-27
contig00099-orf00033	hypothetical protein TDE0563 [Treponema denticola ATCC 35405]	gi|42526079|ref|NP 971177.1|	34.15	2E-11
contig00101-orf00002	UDP-N-acetylglucosamine pyrophosphorylase [Neisseria meningitidis MC58]	gi|15675978|ref|NP 273104.1|	93.82	0
contig00101-orf00004	hypothetical protein NGO2054 [Neisseria gonorrhoeae FA 1090]	gi|59802361|ref|YP 209073.1|	49.32	6E-15
contig00101-orf00007	hydrolase [Neisseria meningitidis Z2491]	gi|15793303|ref|NP 283125.1|	80.48	1E-93
contig00101-orf00008	putative ABC transporter, thiamine-binding periplasmic protein [Neisseria gonorrhoeae FA 1090]	gi|59802363|ref|YP 209075.1|	82.8	8E-152
contig00101-orf00009	#N/A	#N/A	#N/A	#N/A
contig00101-orf00010	5'-3' exonuclease [Streptomyces avermitilis MA-4680]	gi|29833256|ref|NP 827890.1|	46.15	4.6
contig00101-orf00012	mafA protein [Neisseria meningitidis MC58]	gi|15676551|ref|NP 273694.1|	89.04	3E-121
contig00101-orf00014	MafB-related protein [Neisseria meningitidis MC58]	gi|15676552|ref|NP 273695.1|	61.81	6E-146
contig00101-orf00016	hypothetical protein NMB0655 [Neisseria meningitidis MC58]	gi|15676554|ref|NP 273697.1|	87.18	1E-119
contig00102-orf00003	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	33.76	1E-50
contig00104-orf00001	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	95.65	2E-32
contig00106-orf00001	hypothetical protein NMA0532 [Neisseria meningitidis Z2491]	gi|15793527|ref|NP 283349.1|	82.82	2E-80
contig00106-orf00002	methylation [Polaromonas sp. JS666]	gi|91790503|ref|YP 551455.1|	32.39	5E-09
contig00106-orf00005	tyrosyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793610|ref|NP 283432.1|	95.59	0
contig00106-orf00006	cobalamin biosynthesis protein N [Methanothermobacter thermautotrophicus str. Delta H]	gi|15678542|ref|NP 275657.1|	30.19	4.5
contig00106-orf00007	translation-associated GTPase [Neisseria meningitidis Z2491]	gi|15793608|ref|NP 283430.1|	98.9	0
contig00106-orf00008	glutamate racemase [Neisseria meningitidis Z2491]	gi|15794906|ref|NP 284728.1|	89.43	2E-122
contig00106-orf00011	hypothetical protein NTHI0694 [Haemophilus influenzae 86-028NP]	gi|68249162|ref|YP 248274.1|	52.05	4E-40
contig00106-orf00012	hypothetical protein NTHI0694 [Haemophilus influenzae 86-028NP]	gi|68249162|ref|YP 248274.1|	71.82	4E-40
contig00106-orf00014	putative inner membrane protein translocase component YidC [Neisseria meningitidis Z2491]	gi|15793542|ref|NP 283364.1|	89.07	0
contig00106-orf00016	hypothetical protein NMA0549 [Neisseria meningitidis Z2491]	gi|15793543|ref|NP 283365.1|	90.41	3E-34
contig00106-orf00017	50S ribosomal protein L34 [Neisseria meningitidis Z2491]	gi|15793545|ref|NP 283367.1|	100	0.000002
contig00106-orf00018	ribonuclease P [Neisseria meningitidis Z2491]	gi|15793544|ref|NP 283366.1|	79.82	1E-44
contig00106-orf00021	hypothetical protein Bxe B2089 [Burkholderia xenovorans LB400]	gi|91778040|ref|YP 553248.1|	28.28	0.14
contig00106-orf00022	putative chromosomal replication protein (DnaA) [Neisseria gonorrhoeae FA 1090]	gi|59800474|ref|YP 207186.1|	86.37	0
contig00106-orf00023	DNA polymerase III subunit beta [Neisseria meningitidis MC58]	gi|15677733|ref|NP 274896.1|	89.65	4E-179

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contig00106-orf00025	hypothetical protein NMA1049 [Neisseria meningitidis Z2491]	gi|15794000|ref|NP 283822.1|	90.12	1E-79
contig00106-orf00028	pmbA protein [Neisseria meningitidis MC58]	gi|15676735|ref|NP 273880.1|	87.33	0
contig00106-orf00030	RfaG protein [Mannheimia succiniciproducens MBEL55E]	gi|52425551|ref|YP 088688.1|	44.96	1E-89
contig00106-orf00032	tRNA-dihydrouridine synthase A [Neisseria meningitidis MC58]	gi|15676263|ref|NP 273397.1|	96.66	0
contig00106-orf00034	protein tyrosine/serine phosphatase [Burkholderia sp. 383]	gi|78061402|ref|YP 371310.1|	36.79	3E-27
contig00107-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	91.77	7E-81
contig00107-orf00002	hypothetical protein MS0981 [Mannheimia succiniciproducens MBEL55E]	gi|52425036|ref|YP 088173.1|	90.84	2E-63
contig00107-orf00004	hypothetical protein MS0980 [Mannheimia succiniciproducens MBEL55E]	gi|52425035|ref|YP 088172.1|	67.01	3E-35
contig00107-orf00007	hypothetical protein NMA1258 [Neisseria meningitidis Z2491]	gi|15794191|ref|NP 284013.1|	88.57	6E-18
contig00107-orf00008	siroheme synthase [Neisseria meningitidis MC58]	gi|15677068|ref|NP 274220.1|	57.3	1E-127
contig00107-orf00009	#N/A	#N/A	#N/A	#N/A
contig00107-orf00010	sulfate adenylyltransferase subunit 2 [Mannheimia succiniciproducens MBEL55E]	gi|52425307|ref|YP 088444.1|	81.79	6E-114
contig00107-orf00012	Cah [Neisseria gonorrhoeae FA 1090]	gi|59801007|ref|YP 207719.1|	87.76	8E-126
contig00107-orf00013	chaperone protein HchA [Pseudomonas aeruginosa UCBPP-PA14]	gi|116049067|ref|YP 792131.1|	65.85	2E-107
contig00107-orf00014	urease accessory protein UreF [Mesorhizobium loti MAFF303099]	gi|13474124|ref|NP 105692.1|	41.38	7.7
contig00107-orf00015	AraC family transcriptional regulator [Pseudomonas entomophila L48]	gi|104781853|ref|YP 608351.1|	41.88	3E-39
contig00107-orf00018	phosphoadenosine phosphosulfate reductase [Mannheimia succiniciproducens MBEL55E]	gi|52425308|ref|YP 088445.1|	58.68	3E-80
contig00107-orf00019	impB/mucB/samB family protein [Neisseria meningitidis Z2491]	gi|15794555|ref|NP 284377.1|	94.02	0
contig00107-orf00021	hypothetical protein NMA1260 [Neisseria meningitidis Z2491]	gi|15794193|ref|NP 284015.1|	76.16	3E-122
contig00107-orf00023	exodeoxyribonuclease V, alpha subunit [Neisseria meningitidis MC58]	gi|15677105|ref|NP 274257.1|	64.44	6E-168
contig00108-orf00001	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677106|ref|NP 274258.1|	72	1E-80
contig00108-orf00002	LolC [Neisseria gonorrhoeae FA 1090]	gi|59801184|ref|YP 207896.1|	82.21	0
contig00108-orf00003	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794317|ref|NP 284139.1|	67.86	2E-26
contig00108-orf00004	recombination protein RecR [Neisseria meningitidis MC58]	gi|15677109|ref|NP 274261.1|	74.75	2E-80
contig00108-orf00005	peptidyl-prolyl cis-trans isomerase-related protein [Neisseria meningitidis MC58]	gi|15677110|ref|NP 274262.1|	62.4	0
contig00108-orf00006	hypothetical protein NMB1239 [Neisseria meningitidis MC58]	gi|15677111|ref|NP 274263.1|	60.34	1E-31
contig00108-orf00007	hypothetical protein NMA1464 [Neisseria meningitidis Z2491]	gi|15794366|ref|NP 284188.1|	61.4	1E-65
contig00108-orf00009	ATP-dependent DNA helicase [Neisseria meningitidis Z2491]	gi|15794554|ref|NP 284376.1|	92.05	0
contig00108-orf00010	hypothetical protein lpl0179 [Legionella pneumophila str. Lens]	gi|54293140|ref|YP 125555.1|	46.81	0.11
contig00108-orf00012	hypothetical protein NGO0932 [Neisseria gonorrhoeae FA 1090]	gi|59801328|ref|YP 208040.1|	85.07	1E-26
contig00108-orf00013	hypothetical protein NGO0932 [Neisseria gonorrhoeae FA 1090]	gi|59801328|ref|YP 208040.1|	78.05	6E-10
contig00108-orf00014	homoserine O-acetyltransferase [Neisseria meningitidis MC58]	gi|15676833|ref|NP 273978.1|	97.35	0
contig00108-orf00016	hypothetical protein NMA1135 [Neisseria meningitidis Z2491]	gi|15794081|ref|NP 283903.1|	93.26	3E-102
contig00108-orf00017	hypothetical protein CJE0661 [Campylobacter jejuni RM1221]	gi|57238243|ref|YP 178676.1|	38.46	4.6
contig00108-orf00019	aminotransferase AlaT [Neisseria meningitidis MC58]	gi|15677327|ref|NP 274482.1|	94.55	0

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contig00108-orf00020	hypothetical protein NMB1100 [Neisseria meningitidis MC58]	gi|15676980|ref|NP 274131.1|	58.33	0.049
contig00108-orf00021	ubiquinone/menaquinone biosynthesis methyltransferase [Neisseria meningitidis MC58]	gi|15676641|ref|NP 273785.1|	94.29	9E-132
contig00108-orf00024	hypothetical protein NGO0320 [Neisseria gonorrhoeae FA 1090]	gi|59800767|ref|YP 207479.1|	68.33	4E-42
contig00108-orf00025	#N/A	#N/A	#N/A	#N/A
contig00108-orf00027	hypothetical protein NGO0683 [Neisseria gonorrhoeae FA 1090]	gi|59801110|ref|YP 207822.1|	51.17	9E-127
contig00108-orf00028	anaerobic C4-dicarboxylate transporter [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603299|ref|NP 246373.1|	76.59	9E-155
contig00108-orf00029	hypothetical protein NMA1654 [Neisseria meningitidis Z2491]	gi|15794548|ref|NP 284370.1|	81.97	1E-23
contig00108-orf00030	putative O-methyltransferase [Neisseria meningitidis MC58]	gi|15677299|ref|NP 274453.1|	77.48	2E-94
contig00108-orf00032	hypothetical protein NGO0747 [Neisseria gonorrhoeae FA 1090]	gi|59801164|ref|YP 207876.1|	54.46	3E-54
contig00108-orf00033	putative phosphoribosylaminoimidazole carboxylase catalytic subunit [Neisseria gonorrhoeae FA 1090]	gi|59801165|ref|YP 207877.1|	92.5	4E-54
contig00108-orf00035	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15794184|ref|NP 284006.1|	96.07	0
contig00108-orf00036	inositol-5-monophosphate dehydrogenase [Neisseria meningitidis MC58]	gi|15677074|ref|NP 274226.1|	98.56	0
contig00108-orf00039	phosphopyruvate hydratase [Neisseria gonorrhoeae FA 1090]	gi|59801045|ref|YP 207757.1|	97.2	0
contig00108-orf00040	hypothetical protein NMA1496 [Neisseria meningitidis Z2491]	gi|15794396|ref|NP 284218.1|	77.17	1E-28
contig00108-orf00044	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	72.73	7E-15
contig00108-orf00045	hypothetical protein UTI89 C0509 [Escherichia coli UTI89]	gi|91209555|ref|YP 539541.1|	28.37	3E-10
contig00108-orf00047	putative ATP-dependent RNA helicase [Neisseria meningitidis MC58]	gi|15677233|ref|NP 274386.1|	96.84	0
contig00108-orf00049	hypothetical protein NMA1579 [Neisseria meningitidis Z2491]	gi|15794472|ref|NP 284294.1|	92.99	4E-161
contig00108-orf00051	membrane protein [Neisseria meningitidis Z2491]	gi|15794077|ref|NP 283899.1|	89.13	4E-43
contig00108-orf00053	hypothetical protein NMA1132 [Neisseria meningitidis Z2491]	gi|15794078|ref|NP 283900.1|	90.86	0
contig00108-orf00054	elongation factor P [Neisseria meningitidis MC58]	gi|15676830|ref|NP 273975.1|	100	6E-102
contig00108-orf00058	DNA gyrase subunit A [Neisseria gonorrhoeae FA 1090]	gi|59801057|ref|YP 207769.1|	92.69	0
contig00108-orf00059	O-acetylhomoserine/O-acetylserine sulfhydrylase [Shewanella sp. MR-7]	gi|114046472|ref|YP 737022.1|	70.77	1E-155
contig00108-orf00061	exodeoxyribonuclease V 135 KD polypeptide [Neisseria meningitidis MC58]	gi|15676683|ref|NP 273827.1|	62.9	0
contig00108-orf00065	recombination associated protein [Neisseria meningitidis MC58]	gi|15676747|ref|NP 273892.1|	96.32	5E-154
contig00108-orf00067	hypothetical protein NMB0850 [Neisseria meningitidis MC58]	gi|15676746|ref|NP 273891.1|	86.96	1E-67
contig00108-orf00069	deoxycytidine triphosphate deaminase [Neisseria gonorrhoeae FA 1090]	gi|59800864|ref|YP 207576.1|	98.93	3E-107
contig00108-orf00075	competence protein [Neisseria meningitidis Z2491]	gi|15793872|ref|NP 283694.1|	73.45	0
contig00108-orf00079	glutamate--cysteine ligase [Neisseria meningitidis Z2491]	gi|15794354|ref|NP 284176.1|	94.86	0
contig00108-orf00081	isopropylmalate isomerase large subunit [Neisseria meningitidis Z2491]	gi|15794355|ref|NP 284177.1|	96.14	0
contig00108-orf00083	entericidin EcnAB [Psychrobacter cryohalolentis K5]	gi|93005997|ref|YP 580434.1|	51.22	0.00003
contig00108-orf00084	isopropylmalate isomerase small subunit [Neisseria meningitidis Z2491]	gi|15794357|ref|NP 284179.1|	96.71	3E-119
contig00108-orf00086	hypothetical protein DP2396 [Desulfotalea psychrophila LSv54]	gi|51246248|ref|YP 066132.1|	36	2E-21
contig00108-orf00090	3-isopropylmalate dehydrogenase [Neisseria meningitidis MC58]	gi|15676918|ref|NP 274065.1|	98.03	0

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contig00108-orf00093	hypothetical protein Bcep18194 B0817 [Burkholderia sp. 383]	gi|78061667|ref|YP 371575.1|	47.46	4E-28
contig00108-orf00095	putative transmembrane protein [Ralstonia metallidurans CH34]	gi|94312390|ref|YP 585600.1|	58.88	5E-93
contig00108-orf00100	hypothetical protein RS05340 [Ralstonia solanacearum GMI1000]	gi|17549514|ref|NP 522854.1|	37.89	3E-87
contig00108-orf00102	S-adenosylmethionine decarboxylase related [Burkholderia cenocepacia HI2424]	gi|116692983|ref|YP 838516.1|	47.32	8E-21
contig00108-orf00104	hypothetical protein RS04763 [Ralstonia solanacearum GMI1000]	gi|17549557|ref|NP 522897.1|	43.85	1E-108
contig00108-orf00107	DNA polymerase III chi subunit [Neisseria meningitidis MC58]	gi|15677419|ref|NP 274575.1|	69.18	5E-53
contig00108-orf00109	putative peptidyl-prolylisomerase [Neisseria gonorrhoeae FA 1090]	gi|59801584|ref|YP 208296.1|	82.38	3E-98
contig00108-orf00111	#N/A	#N/A	#N/A	#N/A
contig00108-orf00114	putative phosphoribosylglycinamidetransformylase [Neisseria gonorrhoeae FA 1090]	gi|59801583|ref|YP 208295.1|	84.54	3E-94
contig00108-orf00115	hypothetical protein NGO1223 [Neisseria gonorrhoeae FA 1090]	gi|59801582|ref|YP 208294.1|	66.3	5E-64
contig00108-orf00117	hypothetical protein NGO0969 [Neisseria gonorrhoeae FA 1090]	gi|59801355|ref|YP 208067.1|	55.32	4E-58
contig00108-orf00118	ribose-5-phosphate isomerase A [Neisseria meningitidis Z2491]	gi|15794604|ref|NP 284426.1|	87.39	6E-106
contig00108-orf00121	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Neisseria gonorrhoeae FA 1090]	gi|59801357|ref|YP 208069.1|	90.32	3E-69
contig00108-orf00122	dihydroxy-acid dehydratase [Neisseria meningitidis Z2491]	gi|15794282|ref|NP 284104.1|	97.19	0
contig00108-orf00124	iron-sulphur protein [Neisseria meningitidis Z2491]	gi|15794544|ref|NP 284366.1|	97.52	0
contig00108-orf00126	hypothetical protein NMB1437 [Neisseria meningitidis MC58]	gi|15677295|ref|NP 274449.1|	96.57	7E-129
contig00108-orf00128	hypothetical protein NGO0904 [Neisseria gonorrhoeae FA 1090]	gi|59801302|ref|YP 208014.1|	95.35	5E-163
contig00108-orf00129	integral membrane protein [Neisseria meningitidis Z2491]	gi|15794541|ref|NP 284363.1|	74.61	1E-162
contig00109-orf00002	putative integrase [Shigella flexneri 5 str. 8401]	gi|110804320|ref|YP 687840.1|	42.9	2E-71
contig00113-orf00001	hypothetical protein NMB1870 [Neisseria meningitidis MC58]	gi|15677705|ref|NP 274866.1|	28.57	0.00009
contig00113-orf00002	hypothetical protein NMB1466 [Neisseria meningitidis MC58]	gi|15677320|ref|NP 274475.1|	70.25	2E-102
contig00113-orf00004	#N/A	#N/A	#N/A	#N/A
contig00113-orf00006	membrane protein [Neisseria meningitidis MC58]	gi|15676492|ref|NP 273631.1|	83.45	1E-120
contig00113-orf00008	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676493|ref|NP 273632.1|	75.31	2E-98
contig00113-orf00011	major outer membrane protein porin P.IB [Neisseria gonorrhoeae FA 1090]	gi|59802130|ref|YP 208842.1|	27.88	7E-25
contig00113-orf00012	oligopeptide ABC transporter periplasmic component [Sodalis glossinidius str. 'morsitans']	gi|85059351|ref|YP 455053.1|	46.14	2E-125
contig00113-orf00015	aminopeptidase [Neisseria meningitidis Z2491]	gi|15794534|ref|NP 284356.1|	94.48	0
contig00113-orf00017	hypothetical protein MHJ 0430 [Mycoplasma hyopneumoniae J]	gi|71893781|ref|YP 279227.1|	30.09	0.004
contig00113-orf00019	oligopeptide transporter permease [Yersinia pseudotuberculosis IP 32953]	gi|51596432|ref|YP 070623.1|	69.93	2E-126
contig00113-orf00022	oligopeptide transport system permease protein OppC [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37526383|ref|NP 929727.1|	68.54	4E-115
contig00113-orf00024	ABC-type transport system, ATPase component [Vibrio vulnificus YJ016]	gi|37676918|ref|NP 937314.1|	59.43	4E-178
contig00113-orf00026	hypothetical protein BH1415 [Bacillus halodurans C-125]	gi|15613978|ref|NP 242281.1|	45.71	7.9
contig00113-orf00027	hypothetical protein PM0613 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602478|ref|NP 245550.1|	33.9	4E-11

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contig00113-orf00028	hypothetical protein ECA0639 [Pectobacterium atrosepticum SCRI1043]	gi|50119588|ref|YP 048755.1|	29.11	0.017
contig00113-orf00029	succinyl-CoA synthetase subunit alpha [Neisseria meningitidis MC58]	gi|15676853|ref|NP 273998.1|	99.32	7E-135
contig00113-orf00032	succinyl-CoA synthetase subunit beta [Neisseria meningitidis Z2491]	gi|15794099|ref|NP 283921.1|	98.97	0
contig00113-orf00034	hypothetical protein NGO0914 [Neisseria gonorrhoeae FA 1090]	gi|59801310|ref|YP 208022.1|	95.79	2E-48
contig00113-orf00036	dihydrolipoamide dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801311|ref|YP 208023.1|	97.9	0
contig00113-orf00042	putative lipoprotein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]	gi|46578660|ref|YP 009468.1|	32.47	3.5
contig00113-orf00044	dihydrolipoamide acetyltransferase [Neisseria meningitidis MC58]	gi|15676849|ref|NP 273994.1|	89.59	1E-152
contig00113-orf00049	alpha-ketoglutarate decarboxylase [Neisseria meningitidis Z2491]	gi|15794095|ref|NP 283917.1|	92.78	0
contig00113-orf00050	type II citrate synthase [Neisseria gonorrhoeae FA 1090]	gi|59801314|ref|YP 208026.1|	95.55	0
contig00113-orf00051	hypothetical protein NMA1147 [Neisseria meningitidis Z2491]	gi|15794093|ref|NP 283915.1|	96.34	3E-37
contig00113-orf00052	succinate dehydrogenase iron-sulfur subunit [Neisseria meningitidis Z2491]	gi|15794092|ref|NP 283914.1|	99.15	4E-138
contig00113-orf00053	succinate dehydrogenase flavoprotein subunit [Neisseria meningitidis Z2491]	gi|15794091|ref|NP 283913.1|	98.98	0
contig00113-orf00054	succinate dehydrogenase hydrophobic membrane anchor protein [Neisseria meningitidis Z2491]	gi|15794090|ref|NP 283912.1|	95.58	4E-59
contig00113-orf00055	succinate dehydrogenase cytochrome B subunit [Neisseria meningitidis Z2491]	gi|15794089|ref|NP 283911.1|	88.24	7E-28
contig00113-orf00057	superoxide dismutase [Neisseria meningitidis Z2491]	gi|15794511|ref|NP 284333.1|	87.34	6E-82
contig00113-orf00058	hypothetical protein BC5231 [Bacillus cereus ATCC 14579]	gi|30023263|ref|NP 834894.1|	33.98	7E-17
contig00113-orf00060	hypothetical protein NMA1784 [Neisseria meningitidis Z2491]	gi|15794677|ref|NP 284499.1|	72.46	5E-62
contig00113-orf00062	putative cysteine synthase/cystathionine beta-synthase [Neisseria gonorrhoeae FA 1090]	gi|59800785|ref|YP 207497.1|	92.9	9E-144
contig00113-orf00064	hypothetical protein NGO0339 [Neisseria gonorrhoeae FA 1090]	gi|59800784|ref|YP 207496.1|	58	2E-56
contig00113-orf00066	diaminopimelate epimerase [Neisseria meningitidis MC58]	gi|15676658|ref|NP 273802.1|	72.79	8E-99
contig00113-orf00067	TetR family transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59800837|ref|YP 207549.1|	97.13	5E-105
contig00113-orf00068	UDP-N-acetylpyruvoylglucosamine reductase [Neisseria meningitidis MC58]	gi|15676709|ref|NP 273853.1|	92.49	0
contig00113-orf00070	hypothetical protein NTHI0422 [Haemophilus influenzae 86-028NP]	gi|68248911|ref|YP 248023.1|	73.16	4E-76
contig00113-orf00073	multidrug efflux protein [Neisseria meningitidis Z2491]	gi|15793978|ref|NP 283800.1|	98.04	0
contig00113-orf00075	putative nitrogen regulatory protein P-II [Neisseria gonorrhoeae FA 1090]	gi|59801542|ref|YP 208254.1|	90.18	5E-52
contig00113-orf00079	phosphoribosylformylglycinamidine synthase [Neisseria meningitidis MC58]	gi|15677824|ref|NP 274988.1|	89.27	0
contig00113-orf00081	hypothetical protein ECA4448 [Pectobacterium atrosepticum SCRI1043]	gi|50123366|ref|YP 052533.1|	43.2	1E-22
contig00113-orf00083	dihydroorotase [Neisseria meningitidis MC58]	gi|15676580|ref|NP 273724.1|	97.67	0
contig00113-orf00085	lipoprotein [Neisseria meningitidis Z2491]	gi|15793852|ref|NP 283674.1|	47.59	3E-37
contig00113-orf00086	hypothetical protein NMA0882 [Neisseria meningitidis Z2491]	gi|15793851|ref|NP 283673.1|	81.67	2E-22
contig00113-orf00087	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793850|ref|NP 283672.1|	71.7	4E-28
contig00113-orf00088	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793850|ref|NP 283672.1|	73.58	1E-42
contig00113-orf00089	hypothetical protein NMA0982 [Neisseria meningitidis Z2491]	gi|15793939|ref|NP 283761.1|	77.82	2E-119
contig00113-orf00090	pilus biogenesis protein [Neisseria meningitidis Z2491]	gi|15793938|ref|NP 283760.1|	66.67	3E-39
contig00113-orf00092	DNA polymerase III subunit delta' [Neisseria meningitidis Z2491]	gi|15793937|ref|NP 283759.1|	66.98	4E-116

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contig00113-orf00093	TPR repeat-containing protein [Bacillus thuringiensis serovar konkukian str. 97-27]	gi|49480843|ref|YP 037826.1|	42.86	2.6
contig00113-orf00095	hypothetical protein lmo0592 [Listeria monocytogenes EGD-e]	gi|16802635|ref|NP 464120.1|	34.09	0.002
contig00113-orf00098	hypothetical protein NMA0850 [Neisseria meningitidis Z2491]	gi|15793820|ref|NP 283642.1|	76.92	0.31
contig00113-orf00100	putative deoxyribonucleotide triphosphate pyrophosphatase [Neisseria meningitidis Z2491]	gi|15793819|ref|NP 283641.1|	76.56	1E-81
contig00113-orf00103	coproporphyrinogen III oxidase [Neisseria meningitidis MC58]	gi|15676563|ref|NP 273707.1|	96.16	0
contig00113-orf00104	outer membrane protein [Neisseria meningitidis Z2491]	gi|15793832|ref|NP 283654.1|	52.85	2E-45
contig00113-orf00105	hypothetical protein NMA0861 [Neisseria meningitidis Z2491]	gi|15793831|ref|NP 283653.1|	96.9	2E-63
contig00113-orf00107	diadenosine tetraphosphatase [Neisseria meningitidis Z2491]	gi|15793830|ref|NP 283652.1|	76.81	7E-119
contig00113-orf00108	transaldolase [Neisseria meningitidis MC58]	gi|15676266|ref|NP 273400.1|	94.59	1E-169
contig00113-orf00112	hypothetical protein NMA2135 [Neisseria meningitidis Z2491]	gi|15795006|ref|NP 284828.1|	91.67	1E-153
contig00113-orf00115	putative SUN-family protein [Neisseria gonorrhoeae FA 1090]	gi|59801095|ref|YP 207807.1|	90.95	0
contig00113-orf00124	hypothetical protein NGO0317 [Neisseria gonorrhoeae FA 1090]	gi|59800764|ref|YP 207476.1|	92.16	2E-76
contig00113-orf00128	hypothetical protein NGO0992 [Neisseria gonorrhoeae FA 1090]	gi|59801376|ref|YP 208088.1|	98.54	1E-112
contig00113-orf00130	hypothetical protein NMA1732 [Neisseria meningitidis Z2491]	gi|15794625|ref|NP 284447.1|	95.27	3E-90
contig00113-orf00133	Laz [Neisseria gonorrhoeae FA 1090]	gi|59801378|ref|YP 208090.1|	70.05	4E-59
contig00113-orf00134	hypothetical protein NGO0995 [Neisseria gonorrhoeae FA 1090]	gi|59801379|ref|YP 208091.1|	73.91	5E-46
contig00113-orf00138	preprotein translocase subunit SecA [Neisseria meningitidis Z2491]	gi|15794628|ref|NP 284450.1|	90.52	0
contig00113-orf00141	glutaminyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15794641|ref|NP 284463.1|	96.09	0
contig00113-orf00143	#N/A	#N/A	#N/A	#N/A
contig00113-orf00144	DeoR family transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59801578|ref|YP 208290.1|	76.92	3E-106
contig00113-orf00146	hypothetical protein NMA1891 [Neisseria meningitidis Z2491]	gi|15794777|ref|NP 284599.1|	82.17	1E-72
contig00113-orf00148	phosphoserine aminotransferase [Neisseria meningitidis Z2491]	gi|15794779|ref|NP 284601.1|	87.5	0
contig00113-orf00149	hypothetical protein NMA1895 [Neisseria meningitidis Z2491]	gi|15794780|ref|NP 284602.1|	94.41	4E-72
contig00113-orf00153	transcription elongation factor NusA [Neisseria meningitidis Z2491]	gi|15794781|ref|NP 284603.1|	90.1	0
contig00113-orf00155	translation initiation factor IF-2 [Neisseria meningitidis Z2491]	gi|15794782|ref|NP 284604.1|	90.16	0
contig00113-orf00157	lipoprotein [Neisseria meningitidis Z2491]	gi|15794660|ref|NP 284482.1|	74.03	1E-89
contig00113-orf00159	ATP phosphoribosyltransferase catalytic subunit [Neisseria meningitidis Z2491]	gi|15794661|ref|NP 284483.1|	91.67	8E-107
contig00113-orf00160	hypothetical protein NMA1769 [Neisseria meningitidis Z2491]	gi|15794662|ref|NP 284484.1|	84.28	2E-129
contig00113-orf00162	histidinol dehydrogenase [Neisseria meningitidis Z2491]	gi|15794663|ref|NP 284485.1|	91.84	0
contig00113-orf00163	sulphate permease ATP-binding protein [Neisseria meningitidis Z2491]	gi|15794045|ref|NP 283867.1|	94.96	0
contig00113-orf00166	sulphate permease inner membrane protein [Neisseria meningitidis Z2491]	gi|15794046|ref|NP 283868.1|	95.44	8E-118
contig00113-orf00169	hypothetical protein NGO1457 [Neisseria gonorrhoeae FA 1090]	gi|59801798|ref|YP 208510.1|	38.71	0.029
contig00113-orf00170	sulfate ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15676777|ref|NP 273922.1|	96.4	2E-139
contig00113-orf00171	hypothetical protein NMB1365 [Neisseria meningitidis MC58]	gi|15677230|ref|NP 274383.1|	64.33	2E-48
contig00113-orf00172	hypothetical protein NGO0337 [Neisseria gonorrhoeae FA 1090]	gi|59800782|ref|YP 207494.1|	46.51	0.001

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contig00113-orf00174	dihydropteridine reductase [Vibrio cholerae O1 biovar eltor str. N16961]	gi|15601395|ref|NP 233026.1|	52.53	2E-60
contig00113-orf00176	hypothetical protein NMA0801 [Neisseria meningitidis Z2491]	gi|15793775|ref|NP 283597.1|	86.67	2E-15
contig00113-orf00179	hypothetical protein NMA0800 [Neisseria meningitidis Z2491]	gi|15793774|ref|NP 283596.1|	49.75	2E-151
contig00113-orf00182	exodeoxyribonuclease V [Neisseria meningitidis Z2491]	gi|15794857|ref|NP 284679.1|	72.13	0
contig00113-orf00184	putative TonB-dependent receptor protein [Neisseria gonorrhoeae FA 1090]	gi|59801342|ref|YP 208054.1|	60.91	5E-172
contig00113-orf00185	outer membrane substrate binding protein [Neisseria meningitidis Z2491]	gi|15794593|ref|NP 284415.1|	68.86	8E-173
contig00113-orf00186	hypothetical protein NMB0772 [Neisseria meningitidis MC58]	gi|15676670|ref|NP 273814.1|	61.7	8E-13
contig00115-orf00001	mtrCDE transcriptional regulator, repressor [Neisseria gonorrhoeae FA 1090]	gi|59801714|ref|YP 208426.1|	77.62	2E-94
contig00115-orf00002	outer membrane protein OprC complement [Chromobacterium violaceum ATCC 12472]	gi|34496350|ref|NP 900565.1|	46.4	3E-155
contig00115-orf00004	#N/A	#N/A	#N/A	#N/A
contig00115-orf00006	hypothetical protein NGO1468 [Neisseria gonorrhoeae FA 1090]	gi|59801808|ref|YP 208520.1|	89.49	9E-132
contig00115-orf00008	hypothetical protein NMB1824 [Neisseria meningitidis MC58]	gi|15677660|ref|NP 274821.1|	97.11	2E-146
contig00115-orf00011	hypothetical protein NMA0634 [Neisseria meningitidis Z2491]	gi|15793622|ref|NP 283444.1|	91.04	2E-32
contig00115-orf00013	hypothetical protein NMB1826 [Neisseria meningitidis MC58]	gi|15677662|ref|NP 274823.1|	98.68	7E-36
contig00115-orf00015	outer membrane ferripyoverdine receptor [Pseudomonas fluorescens Pf-5]	gi|70731448|ref|YP 261189.1|	30.94	5E-95
contig00115-orf00017	hypothetical protein TK0088 [Thermococcus kodakarensis KOD1]	gi|57640023|ref|YP 182501.1|	30.34	0.01
contig00115-orf00019	putative ABC transporter ATP-binding protein [Pectobacterium atrosepticum SCRI1043]	gi|50119822|ref|YP 048989.1|	41.58	1E-123
contig00115-orf00022	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	85.71	1E-10
contig00115-orf00024	GntR family transcriptional regulator [Neisseria meningitidis MC58]	gi|15677558|ref|NP 274714.1|	86.33	7E-128
contig00115-orf00027	L-lactate permease [Shewanella oneidensis MR-1]	gi|24372416|ref|NP 716458.1|	76.88	0
contig00115-orf00033	aminopeptidase N [Neisseria meningitidis MC58]	gi|15677275|ref|NP 274428.1|	97.23	0
contig00116-orf00001	C-5 cytosine-specific DNA methylase family protein [Methylococcus capsulatus str. Bath]	gi|53804329|ref|YP 114062.1|	67.82	4E-111
contig00116-orf00002	hypothetical protein MCA1617 [Methylococcus capsulatus str. Bath]	gi|53804328|ref|YP 114063.1|	46.15	0.001
contig00116-orf00003	hypothetical protein MCA1617 [Methylococcus capsulatus str. Bath]	gi|53804328|ref|YP 114063.1|	60.71	1E-97
contig00116-orf00005	alanyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677445|ref|NP 274601.1|	86.83	0
contig00116-orf00006	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Neisseria meningitidis MC58]	gi|15677444|ref|NP 274600.1|	89.36	0
contig00116-orf00008	phopholipase D-family protein [Neisseria meningitidis MC58]	gi|15677292|ref|NP 274446.1|	74.02	0
contig00116-orf00010	adenosine deaminase [Acinetobacter sp. ADP1]	gi|50084431|ref|YP 045941.1|	67.77	6E-128
contig00116-orf00012	hypothetical protein NMB1470 [Neisseria meningitidis MC58]	gi|15677324|ref|NP 274479.1|	79.1	2E-70
contig00116-orf00013	tryptophanyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15794575|ref|NP 284397.1|	95.54	1E-177
contig00116-orf00016	clpB protein [Neisseria meningitidis MC58]	gi|15677326|ref|NP 274481.1|	90.92	0
contig00116-orf00018	hypothetical protein NGO0371 [Neisseria gonorrhoeae FA 1090]	gi|59800815|ref|YP 207527.1|	81.46	2E-143
contig00116-orf00021	hypothetical protein MS1630 [Mannheimia succiniciproducens MBEL55E]	gi|52425685|ref|YP 088822.1|	54.15	1E-93

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contig00116-orf00024	divalent cation transporter [Saccharophagus degradans 2-40]	gi|90022792|ref|YP 528619.1|	21.79	5E-09
contig00116-orf00027	prolipoprotein diacylglyceryl transferase [Neisseria meningitidis Z2491]	gi|15794204|ref|NP 284026.1|	84.04	2E-131
contig00116-orf00029	hypothetical protein NMA1274 [Neisseria meningitidis Z2491]	gi|15794205|ref|NP 284027.1|	91.22	0
contig00116-orf00032	acetylglutamate kinase [Neisseria meningitidis MC58]	gi|15676958|ref|NP 274107.1|	90.94	6E-126
contig00116-orf00033	exopolyphosphatase [Neisseria meningitidis MC58]	gi|15677321|ref|NP 274476.1|	85.4	0
contig00116-orf00035	transglycosylase [Neisseria meningitidis Z2491]	gi|15794568|ref|NP 284390.1|	88.95	1E-87
contig00116-orf00036	hypothetical protein NGO1032 [Neisseria gonorrhoeae FA 1090]	gi|59801408|ref|YP 208120.1|	88.26	0
contig00116-orf00037	putative single-stranded DNA binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801407|ref|YP 208119.1|	80.46	3E-65
contig00116-orf00038	hypothetical protein PM1949 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603814|ref|NP 246888.1|	90.71	4E-157
contig00116-orf00039	hypothetical protein PM1948 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603813|ref|NP 246887.1|	88.33	2E-153
contig00116-orf00041	hypothetical protein PM1947 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603812|ref|NP 246886.1|	78.82	0
contig00116-orf00043	filamentous hemagglutinin / adhesin [Ralstonia eutropha H16]	gi|116694202|ref|YP 728413.1|	32.58	9E-35
contig00116-orf00045	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15677610|ref|NP 274768.1|	36.85	0
contig00116-orf00046	putative hemolysin activation protein HecB [Neisseria meningitidis MC58]	gi|15677604|ref|NP 274762.1|	64.26	0
contig00116-orf00049	hypothetical protein SPO0394 [Ruegeria pomeroyi DSS-3]	gi|56695309|ref|YP 165657.1|	50.79	0.0003
contig00116-orf00052	rhodanese-like protein [Ralstonia metallidurans CH34]	gi|94311307|ref|YP 584517.1|	43.2	4E-21
contig00116-orf00054	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794513|ref|NP 284335.1|	96.55	5E-44
contig00117-orf00003	ribonuclease II family protein [Neisseria meningitidis MC58]	gi|15677073|ref|NP 274225.1|	89.25	0
contig00117-orf00005	molybdopterin-guanine dinucleotide biosynthesis protein A [Neisseria meningitidis Z2491]	gi|15794329|ref|NP 284151.1|	69.44	1E-69
contig00117-orf00006	NarX/NarQ [Neisseria gonorrhoeae FA 1090]	gi|59801168|ref|YP 207880.1|	58.75	0
contig00117-orf00007	NarL/NarP [Neisseria gonorrhoeae FA 1090]	gi|59801167|ref|YP 207879.1|	84.65	4E-98
contig00117-orf00009	thiol:disulfide interchange protein precursor [Neisseria meningitidis MC58]	gi|15677372|ref|NP 274527.1|	77.83	0
contig00117-orf00012	uracil-DNA glycosylase [Neisseria meningitidis MC58]	gi|15677095|ref|NP 274247.1|	70.32	6E-92
contig00117-orf00013	hypothetical protein PM1470 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603335|ref|NP 246409.1|	80.61	9E-73
contig00117-orf00014	hypothetical protein all0364 [Nostoc sp. PCC 7120]	gi|17227860|ref|NP 484408.1|	46.95	3E-31
contig00117-orf00015	VCBS [Rhodoferax ferrireducens T118]	gi|89901489|ref|YP 523960.1|	50	0.0000002
contig00117-orf00017	alcohol dehydrogenase class-III [Neisseria meningitidis Z2491]	gi|15794412|ref|NP 284234.1|	97.62	3E-142
contig00117-orf00018	esterase D [Neisseria meningitidis MC58]	gi|15677171|ref|NP 274324.1|	95.27	1E-155
contig00117-orf00020	peptidyl-prolyl cis-trans isomerase B [Neisseria meningitidis Z2491]	gi|15793958|ref|NP 283780.1|	96.45	8E-83
contig00117-orf00022	NadC family protein [Neisseria meningitidis MC58]	gi|15676690|ref|NP 273834.1|	91.3	0
contig00117-orf00023	3-dehydroquinate dehydratase [Neisseria gonorrhoeae FA 1090]	gi|59801157|ref|YP 207869.1|	55.42	1E-62
contig00117-orf00025	hypothetical protein NMA1760 [Neisseria meningitidis Z2491]	gi|15794653|ref|NP 284475.1|	89.61	2E-170
contig00117-orf00027	hypothetical protein NMB1570 [Neisseria meningitidis MC58]	gi|15677420|ref|NP 274576.1|	94.07	0
contig00117-orf00028	aminopeptidase A [Neisseria meningitidis Z2491]	gi|15794651|ref|NP 284473.1|	94.23	0
contig00117-orf00030	hypothetical protein Mmcs 0699 [Mycobacterium sp. MCS]	gi|108797679|ref|YP 637876.1|	33.62	3E-09

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contig00117-orf00031	mannose-1-phosphate guanylyl transferase (GDP) [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	gi|19703885|ref|NP 603447.1|	60	6E-34
contig00117-orf00033	hypothetical protein BT9727 1913 [Bacillus thuringiensis serovar konkukian str. 97-27]	gi|49477495|ref|YP 036243.1|	40	4.5
contig00117-orf00035	TonB-dependent receptor [Neisseria meningitidis MC58]	gi|15676857|ref|NP 274002.1|	94.13	0
contig00117-orf00037	alpha amylase, catalytic region [Arthrobacter sp. FB24]	gi|116670577|ref|YP 831510.1|	57.3	0
contig00118-orf00001	DNA-binding protein [Neisseria meningitidis Z2491]	gi|15794211|ref|NP 284033.1|	96.55	3E-43
contig00119-orf00002	hypothetical protein Gmet A3576 [Geobacter metallireducens GS-15]	gi|78214265|ref|YP 380336.1|	29.03	0.029
contig00119-orf00004	hypothetical protein Swol 0432 [Syntrophomonas wolfei subsp. wolfei str. Goettingen]	gi|114565987|ref|YP 753141.1|	48.81	2E-18
contig00119-orf00005	hypothetical protein SAR2498 [Staphylococcus aureus subsp. aureus MRSA252]	gi|49484624|ref|YP 041848.1|	57.14	0.00001
contig00119-orf00007	hypothetical protein Ava B0327 [Anabaena variabilis ATCC 29413]	gi|75812607|ref|YP 320226.1|	35	0.0008
contig00119-orf00010	hypothetical protein NMB1665 [Neisseria meningitidis MC58]	gi|15677514|ref|NP 274670.1|	75.89	5E-44
contig00119-orf00011	hypothetical protein NMB1666 [Neisseria meningitidis MC58]	gi|15677515|ref|NP 274671.1|	76.83	6E-26
contig00119-orf00013	#N/A	#N/A	#N/A	#N/A
contig00119-orf00016	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	96.94	4E-52
contig00120-orf00001	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15677610|ref|NP 274768.1|	51.46	4E-38
contig00122-orf00004	calcium binding hemolysin [Chromobacterium violaceum ATCC 12472]	gi|34495971|ref|NP 900186.1|	25.95	1E-45
contig00122-orf00005	hypothetical protein HD0394 [Haemophilus ducreyi 35000HP]	gi|33151620|ref|NP 872973.1|	62.42	2E-44
contig00122-orf00008	anaerobic ribonucleoside triphosphate reductase [Haemophilus ducreyi	gi|33151619|ref|NP 872972.1|	80.44	0
contig00122-orf00009	#N/A	#N/A	#N/A	#N/A
contig00122-orf00010	hypothetical protein NGO0860 [Neisseria gonorrhoeae FA 1090]	gi|59801262|ref|YP 207974.1|	43.21	4E-11
contig00122-orf00011	Pirin-related protein [Ralstonia eutropha H16]	gi|113867305|ref|YP 725794.1|	57.79	3E-92
contig00122-orf00012	putative transcriptional regulator [Bacillus subtilis subsp. subtilis str. 168]	gi|16077596|ref|NP 388410.1|	75	1E-15
contig00122-orf00013	hypothetical protein NGO0588 [Neisseria gonorrhoeae FA 1090]	gi|59801019|ref|YP 207731.1|	57.23	1E-44
contig00123-orf00001	methionyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59802352|ref|YP 209064.1|	98.24	0
contig00123-orf00003	#N/A	#N/A	#N/A	#N/A
contig00123-orf00004	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793232|ref|NP 283054.1|	93.15	0
contig00124-orf00001	F0F1 ATP synthase subunit epsilon [Neisseria meningitidis MC58]	gi|15677763|ref|NP 274927.1|	87.5	3E-16
contig00124-orf00002	F0F1 ATP synthase subunit beta [Neisseria meningitidis MC58]	gi|15677764|ref|NP 274928.1|	97.63	0
contig00124-orf00004	F0F1 ATP synthase subunit gamma [Neisseria meningitidis Z2491]	gi|15793516|ref|NP 283338.1|	87.91	2E-102
contig00124-orf00006	F0F1 ATP synthase subunit alpha [Neisseria meningitidis Z2491]	gi|15793515|ref|NP 283337.1|	96.12	0
contig00124-orf00007	F0F1 ATP synthase subunit delta [Neisseria gonorrhoeae FA 1090]	gi|59802444|ref|YP 209156.1|	78.53	1E-72
contig00124-orf00008	F0F1 ATP synthase subunit B [Neisseria meningitidis Z2491]	gi|15793513|ref|NP 283335.1|	89.74	2E-61
contig00124-orf00009	F0F1 ATP synthase subunit C [Neisseria meningitidis Z2491]	gi|15793512|ref|NP 283334.1|	100	2E-22
contig00124-orf00010	F0F1 ATP synthase subunit A [Neisseria meningitidis Z2491]	gi|15793511|ref|NP 283333.1|	92.01	4E-152
contig00124-orf00013	chromosome segregation proteins [Neisseria meningitidis Z2491]	gi|15793507|ref|NP 283329.1|	87.72	6E-137

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contig00124-orf00014	serine/threonine kinase [Nostoc sp. PCC 7120]	gi|17229361|ref|NP 485909.1|	24.47	2.3
contig00124-orf00015	putative transport protein [Neisseria gonorrhoeae FA 1090]	gi|59801910|ref|YP 208622.1|	87.61	0
contig00124-orf00016	anhydro-N-acetylmuramic acid kinase [Neisseria gonorrhoeae FA 1090]	gi|59801912|ref|YP 208624.1|	70.6	3E-147
contig00124-orf00017	CcoP [Neisseria gonorrhoeae FA 1090]	gi|59801719|ref|YP 208431.1|	86.16	3E-155
contig00124-orf00018	hypothetical protein NGO1372 [Neisseria gonorrhoeae FA 1090]	gi|59801720|ref|YP 208432.1|	67.86	1E-14
contig00124-orf00019	cytochrome oxidase subunit [Neisseria meningitidis Z2491]	gi|15794861|ref|NP 284683.1|	93.6	1E-107
contig00124-orf00021	CcoN [Neisseria gonorrhoeae FA 1090]	gi|59801722|ref|YP 208434.1|	95.09	0
contig00124-orf00023	hypothetical protein NMB1726 [Neisseria meningitidis MC58]	gi|15677572|ref|NP 274729.1|	73.24	0
contig00124-orf00024	hypothetical protein NMA1982 [Neisseria meningitidis Z2491]	gi|15794864|ref|NP 284686.1|	53.95	2E-32
contig00124-orf00025	nitrilase [Neisseria meningitidis MC58]	gi|15676353|ref|NP 273489.1|	71.53	2E-116
contig00124-orf00027	1-deoxy-D-xylulose-5-phosphate synthase [Neisseria meningitidis MC58]	gi|15677702|ref|NP 274863.1|	89.12	0
contig00124-orf00029	putative oxidoreductase [Neisseria gonorrhoeae FA 1090]	gi|59801853|ref|YP 208565.1|	69.66	3E-101
contig00124-orf00030	carbamoyl phosphate synthase small subunit [Streptococcus agalactiae NEM316]	gi|25011129|ref|NP 735524.1|	43.24	3.4
contig00124-orf00031	putative lipopolysaccharide glucosyltransferase [Sodalis glossinidius str. 'morsitans']	gi|85060179|ref|YP 455881.1|	44.8	7E-74
contig00124-orf00032	hypothetical protein RSc0467 [Ralstonia solanacearum GMI1000]	gi|17545186|ref|NP 518588.1|	27.66	4.5
contig00124-orf00033	Holliday junction resolvase [Neisseria meningitidis Z2491]	gi|15794525|ref|NP 284347.1|	88.14	7E-63
contig00124-orf00034	lipid A biosynthesis lauroyl acyltransferase [Neisseria meningitidis Z2491]	gi|15794524|ref|NP 284346.1|	76.47	6E-132
contig00124-orf00036	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	100	1E-28
contig00125-orf00001	inorganic phosphate transporter [Chlamydia trachomatis D/UW-3/CX]	gi|15605425|ref|NP 220211.1|	30.77	4.5
contig00125-orf00002	hypothetical protein NMA0778 [Neisseria meningitidis Z2491]	gi|15793753|ref|NP 283575.1|	38.46	6E-10
contig00125-orf00003	acyltransferase 3 [Pseudomonas syringae pv. syringae B728a]	gi|66048311|ref|YP 238152.1|	38.3	2
contig00126-orf00001	#N/A	#N/A	#N/A	#N/A
contig00127-orf00002	PilT protein-like protein [Syntrophomonas wolfei subsp. wolfei str. Goettingen]	gi|114565795|ref|YP 752949.1|	31.37	4.5
contig00128-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	98.33	4E-28
contig00131-orf00001	excinuclease ABC subunit C [Neisseria meningitidis Z2491]	gi|15794433|ref|NP 284255.1|	97.53	0
contig00131-orf00002	short chain dehydrogenase/reductase family oxidoreductase [Neisseria meningitidis MC58]	gi|15676819|ref|NP 273964.1|	80	7E-124
contig00131-orf00004	putative C-type cytochrome [Neisseria gonorrhoeae FA 1090]	gi|59801447|ref|YP 208159.1|	85.07	9E-53
contig00131-orf00008	tautomerase [Neisseria meningitidis Z2491]	gi|15794578|ref|NP 284400.1|	78.26	3E-24
contig00131-orf00009	hypothetical protein NMA1207 [Neisseria meningitidis Z2491]	gi|15794151|ref|NP 283973.1|	85.89	8E-150
contig00131-orf00011	inosine/uridine-preferring nucleoside hydrolase [Silicibacter sp. TM1040]	gi|99080775|ref|YP 612929.1|	53.05	3E-85
contig00131-orf00013	hypothetical protein HH0773 [Helicobacter hepaticus ATCC 51449]	gi|32266272|ref|NP 860304.1|	45.58	2E-128
contig00131-orf00015	endonuclease/exonuclease/phosphatase [Psychrobacter cryohalolentis K5]	gi|93004917|ref|YP 579354.1|	57.26	4E-75
contig00131-orf00016	ferredoxin [Neisseria meningitidis Z2491]	gi|15793090|ref|NP 282912.1|	65.95	3E-62
contig00131-orf00019	aldehyde dehydrogenase [Neisseria meningitidis Z2491]	gi|15794458|ref|NP 284280.1|	82.1	0
contig00131-orf00021	uracil permease [Neisseria meningitidis MC58]	gi|15677181|ref|NP 274334.1|	91.29	5E-159

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contig00131-orf00024	TolC protein [Mannheimia succiniciproducens MBEL55E]	gi|52425359|ref|YP 088496.1|	58.21	4E-35
contig00131-orf00026	TolC protein [Mannheimia succiniciproducens MBEL55E]	gi|52425359|ref|YP 088496.1|	43.22	2E-52
contig00131-orf00027	hypothetical protein PM1981 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603846|ref|NP 246920.1|	48.79	1E-96
contig00131-orf00029	hypothetical protein Nham 1894 [Nitrobacter hamburgensis X14]	gi|92117433|ref|YP 577162.1|	37.18	0.0002
contig00132-orf00002	hypothetical protein Tery 3131 [Trichodesmium erythraeum IMS101]	gi|113476673|ref|YP 722734.1|	19.73	0.65
contig00132-orf00004	Smc-like [Mycoplasma gallisepticum R]	gi|31544374|ref|NP 852952.1|	28.32	0.009
contig00134-orf00001	cytochrome c5 [Neisseria meningitidis MC58]	gi|15677525|ref|NP 274681.1|	76.84	5E-106
contig00134-orf00002	aromatic amino acid aminotransferase [Neisseria meningitidis MC58]	gi|15677526|ref|NP 274682.1|	95.21	0
contig00134-orf00003	dihydropteroate synthase [Neisseria meningitidis MC58]	gi|15677539|ref|NP 274695.1|	91.17	3E-134
contig00134-orf00005	MrsA [Neisseria gonorrhoeae FA 1090]	gi|59801691|ref|YP 208403.1|	95.49	0
contig00134-orf00007	putative dedA protein [Neisseria meningitidis MC58]	gi|15677537|ref|NP 274693.1|	87.5	1E-95
contig00134-orf00010	L-asparaginase [Neisseria meningitidis MC58]	gi|15677536|ref|NP 274692.1|	93.64	4E-171
contig00134-orf00011	hypothetical protein NMA1946 [Neisseria meningitidis Z2491]	gi|15794829|ref|NP 284651.1|	86.38	1E-122
contig00134-orf00015	thiamine monophosphate kinase [Neisseria meningitidis Z2491]	gi|15794978|ref|NP 284800.1|	70.13	2E-119
contig00134-orf00016	phosphatidylglycerophosphatase A [Neisseria meningitidis Z2491]	gi|15794977|ref|NP 284799.1|	68.99	1E-48
contig00134-orf00017	ApaG [Mesorhizobium loti MAFF303099]	gi|13474703|ref|NP 106272.1|	43.12	2E-18
contig00134-orf00019	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	91.82	3E-82
contig00135-orf00003	hypothetical protein NMB1866 [Neisseria meningitidis MC58]	gi|15677701|ref|NP 274862.1|	97.96	0
contig00135-orf00005	hypothetical protein PA14 33120 [Pseudomonas aeruginosa UCBPP-PA14]	gi|116050384|ref|YP 790799.1|	27.27	0.0002
contig00135-orf00007	glutamate-1-semialdehyde aminotransferase [Neisseria gonorrhoeae FA 1090]	gi|59800508|ref|YP 207220.1|	91.78	0
contig00135-orf00011	hypothetical protein MS1440 [Mannheimia succiniciproducens MBEL55E]	gi|52425495|ref|YP 088632.1|	63.19	1E-96
contig00135-orf00015	putative adhesin/invasin [Neisseria meningitidis MC58]	gi|15677822|ref|NP 274986.1|	25.16	0.0001
contig00136-orf00001	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Neisseria meningitidis MC58]	gi|15676373|ref|NP 273509.1|	94.21	0
contig00136-orf00003	30S ribosomal protein S20 [Neisseria meningitidis Z2491]	gi|15794902|ref|NP 284724.1|	100	3E-40
contig00136-orf00006	putative phospholipase [Neisseria gonorrhoeae FA 1090]	gi|59801830|ref|YP 208542.1|	76.62	3E-158
contig00136-orf00008	hypothetical protein NMB0465 [Neisseria meningitidis MC58]	gi|15676376|ref|NP 273512.1|	80.26	1E-87
contig00136-orf00009	aspartyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15794899|ref|NP 284721.1|	96.18	0
contig00136-orf00011	LmbE family protein [Pseudomonas putida KT2440]	gi|26991619|ref|NP 747044.1|	32.31	8E-48
contig00136-orf00013	UDP-2,3-diacylglucosamine hydrolase [Neisseria meningitidis MC58]	gi|15676450|ref|NP 273589.1|	65.24	1E-75
contig00136-orf00015	putative carboxypeptidase, penicillin binding protein [Neisseria gonorrhoeae FA 1090]	gi|59800568|ref|YP 207280.1|	58.63	8E-148
contig00136-orf00017	histidinol-phosphate aminotransferase [Neisseria meningitidis Z2491]	gi|15794664|ref|NP 284486.1|	72.63	4E-148
contig00136-orf00019	imidazoleglycerol-phosphate dehydratase [Neisseria meningitidis Z2491]	gi|15794665|ref|NP 284487.1|	72.13	1E-117
contig00136-orf00022	hypothetical protein SMc02493 [Sinorhizobium meliloti 1021]	gi|15966795|ref|NP 387148.1|	31.64	1E-15
contig00136-orf00024	hypothetical protein all4935 [Nostoc sp. PCC 7120]	gi|17232427|ref|NP 488975.1|	21.21	3E-09
contig00136-orf00026	iron-regulated outer membrane protein FrpB [Neisseria meningitidis MC58]	gi|15677816|ref|NP 274980.1|	37.76	4E-109

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contig00136-orf00027	hypothetical protein NGO1505 [Neisseria gonorrhoeae FA 1090]	gi|59801843|ref|YP 208555.1|	68.8	3E-40
contig00136-orf00029	MutT-related protein [Neisseria meningitidis Z2491]	gi|15794912|ref|NP 284734.1|	71.1	3E-103
contig00138-orf00001	tetraacyldisaccharide 4'-kinase [Neisseria meningitidis MC58]	gi|15676570|ref|NP 273714.1|	84.62	2E-68
contig00138-orf00003	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793842|ref|NP 283664.1|	24.66	0.073
contig00138-orf00005	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793842|ref|NP 283664.1|	38.04	2E-21
contig00138-orf00008	hypothetical protein NMA0874 [Neisseria meningitidis Z2491]	gi|15793843|ref|NP 283665.1|	100	3E-28
contig00138-orf00009	3-deoxy-manno-octulosonate cytidylyltransferase [Neisseria meningitidis Z2491]	gi|15793844|ref|NP 283666.1|	95.26	4E-126
contig00138-orf00012	hypothetical protein NMA0876 [Neisseria meningitidis Z2491]	gi|15793845|ref|NP 283667.1|	78.57	3E-39
contig00138-orf00014	adenylate kinase [Neisseria meningitidis Z2491]	gi|15793988|ref|NP 283810.1|	99.07	3E-117
contig00138-orf00015	orotidine 5'-phosphate decarboxylase [Neisseria gonorrhoeae FA 1090]	gi|59800845|ref|YP 207557.1|	98.35	1E-122
contig00138-orf00016	NADH dehydrogenase [Shewanella denitrificans OS217]	gi|91792489|ref|YP 562140.1|	38.1	3E-29
contig00138-orf00017	putative sugar kinase / ADP-heptose synthase [Neisseria gonorrhoeae FA 1090]	gi|59800846|ref|YP 207558.1|	94.38	2E-162
contig00138-orf00019	ADP-L-glycero-D-mannoheptose-6-epimerase [Neisseria meningitidis MC58]	gi|15676725|ref|NP 273870.1|	95.21	0
contig00138-orf00020	hypothetical protein NGO0460 [Neisseria gonorrhoeae FA 1090]	gi|59800898|ref|YP 207610.1|	86.08	0
contig00138-orf00021	hypothetical protein NMA1666 [Neisseria meningitidis Z2491]	gi|15794560|ref|NP 284382.1|	90.96	0
contig00138-orf00022	aldose-1-epimerase [Cytophaga hutchinsonii ATCC 33406]	gi|110637076|ref|YP 677283.1|	32.08	4E-33
contig00138-orf00025	hypothetical protein NGO0657 [Neisseria gonorrhoeae FA 1090]	gi|59801084|ref|YP 207796.1|	95.99	0
contig00138-orf00027	pyridoxamine 5'-phosphate oxidase [Neisseria meningitidis Z2491]	gi|15794465|ref|NP 284287.1|	81.9	2E-92
contig00138-orf00029	deoxyuridine 5'-triphosphate nucleotidohydrolase [Neisseria gonorrhoeae FA 1090]	gi|59800897|ref|YP 207609.1|	81.08	2E-64
contig00138-orf00031	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15794072|ref|NP 283894.1|	95.9	0
contig00139-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	91.18	2E-11
contig00139-orf00003	hypothetical protein NMA2056 [Neisseria meningitidis Z2491]	gi|15794934|ref|NP 284756.1|	87.84	0
contig00139-orf00006	putative adhesin/invasin [Neisseria meningitidis MC58]	gi|15677822|ref|NP 274986.1|	40.06	6E-39
contig00141-orf00002	O-sialoglycoprotein endopeptidase [Neisseria meningitidis Z2491]	gi|15793645|ref|NP 283467.1|	81.92	1E-141
contig00141-orf00004	phospho-2-dehydro-3-deoxyheptonate aldolase [Neisseria meningitidis Z2491]	gi|15795051|ref|NP 284873.1|	88.79	9E-175
contig00141-orf00006	hypothetical protein VP0670 [Vibrio parahaemolyticus RIMD 2210633]	gi|28897444|ref|NP 797049.1|	60	4.5
contig00141-orf00008	3-deoxy-D-manno-octulosonic-acid transferase [Neisseria meningitidis MC58]	gi|15675962|ref|NP 273080.1|	61.46	3E-141
contig00141-orf00010	Hsf [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603435|ref|NP 246509.1|	56.92	2E-22
contig00141-orf00012	Plp4 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602451|ref|NP 245523.1|	72.66	7E-55
contig00141-orf00014	type IV pilus assembly protein [Neisseria meningitidis Z2491]	gi|15795030|ref|NP 284852.1|	80.5	0
contig00141-orf00015	PilG [Neisseria gonorrhoeae FA 1090]	gi|59801994|ref|YP 208706.1|	72.21	3E-161
contig00141-orf00016	type IV prepilin peptidase [Neisseria meningitidis MC58]	gi|15676247|ref|NP 273381.1|	75.3	2E-88
contig00141-orf00017	putative kinase [Neisseria meningitidis MC58]	gi|15677989|ref|NP 273380.1|	53.81	3E-51
contig00141-orf00019	bifunctional riboflavin kinase/FMN adenylyltransferase [Neisseria meningitidis MC58]	gi|15677670|ref|NP 274831.1|	77.14	2E-112

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contig00141-orf00020	bifunctional riboflavin kinase/FMN adenylyltransferase [Neisseria meningitidis MC58]	gi|15677670|ref|NP 274831.1|	78.57	0.000002
contig00141-orf00021	hypothetical protein HD1060 [Haemophilus ducreyi 35000HP]	gi|33152189|ref|NP 873542.1|	45.21	5E-10
contig00141-orf00022	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [Neisseria meningitidis Z2491]	gi|15793614|ref|NP 283436.1|	90.65	2E-164
contig00141-orf00023	lipoprotein signal peptidase [Neisseria gonorrhoeae FA 1090]	gi|59800534|ref|YP 207246.1|	75	1E-59
contig00141-orf00024	hypothetical protein MS0269 [Mannheimia succiniciproducens MBEL55E]	gi|52424324|ref|YP 087461.1|	64.35	1E-33
contig00141-orf00028	putative outer membrane protein OmpU [Neisseria gonorrhoeae FA 1090]	gi|59802013|ref|YP 208725.1|	60.34	1E-157
contig00141-orf00029	hypothetical protein Rfer 1117 [Rhodoferax ferrireducens T118]	gi|89899918|ref|YP 522389.1|	44.44	3.5
contig00141-orf00032	hypothetical protein NMB0570 [Neisseria meningitidis MC58]	gi|15676475|ref|NP 273614.1|	81.14	0
contig00141-orf00035	Na(+)-translocating NADH-quinone reductase subunit A [Neisseria meningitidis Z2491]	gi|15793727|ref|NP 283549.1|	97.09	0
contig00141-orf00037	Na(+)-translocating NADH-quinone reductase subunit B [Neisseria meningitidis Z2491]	gi|15793726|ref|NP 283548.1|	96.1	0
contig00141-orf00040	Na(+)-translocating NADH-quinone reductase subunit C [Neisseria meningitidis Z2491]	gi|15793725|ref|NP 283547.1|	93.02	7E-138
contig00141-orf00041	Na(+)-translocating NADH-quinone reductase subunit D [Neisseria meningitidis Z2491]	gi|15793724|ref|NP 283546.1|	93.66	1E-106
contig00141-orf00043	Na(+)-translocating NADH-quinone reductase subunit E [Neisseria gonorrhoeae FA 1090]	gi|59801761|ref|YP 208473.1|	97.35	7E-98
contig00141-orf00045	Na(+)-translocating NADH-quinone reductase subunit F [Neisseria gonorrhoeae FA 1090]	gi|59801762|ref|YP 208474.1|	98.52	0
contig00141-orf00047	hypothetical protein NMA1916 [Neisseria meningitidis Z2491]	gi|15794801|ref|NP 284623.1|	71.32	3E-158
contig00142-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	90.52	2E-55
contig00142-orf00004	hypothetical protein MS2110 [Mannheimia succiniciproducens MBEL55E]	gi|52426165|ref|YP 089302.1|	41.38	1E-25
contig00142-orf00006	ribosomal protein L11 methyltransferase [Neisseria meningitidis Z2491]	gi|15793585|ref|NP 283407.1|	89.83	2E-153
contig00142-orf00009	acetyl-CoA carboxylase, biotin carboxylase [Neisseria gonorrhoeae FA 1090]	gi|59800511|ref|YP 207223.1|	92.27	0
contig00142-orf00010	hypothetical protein BPP1343 [Bordetella parapertussis 12822]	gi|33596003|ref|NP 883646.1|	85.71	5E-25
contig00142-orf00011	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit [Neisseria gonorrhoeae FA 1090]	gi|59800512|ref|YP 207224.1|	98.21	5E-24
contig00143-orf00001	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	92.91	4E-74
contig00143-orf00002	transposase (fragment) [Neisseria meningitidis Z2491]	gi|15795054|ref|NP 284876.1|	98.15	4E-24
contig00145-orf00001	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	76.17	6E-87
contig00145-orf00003	hypothetical protein PSPPH 1863 [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71734619|ref|YP 274094.1|	42.42	1.6
contig00145-orf00004	AspS [Buchnera aphidicola str. Cc (Cinara cedri)]	gi|116515132|ref|YP 802761.1|	46.15	0.69
contig00145-orf00007	filamentous haemagglutinin [Xanthomonas axonopodis pv. citri str. 306]	gi|21242559|ref|NP 642141.1|	53.39	1E-27

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contig00148-orf00002	hypothetical protein NMB1293 [Neisseria meningitidis MC58]	gi|15677160|ref|NP 274313.1|	58.18	8E-27
contig00148-orf00003	hypothetical protein NMB0516 [Neisseria meningitidis MC58]	gi|15676425|ref|NP 273562.1|	97.14	6E-117
contig00148-orf00005	hypothetical protein NGO0607 [Neisseria gonorrhoeae FA 1090]	gi|59801035|ref|YP 207747.1|	76	2E-95
contig00148-orf00007	hypothetical protein NMA1400 [Neisseria meningitidis Z2491]	gi|15794312|ref|NP 284134.1|	68.98	1E-128
contig00148-orf00009	aspartyl/glutamyl-tRNA amidotransferase subunit B [Neisseria meningitidis Z2491]	gi|15794463|ref|NP 284285.1|	98.32	0
contig00148-orf00010	hypothetical protein NGO0661 [Neisseria gonorrhoeae FA 1090]	gi|59801088|ref|YP 207800.1|	68.93	5E-104
contig00148-orf00012	Glu-tRNA(Gln) amidotransferase subunit A [Neisseria meningitidis MC58]	gi|15677221|ref|NP 274374.1|	87.55	0
contig00148-orf00014	aspartyl/glutamyl-tRNA amidotransferase subunit C [Neisseria meningitidis Z2491]	gi|15794460|ref|NP 284282.1|	84.38	3E-39
contig00148-orf00016	rod shape-determining protein [Aromatoleum aromaticum EbN1]	gi|56477147|ref|YP 158736.1|	61.05	1E-114
contig00148-orf00017	rod shape-determining protein MreC [Polaromonas sp. JS666]	gi|91786134|ref|YP 547086.1|	37.69	8E-38
contig00148-orf00018	rod shape-determining protein MreD [Chromobacterium violaceum ATCC	gi|34499814|ref|NP 904029.1|	37.76	6E-24
contig00148-orf00019	penicillin-binding protein 2 [Chromobacterium violaceum ATCC 12472]	gi|34499815|ref|NP 904030.1|	55.59	0
contig00148-orf00022	rod shape-determining [Chromobacterium violaceum ATCC 12472]	gi|34499816|ref|NP 904031.1|	63.58	8E-95
contig00148-orf00023	hypothetical protein NGO0664 [Neisseria gonorrhoeae FA 1090]	gi|59801091|ref|YP 207803.1|	81.19	3E-76
contig00148-orf00026	CysJ protein [Mannheimia succiniciproducens MBEL55E]	gi|52425305|ref|YP 088442.1|	54.81	5E-162
contig00148-orf00028	phosphoglucomutase [Neisseria meningitidis Z2491]	gi|15793957|ref|NP 283779.1|	92.39	0
contig00148-orf00030	hypothetical protein PM1973 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603838|ref|NP 246912.1|	65.7	4E-97
contig00148-orf00031	hypothetical protein NMB1229 [Neisseria meningitidis MC58]	gi|15677101|ref|NP 274253.1|	82.64	2E-47
contig00148-orf00034	homoserine dehydrogenase [Neisseria meningitidis Z2491]	gi|15794308|ref|NP 284130.1|	96.32	0
contig00148-orf00037	hypothetical protein NMB1227 [Neisseria meningitidis MC58]	gi|15677099|ref|NP 274251.1|	43.44	6E-21
contig00148-orf00041	thiol peroxidase [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71736685|ref|YP 274830.1|	71.52	7E-60
contig00148-orf00042	#N/A	#N/A	#N/A	#N/A
contig00148-orf00044	coproporphyrinogen III oxidase [Chromobacterium violaceum ATCC 12472]	gi|34496212|ref|NP 900427.1|	71.48	2E-126
contig00148-orf00046	serine hydroxymethyltransferase [Neisseria meningitidis MC58]	gi|15676940|ref|NP 274089.1|	96.63	0
contig00148-orf00047	#N/A	#N/A	#N/A	#N/A
contig00148-orf00048	cell division control protein 48 [Haloarcula marismortui ATCC 43049]	gi|55377649|ref|YP 135499.1|	35.29	2.7
contig00148-orf00050	sugar efflux transporter [Pseudomonas entomophila L48]	gi|104781420|ref|YP 607918.1|	56.18	4E-108
contig00148-orf00052	recombination factor protein RarA [Neisseria gonorrhoeae FA 1090]	gi|59801120|ref|YP 207832.1|	97.92	0
contig00148-orf00057	methyl-accepting chemotaxis protein [Vibrio fischeri ES114]	gi|59714256|ref|YP 207031.1|	29.03	1.8
contig00148-orf00060	lipoprotein [Neisseria meningitidis Z2491]	gi|15794344|ref|NP 284166.1|	60.16	5E-32
contig00148-orf00062	threonine synthase [Neisseria meningitidis Z2491]	gi|15794345|ref|NP 284167.1|	93.38	0
contig00148-orf00064	hypothetical protein NMB0800 [Neisseria meningitidis MC58]	gi|15676698|ref|NP 273842.1|	92.55	2E-44
contig00148-orf00065	cell division protein [Neisseria meningitidis Z2491]	gi|15793964|ref|NP 283786.1|	92.39	3E-91
contig00148-orf00067	ATP-dependent zinc metallopeptidase [Neisseria meningitidis Z2491]	gi|15793963|ref|NP 283785.1|	91.24	0
contig00148-orf00068	thioredoxin reductase [Neisseria meningitidis MC58]	gi|15677190|ref|NP 274343.1|	88.29	4E-152

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contig00148-orf00072	delta-aminolevulinic acid dehydratase [Neisseria meningitidis Z2491]	gi|15793967|ref|NP 283789.1|	91.29	6E-173
contig00148-orf00075	hypothetical protein plu0311 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37524328|ref|NP 927672.1|	34.85	4E-19
contig00148-orf00076	putative ATP-dependent helicase, MgpS [Rhodobacter sphaeroides 2.4.1]	gi|77462980|ref|YP 352484.1|	31.82	6
contig00148-orf00077	integral membrane transporter [Neisseria meningitidis Z2491]	gi|15794467|ref|NP 284289.1|	91.8	0
contig00148-orf00079	hypothetical protein NMB1345 [Neisseria meningitidis MC58]	gi|15677211|ref|NP 274364.1|	66.15	0
contig00149-orf00001	ferredoxin, 4Fe-4S type [Neisseria meningitidis MC58]	gi|15676051|ref|NP 273181.1|	98.8	2E-46
contig00149-orf00002	putative DNA methylase [Neisseria gonorrhoeae FA 1090]	gi|59802181|ref|YP 208893.1|	70.43	8E-70
contig00149-orf00006	hypothetical protein NMB0119 [Neisseria meningitidis MC58]	gi|15676047|ref|NP 273177.1|	85.71	3E-121
contig00149-orf00009	DNA topoisomerase I [Neisseria meningitidis Z2491]	gi|15793183|ref|NP 283005.1|	97.92	0
contig00149-orf00010	hypothetical protein NMA0157 [Neisseria meningitidis Z2491]	gi|15793184|ref|NP 283006.1|	75.82	4E-57
contig00149-orf00011	DNA processing chain A [Neisseria meningitidis MC58]	gi|15676044|ref|NP 273174.1|	74.47	2E-13
contig00149-orf00013	DNA processing chain A [Neisseria meningitidis MC58]	gi|15676044|ref|NP 273174.1|	86.69	1E-136
contig00149-orf00016	nitrogen assimilation regulatory protein NtrX [Neisseria meningitidis MC58]	gi|15676043|ref|NP 273173.1|	71.79	2E-160
contig00149-orf00017	putative two-component system sensor kinase [Neisseria gonorrhoeae FA 1090]	gi|59802187|ref|YP 208899.1|	76.8	0
contig00149-orf00018	hypothetical protein NMA0161 [Neisseria meningitidis Z2491]	gi|15793188|ref|NP 283010.1|	73.86	2E-71
contig00149-orf00019	putative 16S RNA methyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802189|ref|YP 208901.1|	92.31	0
contig00149-orf00021	#N/A	#N/A	#N/A	#N/A
contig00149-orf00022	hypothetical protein NMA2220 [Neisseria meningitidis Z2491]	gi|15795089|ref|NP 284911.1|	41.1	0.0001
contig00149-orf00023	hypothetical protein ebA148 [Aromatoleum aromaticum EbN1]	gi|56475515|ref|YP 157104.1|	62.5	4E-54
contig00149-orf00025	methionyl-tRNA formyltransferase [Neisseria meningitidis Z2491]	gi|15793190|ref|NP 283012.1|	90.58	9E-142
contig00149-orf00028	peptide deformylase [Neisseria meningitidis Z2491]	gi|15793191|ref|NP 283013.1|	97.6	4E-88
contig00149-orf00029	hypothetical protein NMB0109 [Neisseria meningitidis MC58]	gi|15676037|ref|NP 273167.1|	57.66	1E-128
contig00149-orf00033	hypothetical protein HD0038 [Haemophilus ducreyi 35000HP]	gi|33151311|ref|NP 872664.1|	48.51	2E-34
contig00149-orf00035	coproporphyrinogen III oxidase [Haemophilus ducreyi 35000HP]	gi|33151310|ref|NP 872663.1|	66.72	0
contig00149-orf00036	TonB-dependent receptor [Chromobacterium violaceum ATCC 12472]	gi|34499351|ref|NP 903566.1|	40.34	3E-57
contig00149-orf00037	hypothetical protein NGO2113 [Neisseria gonorrhoeae FA 1090]	gi|59802413|ref|YP 209125.1|	91.26	2E-158
contig00149-orf00038	putative para-aminobenzoate synthase component [Neisseria gonorrhoeae FA 1090]	gi|59802412|ref|YP 209124.1|	80.32	0
contig00149-orf00040	hypothetical protein Bcep18194 B2943 [Burkholderia sp. 383]	gi|78063790|ref|YP 373698.1|	39.52	7E-79
contig00149-orf00041	acyl carrier protein [Neisseria meningitidis Z2491]	gi|15793075|ref|NP 282897.1|	97.44	3E-36
contig00149-orf00042	3-oxoacyl-(acyl carrier protein) synthase II [Neisseria gonorrhoeae FA 1090]	gi|59802084|ref|YP 208796.1|	90.1	0
contig00149-orf00046	hypothetical protein NGO1880 [Neisseria gonorrhoeae FA 1090]	gi|59802201|ref|YP 208913.1|	51.76	3E-37
contig00149-orf00047	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793193|ref|NP 283015.1|	50	2E-43
contig00149-orf00050	PykA [Neisseria gonorrhoeae FA 1090]	gi|59802202|ref|YP 208914.1|	93.88	0
contig00149-orf00051	hypoxanthine-guanine phosphoribosyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802343|ref|YP 209055.1|	95.65	7E-90

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contig00149-orf00052	putative sugar transport PTS system IIA protein [Neisseria gonorrhoeae FA 1090]	gi|59802344|ref|YP 209056.1|	83.45	4E-65
contig00149-orf00054	PtsH [Neisseria gonorrhoeae FA 1090]	gi|59802345|ref|YP 209057.1|	96.63	2E-41
contig00149-orf00056	phosphoenolpyruvate-protein phosphotransferase [Neisseria meningitidis Z2491]	gi|15793400|ref|NP 283222.1|	85.54	0
contig00149-orf00061	ATP-dependent helicase hrpA [Chromobacterium violaceum ATCC 12472]	gi|34496971|ref|NP 901186.1|	64.38	0
contig00150-orf00001	HAD superfamily hydrolase [Enterococcus faecalis V583]	gi|29377610|ref|NP 816764.1|	31.03	4.3
contig00150-orf00004	sensory transduction histidine kinase [Methanosarcina acetivorans C2A]	gi|20089508|ref|NP 615583.1|	37.84	2.1
contig00151-orf00003	transmembrane protein [Chromobacterium violaceum ATCC 12472]	gi|34498417|ref|NP 902632.1|	46.17	1E-85
contig00151-orf00004	dATP pyrophosphohydrolase [Neisseria meningitidis MC58]	gi|15676542|ref|NP 273685.1|	80.14	2E-64
contig00151-orf00007	inorganic pyrophosphatase [Neisseria meningitidis MC58]	gi|15676541|ref|NP 273684.1|	96.05	1E-87
contig00151-orf00009	DNA polymerase III, epsilon subunit [Neisseria meningitidis MC58]	gi|15677307|ref|NP 274462.1|	54.04	3E-136
contig00151-orf00010	hypothetical protein NMA1921 [Neisseria meningitidis Z2491]	gi|15794806|ref|NP 284628.1|	54.55	8E-70
contig00151-orf00012	phosphomethylpyrimidine kinase [Neisseria meningitidis MC58]	gi|15677466|ref|NP 274622.1|	81.34	1E-111
contig00151-orf00015	ribokinase-like domain-containing protein [Shewanella frigidimarina NCIMB	gi|114563075|ref|YP 750588.1|	50.34	4E-80
contig00151-orf00016	hypothetical protein NGO1295 [Neisseria gonorrhoeae FA 1090]	gi|59801649|ref|YP 208361.1|	80.68	3E-172
contig00151-orf00018	hypothetical protein NGO1298 [Neisseria gonorrhoeae FA 1090]	gi|59801652|ref|YP 208364.1|	95.56	8E-42
contig00151-orf00020	hypothetical protein NGO1297 [Neisseria gonorrhoeae FA 1090]	gi|59801651|ref|YP 208363.1|	98.23	0
contig00151-orf00023	hypothetical protein NMB1564 [Neisseria meningitidis MC58]	gi|15677415|ref|NP 274571.1|	90.65	5E-67
contig00151-orf00026	GntR family transcriptional regulator [Neisseria meningitidis Z2491]	gi|15794644|ref|NP 284466.1|	81.01	2E-105
contig00151-orf00028	tRNA (uracil-5-)-methyltransferase [Neisseria meningitidis MC58]	gi|15677527|ref|NP 274683.1|	76.94	4E-155
contig00151-orf00030	transmembrane protein [Chromobacterium violaceum ATCC 12472]	gi|34498006|ref|NP 902221.1|	49.19	2E-58
contig00151-orf00032	chorismate synthase [Neisseria meningitidis Z2491]	gi|15794822|ref|NP 284644.1|	94.81	0
contig00151-orf00036	hypothetical protein NMA1940 [Neisseria meningitidis Z2491]	gi|15794823|ref|NP 284645.1|	92.79	1E-53
contig00151-orf00041	iron-regulated protein FrpC [Neisseria meningitidis MC58]	gi|15677274|ref|NP 274427.1|	28.13	2E-51
contig00151-orf00042	NosL [Neisseria gonorrhoeae FA 1090]	gi|59801745|ref|YP 208457.1|	78.66	6E-72
contig00151-orf00043	hypothetical protein NGO1398 [Neisseria gonorrhoeae FA 1090]	gi|59801746|ref|YP 208458.1|	92.39	1E-118
contig00151-orf00044	putative ABC transporter, ATP-binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801747|ref|YP 208459.1|	90.27	2E-142
contig00151-orf00046	copper ABC transporter, periplasmic copper-binding protein [Neisseria meningitidis MC58]	gi|15676483|ref|NP 273622.1|	86.92	8E-171
contig00151-orf00050	nitrous-oxide reductase [Sinorhizobium meliloti 1021]	gi|16263096|ref|NP 435889.1|	67.74	0
contig00151-orf00053	regulatory protein NosR [Rhodopseudomonas palustris CGA009]	gi|39935129|ref|NP 947405.1|	48.28	0
contig00151-orf00054	acetyl-CoA carboxylase subunit beta [Neisseria meningitidis Z2491]	gi|15793849|ref|NP 283671.1|	92.1	2E-152
contig00151-orf00057	tryptophan synthase subunit alpha [Neisseria meningitidis Z2491]	gi|15793848|ref|NP 283670.1|	82.38	5E-113
contig00151-orf00059	hypothetical protein MS0943 [Mannheimia succiniciproducens MBEL55E]	gi|52424998|ref|YP 088135.1|	58.9	3E-69
contig00151-orf00060	apolipoprotein N-acyltransferase [Neisseria meningitidis MC58]	gi|15676611|ref|NP 273755.1|	76.76	0
contig00151-orf00061	RNA polymerase factor sigma-32 [Neisseria meningitidis MC58]	gi|15676610|ref|NP 273754.1|	95.47	1E-153
contig00151-orf00063	hypothetical protein NMA0501 [Neisseria meningitidis Z2491]	gi|15793500|ref|NP 283322.1|	67.39	7E-46
contig00151-orf00064	30S ribosomal protein S21 [Neisseria meningitidis Z2491]	gi|15793501|ref|NP 283323.1|	98.57	1E-20

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00151-orf00065	hypothetical protein NMA0984 [Neisseria meningitidis Z2491]	gi|15793941|ref|NP 283763.1|	96.12	1E-51
contig00151-orf00066	uracil phosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15793942|ref|NP 283764.1|	97.6	5E-113
contig00151-orf00068	hypothetical protein NMA0986 [Neisseria meningitidis Z2491]	gi|15793943|ref|NP 283765.1|	66.67	8E-19
contig00152-orf00001	hypothetical protein PD1328 [Xylella fastidiosa Temecula1]	gi|28199212|ref|NP 779526.1|	96	0.000003
contig00152-orf00003	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Neisseria meningitidis Z2491]	gi|15794672|ref|NP 284494.1|	77.96	3E-78
contig00152-orf00005	hypothetical protein BPSL2046 [Burkholderia pseudomallei K96243]	gi|53719658|ref|YP 108644.1|	34.66	3E-19
contig00152-orf00006	inner membrane protein [Neisseria meningitidis Z2491]	gi|15794561|ref|NP 284383.1|	76.5	7E-82
contig00152-orf00008	ferredoxin [Neisseria meningitidis Z2491]	gi|15794562|ref|NP 284384.1|	91.81	0
contig00152-orf00014	transketolase [Neisseria meningitidis MC58]	gi|15677313|ref|NP 274468.1|	97.57	0
contig00152-orf00018	hypothetical protein plu0461 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37524470|ref|NP 927814.1|	44.44	1E-156
contig00152-orf00021	hypothetical protein NGO0461 [Neisseria gonorrhoeae FA 1090]	gi|59800899|ref|YP 207611.1|	88.03	3E-129
contig00152-orf00022	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	68.1	3E-34
contig00154-orf00002	surface fibril protein [Neisseria meningitidis Z2491]	gi|15794144|ref|NP 283966.1|	66	1E-30
contig00155-orf00001	methylation [Rhodoferax ferrireducens T118]	gi|89900059|ref|YP 522530.1|	50	2E-21
contig00155-orf00004	#N/A	#N/A	#N/A	#N/A
contig00156-orf00001	hypothetical protein NGO0253 [Neisseria gonorrhoeae FA 1090]	gi|59800705|ref|YP 207417.1|	79.08	7E-61
contig00157-orf00001	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	91.64	1E-154
contig00158-orf00001	hypothetical protein NMA0963 [Neisseria meningitidis Z2491]	gi|15793920|ref|NP 283742.1|	88.81	3E-70
contig00161-orf00001	RNA methyltransferase [Neisseria meningitidis MC58]	gi|15676825|ref|NP 273970.1|	95.18	9E-135
contig00161-orf00003	hypothetical protein NGO0457 [Neisseria gonorrhoeae FA 1090]	gi|59800896|ref|YP 207608.1|	86.75	2E-31
contig00161-orf00004	hypothetical protein mll2427 [Mesorhizobium loti MAFF303099]	gi|13472209|ref|NP 103776.1|	58.93	2E-75
contig00161-orf00005	dihydrodipicolinate synthase [Neisseria meningitidis MC58]	gi|15676823|ref|NP 273968.1|	89.69	6E-148
contig00161-orf00006	hypothetical protein NGO0948 [Neisseria gonorrhoeae FA 1090]	gi|59801339|ref|YP 208051.1|	72.07	3E-155
contig00161-orf00008	hypothetical protein NMB1475 [Neisseria meningitidis MC58]	gi|15677329|ref|NP 274484.1|	87.69	2E-140
contig00161-orf00010	hypothetical protein NMB1496 [Neisseria meningitidis MC58]	gi|15677349|ref|NP 274504.1|	72.04	6E-78
contig00162-orf00001	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus N315]	gi|15925944|ref|NP 373477.1|	54.88	1E-94
contig00162-orf00004	hypothetical protein NMB1870 [Neisseria meningitidis MC58]	gi|15677705|ref|NP 274866.1|	40.68	5E-41
contig00162-orf00006	hypothetical protein NGO0669 [Neisseria gonorrhoeae FA 1090]	gi|59801096|ref|YP 207808.1|	65.6	4E-97
contig00162-orf00007	SpoU methylase family protein [Neisseria meningitidis Z2491]	gi|15794453|ref|NP 284275.1|	86.21	4E-128
contig00162-orf00008	extragenic suppressor protein SuhB [Neisseria meningitidis MC58]	gi|15677212|ref|NP 274365.1|	93.49	1E-139
contig00162-orf00009	#N/A	#N/A	#N/A	#N/A
contig00162-orf00010	hypothetical protein c0360 [Escherichia coli CFT073]	gi|26246258|ref|NP 752297.1|	35.88	3E-60
contig00162-orf00011	putative cytoplasmic membrane export protein [Escherichia coli CFT073]	gi|26246259|ref|NP 752298.1|	61.97	0
contig00162-orf00012	putative membrane spanning export protein [Escherichia coli CFT073]	gi|26246260|ref|NP 752299.1|	60.44	1E-135
contig00162-orf00014	CysN protein [Mannheimia succiniciproducens MBEL55E]	gi|52425306|ref|YP 088443.1|	61.24	6E-137

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00162-orf00020	major facilitator transporter [Rhodospirillum rubrum ATCC 11170]	gi|83593671|ref|YP 427423.1|	29.23	2E-21
contig00162-orf00021	hypothetical protein PA3720 [Pseudomonas aeruginosa PAO1]	gi|15598915|ref|NP 252409.1|	34.04	0.0007
contig00162-orf00022	ferric vulnibactin outer membrane receptor [Vibrio vulnificus YJ016]	gi|37676969|ref|NP 937365.1|	42.13	4E-125
contig00162-orf00024	TetR family transcriptional regulator [Novosphingobium aromaticivorans DSM 12444]	gi|87199491|ref|YP 496748.1|	32.43	5E-08
contig00162-orf00029	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	43.17	2E-59
contig00162-orf00032	gamma-glutamyl phosphate reductase [Chromobacterium violaceum ATCC	gi|34499744|ref|NP 903959.1|	65.55	5E-154
contig00162-orf00037	ADP-heptose:LPS heptosyltransferase II [Neisseria meningitidis MC58]	gi|15677379|ref|NP 274534.1|	78.14	6E-158
contig00162-orf00038	cold shock DNA-binding domain-containing protein [Pseudoalteromonas haloplanktis TAC125]	gi|77360541|ref|YP 340116.1|	32.74	4E-22
contig00162-orf00039	#N/A	#N/A	#N/A	#N/A
contig00162-orf00040	hypothetical protein NGO0319 [Neisseria gonorrhoeae FA 1090]	gi|59800766|ref|YP 207478.1|	62.64	1E-179
contig00162-orf00041	inorganic polyphosphate/ATP-NAD kinase [Neisseria gonorrhoeae FA 1090]	gi|59800834|ref|YP 207546.1|	87.16	4E-149
contig00162-orf00042	hypothetical protein NMA1018 [Neisseria meningitidis Z2491]	gi|15793974|ref|NP 283796.1|	58.95	1E-45
contig00162-orf00043	hypothetical protein NMB0809 [Neisseria meningitidis MC58]	gi|15676707|ref|NP 273851.1|	83.85	1E-126
contig00162-orf00044	hypothetical protein ebA7253 [Aromatoleum aromaticum EbN1]	gi|56479547|ref|YP 161136.1|	28.48	0.027
contig00162-orf00046	hydroxyacylglutathione hydrolase [Neisseria meningitidis MC58]	gi|15677825|ref|NP 274989.1|	77.91	3E-115
contig00162-orf00048	putative type IV pilin protein [Neisseria gonorrhoeae FA 1090]	gi|59801783|ref|YP 208495.1|	45.71	6E-18
contig00162-orf00049	AcrA/AcrE family protein [Neisseria meningitidis MC58]	gi|15676454|ref|NP 273593.1|	80.15	1E-159
contig00162-orf00052	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793705|ref|NP 283527.1|	88.84	0
contig00162-orf00054	Gst protein [Mannheimia succiniciproducens MBEL55E]	gi|52425672|ref|YP 088809.1|	55.56	4E-62
contig00163-orf00001	insertion element IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15794668|ref|NP 284490.1|	96.36	5E-25
contig00165-orf00001	transposase (fragment) [Neisseria meningitidis Z2491]	gi|15795054|ref|NP 284876.1|	97.67	2E-17
contig00167-orf00001	deoxyguanosine kinase [Chromobacterium violaceum ATCC 12472]	gi|34497089|ref|NP 901304.1|	46.6	3E-47
contig00167-orf00004	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine-pyrophosphokinase [Neisseria gonorrhoeae FA 1090]	gi|59800770|ref|YP 207482.1|	73.29	2E-50
contig00167-orf00005	hypothetical protein NMB0746 [Neisseria meningitidis MC58]	gi|15676644|ref|NP 273788.1|	84.68	1E-59
contig00167-orf00007	hypothetical protein NMB0747 [Neisseria meningitidis MC58]	gi|15676645|ref|NP 273789.1|	67.72	5E-61
contig00167-orf00009	hypothetical protein NGO0326 [Neisseria gonorrhoeae FA 1090]	gi|59800772|ref|YP 207484.1|	97.18	2E-32
contig00167-orf00013	GTP-binding protein EngA [Neisseria gonorrhoeae FA 1090]	gi|59800867|ref|YP 207579.1|	97.81	0
contig00167-orf00015	hypothetical protein NMB0853 [Neisseria meningitidis MC58]	gi|15676749|ref|NP 273894.1|	76.08	7E-73
contig00167-orf00016	histidyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15676750|ref|NP 273895.1|	96.29	0
contig00167-orf00019	hypothetical protein NMA1085 [Neisseria meningitidis Z2491]	gi|15794033|ref|NP 283855.1|	84.72	1E-132
contig00167-orf00021	cardiolipin synthetase [Psychrobacter cryohalolentis K5]	gi|93006556|ref|YP 580993.1|	44.72	2E-104
contig00167-orf00024	uroporphyrinogen decarboxylase [Neisseria meningitidis MC58]	gi|15676679|ref|NP 273823.1|	96.31	0
contig00167-orf00026	hypothetical protein NMB0779 [Neisseria meningitidis MC58]	gi|15676677|ref|NP 273821.1|	73.71	8E-171
contig00167-orf00027	hypothetical protein NGO0360 [Neisseria gonorrhoeae FA 1090]	gi|59800804|ref|YP 207516.1|	66.37	2E-124

Query	DanAnn Database Subject	Subject ID	% ID	E value
contig00167-orf00028	uroporphyrinogen-III synthase [Neisseria meningitidis MC58]	gi|15676675|ref|NP 273819.1|	65.5	2E-81
contig00167-orf00029	hypothetical protein Pcryo 0048 [Psychrobacter cryohalolentis K5]	gi|93004879|ref|YP 579316.1|	50.6	5E-12
contig00167-orf00032	heat shock protein DnaJ-like [Psychrobacter cryohalolentis K5]	gi|93004878|ref|YP 579315.1|	50.76	2E-79
contig00167-orf00033	hypothetical protein NMA1248 [Neisseria meningitidis Z2491]	gi|15794183|ref|NP 284005.1|	58.59	2E-33
contig00167-orf00035	magnesium and cobalt transport protein [Chromobacterium violaceum ATCC 12472]	gi|34496718|ref|NP 900933.1|	50.51	9E-83
contig00167-orf00036	putative Mg2+ transporter protein [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	gi|73661864|ref|YP 300645.1|	59.38	3E-19
contig00167-orf00038	acyl CoA thioester hydrolase family protein [Neisseria meningitidis MC58]	gi|15677335|ref|NP 274490.1|	90	3E-80
contig00167-orf00041	hypothetical protein RPB 1952 [Rhodopseudomonas palustris HaA2]	gi|86749075|ref|YP 485571.1|	54.55	3E-53
contig00168-orf00001	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	91.45	5E-78
contig00169-orf00001	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794386|ref|NP 284208.1|	95.97	2E-66

Appendix C

BLAST analysis of *N. sicca* 4320 ORFs with nr database.

The amino acid sequences of the identified *N. sicca* 4320 ORFs were BLASTed against the NCBI nr database. Query: *N. sicca* 4320 ORF. Subject: Database match to query. Subject ID: Identification number of match to query. %ID: Percent identity between query and subject. E Value: Expectation value; number of similar matches that would occur by chance.

Query	NR Database Subject	Subject ID	% ID	E value
contig00001-orf00001	glutathione synthetase [Neisseria gonorrhoeae FA 1090]	gi|59801576|ref|YP 208288.1|	93.04	2E-165
contig00001-orf00003	diacylglycerol kinase [Neisseria gonorrhoeae FA 1090]	gi|59801575|ref|YP 208287.1|	73.81	8E-46
contig00001-orf00004	hypothetical protein NMA1745 [Neisseria meningitidis Z2491]	gi|15794638|ref|NP 284460.1|	85.31	1E-66
contig00001-orf00005	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Neisseria meningitidis Z2491]	gi|15794637|ref|NP 284459.1|	94.81	0
contig00001-orf00008	long-chain-fatty-acid--CoA-ligase [Neisseria meningitidis MC58]	gi|15677406|ref|NP 274562.1|	89.67	0
contig00001-orf00010	PhoH-related protein [Neisseria meningitidis MC58]	gi|15676741|ref|NP 273886.1|	85.06	5E-143
contig00001-orf00012	guanosine-3',5'-bis(diphosphate) 3'-pyrophophohydrolase [Neisseria meningitidis Z2491]	gi|15794802|ref|NP 284624.1|	89.55	0
contig00001-orf00013	DNA-directed RNA polymerase omega chain [Neisseria meningitidis MC58]	gi|15677509|ref|NP 274665.1|	92.65	2E-29
contig00001-orf00015	KguA [Neisseria gonorrhoeae FA 1090]	gi|59801662|ref|YP 208374.1|	78.54	4E-85
contig00001-orf00016	adenine phosphoribosyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801663|ref|YP 208375.1|	90.32	1E-90
contig00001-orf00019	putative soluble lytic murein transglycosylase [Neisseria meningitidis MC58]	gi|15677779|ref|NP 274943.1|	71.9	0
contig00001-orf00020	#N/A	gi|13517946|gb|AAK29066.1|AF345 899 2	55.17	8E-37
contig00002-orf00001	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	gi|59801514|ref|YP 208226.1|	44.93	5E-11
contig00002-orf00003	hypothetical protein NMA1167 [Neisseria meningitidis Z2491]	gi|15794112|ref|NP 283934.1|	58.22	1E-98
contig00002-orf00005	hypothetical protein NMA1168 [Neisseria meningitidis Z2491]	gi|15794113|ref|NP 283935.1|	69.44	5E-08
contig00002-orf00006	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801535|ref|YP 208247.1|	53.97	4E-10
contig00002-orf00007	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801534|ref|YP 208246.1|	75	3E-13
contig00002-orf00008	hypothetical protein NMA0778 [Neisseria meningitidis Z2491]	gi|15793753|ref|NP 283575.1|	78.57	5E-27
contig00003-orf00001	putative phage integrase [Shigella boydii Sb227]	gi|82542847|ref|YP 406794.1|	51.08	1E-62
contig00004-orf00003	#N/A	gi|53732540|ref|ZP 00154607.2|	72.35	0
contig00004-orf00006	NH(3)-dependent NAD synthetase [Neisseria meningitidis Z2491]	gi|15794469|ref|NP 284291.1|	77.1	5E-113
contig00004-orf00008	putative cation transport ATPase, E1-E2 family protein [Photobacterium sp. SKA34]	gi|89076680|ref|ZP 01162972.1|	42.42	6.2
contig00004-orf00009	site-specific recombinase [Neisseria meningitidis Z2491]	gi|15794385|ref|NP 284207.1|	86.04	0
contig00005-orf00001	hypothetical protein NGO0318 [Neisseria gonorrhoeae FA 1090]	gi|59800765|ref|YP 207477.1|	89.49	0
contig00005-orf00002	acetate kinase [Neisseria meningitidis MC58]	gi|15677371|ref|NP 274526.1|	93.72	0
contig00005-orf00006	hypothetical protein NMB1517 [Neisseria meningitidis MC58]	gi|15677370|ref|NP 274525.1|	74.26	3E-35
contig00005-orf00007	FixS [Neisseria gonorrhoeae FA 1090]	gi|59801361|ref|YP 208073.1|	95.83	1E-20
contig00005-orf00008	putative transporter [Neisseria meningitidis MC58]	gi|15677368|ref|NP 274523.1|	81.73	0
contig00006-orf00001	endopeptidase [Neisseria meningitidis Z2491]	gi|15794419|ref|NP 284241.1|	96.12	1E-101
contig00006-orf00003	trigger factor [Neisseria meningitidis Z2491]	gi|15794420|ref|NP 284242.1|	96.33	0
contig00006-orf00007	lipoprotein [Chromobacterium violaceum ATCC 12472]	gi|34498817|ref|NP 903032.1|	44.38	2E-34
contig00006-orf00009	phosphoenolpyruvate synthase [Neisseria meningitidis MC58]	gi|15676521|ref|NP 273662.1|	97.36	0
contig00006-orf00010	hypothetical protein NMA0827 [Neisseria meningitidis Z2491]	gi|15793798|ref|NP 283620.1|	87.18	4E-137

Query	NR Database Subject	Subject ID	% ID	E value
contig00006-orf00013	#N/A	gi|42629454|ref|ZP 00155000.1|	53.41	3E-77
contig00007-orf00001	integrase/recombinase XerD [Neisseria meningitidis MC58]	gi|15676649|ref|NP 273793.1|	70.45	2E-108
contig00008-orf00001	oligoribonuclease [Neisseria meningitidis Z2491]	gi|15793584|ref|NP 283406.1|	87.01	6E-88
contig00008-orf00005	enoyl-(acyl carrier protein) reductase [Neisseria meningitidis Z2491]	gi|15795023|ref|NP 284845.1|	96.54	3E-138
contig00008-orf00008	large conductance mechanosensitive channel protein [Methylobacillus flagellatus KT]	gi|91775002|ref|YP 544758.1|	63.83	1E-28
contig00008-orf00011	Hsp33-like chaperonin [Neisseria meningitidis Z2491]	gi|15793446|ref|NP 283268.1|	83.45	3E-118
contig00008-orf00014	ubiquinone biosynthesis protein [Chromobacterium violaceum ATCC 12472]	gi|34498422|ref|NP 902637.1|	43.97	3E-130
contig00008-orf00016	#N/A	gi|7274420|gb|AAF44765.1|AF2351 48 1	86.92	1E-61
contig00008-orf00017	hypothetical protein NMB2002 [Neisseria meningitidis MC58]	gi|15677830|ref|NP 274994.1|	88.41	3E-30
contig00008-orf00022	putative amino acid symporter [Neisseria meningitidis MC58]	gi|15676121|ref|NP 273252.1|	87.1	0
contig00008-orf00026	glucose-inhibited division protein B [Neisseria meningitidis Z2491]	gi|15793106|ref|NP 282928.1|	74.76	8E-85
contig00008-orf00028	hypothetical protein MK1300 [Methanopyrus kandleri AV19]	gi|20094736|ref|NP 614583.1|	52	6.2
contig00008-orf00032	ribosomal large subunit pseudouridine synthase C [Neisseria meningitidis Z2491]	gi|15793099|ref|NP 282921.1|	87.31	2E-152
contig00008-orf00039	ribonuclease E [Neisseria meningitidis MC58]	gi|15676123|ref|NP 273254.1|	78.95	0
contig00008-orf00039	ribonuclease E [Neisseria meningitidis MC58]	gi|15676123|ref|NP 273254.1|	51.43	1.1
contig00008-orf00041	hypothetical protein NMB1129 [Neisseria meningitidis MC58]	gi|15677006|ref|NP 274158.1|	76.47	3E-29
contig00008-orf00043	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793078|ref|NP 282900.1|	81.44	2E-166
contig00008-orf00046	integral membrane signal transducer protein [Neisseria meningitidis Z2491]	gi|15794998|ref|NP 284820.1|	73.25	1E-153
contig00008-orf00048	50S ribosomal protein L3 [Neisseria meningitidis MC58]	gi|15676069|ref|NP 273200.1|	99.07	1E-105
contig00008-orf00049	50S ribosomal protein L4 [Neisseria meningitidis MC58]	gi|15676070|ref|NP 273201.1|	99.03	3E-110
contig00008-orf00050	50S ribosomal protein L23 [Neisseria meningitidis Z2491]	gi|15793155|ref|NP 282977.1|	100	6E-27
contig00008-orf00052	50S ribosomal protein L2 [Neisseria meningitidis Z2491]	gi|15793154|ref|NP 282976.1|	99.28	1E-141
contig00008-orf00053	30S ribosomal protein S19 [Neisseria gonorrhoeae FA 1090]	gi|59802156|ref|YP 208868.1|	100	3E-09
contig00008-orf00054	50S ribosomal protein L22 [Neisseria meningitidis MC58]	gi|15676074|ref|NP 273205.1|	99.08	6E-54
contig00008-orf00055	30S ribosomal protein S3 [Neisseria meningitidis MC58]	gi|15676075|ref|NP 273206.1|	96.31	2E-114
contig00008-orf00056	50S ribosomal protein L16 [Neisseria meningitidis MC58]	gi|15676076|ref|NP 273207.1|	96.43	1E-14
contig00008-orf00057	50S ribosomal protein L29 [Neisseria meningitidis MC58]	gi|15676077|ref|NP 273208.1|	95.24	1E-26
contig00008-orf00058	50S ribosomal protein L24 [Neisseria meningitidis MC58]	gi|15676080|ref|NP 273211.1|	94.03	2E-30
contig00008-orf00059	50S ribosomal protein L5 [Neisseria gonorrhoeae FA 1090]	gi|59802148|ref|YP 208860.1|	100	3E-11
contig00008-orf00060	30S ribosomal protein S14 [Neisseria meningitidis MC58]	gi|15676082|ref|NP 273213.1|	94.06	5E-47
contig00008-orf00062	50S ribosomal protein L6 [Neisseria meningitidis MC58]	gi|15676084|ref|NP 273215.1|	96.08	1E-49
contig00008-orf00064	50S ribosomal protein L15 [Neisseria meningitidis MC58]	gi|15676088|ref|NP 273219.1|	83.53	1E-33
contig00008-orf00065	preprotein translocase subunit SecY [Neisseria meningitidis MC58]	gi|15676089|ref|NP 273220.1|	86.27	0
contig00008-orf00066	30S ribosomal protein S13 [Chromobacterium violaceum ATCC 12472]	gi|34499618|ref|NP 903833.1|	100	2E-12
contig00008-orf00067	DNA-directed RNA polymerase subunit alpha [Neisseria meningitidis MC58]	gi|15676095|ref|NP 273226.1|	94.21	6E-174

Query	NR Database Subject	Subject ID	% ID	E value
contig00008-orf00070	oxidoreductase [Neisseria meningitidis Z2491]	gi|15793372|ref|NP 283194.1|	93.41	3E-174
contig00008-orf00071	hypothetical protein PFL 2399 [Pseudomonas fluorescens Pf-5]	gi|70729767|ref|YP 259506.1|	45.39	2E-31
contig00008-orf00072	hypothetical protein MS2110 [Mannheimia succiniciproducens MBEL55E]	gi|52426165|ref|YP 089302.1|	53.42	1E-59
contig00008-orf00075	thiamin-phosphate pyrophosphorylase [Neisseria meningitidis MC58]	gi|15677891|ref|NP 275059.1|	95.08	4E-84
contig00008-orf00076	putative oxidoreductase [Gluconobacter oxydans 621H]	gi|58038345|ref|YP 190314.1|	59.23	2E-99
contig00008-orf00077	hypothetical protein Atu0997 [Agrobacterium tumefaciens str. C58]	gi|15888340|ref|NP 354021.1|	63.74	2E-27
contig00008-orf00079	cysteinyl-tRNA synthetase [Mesoplasma florum L1]	gi|50364902|ref|YP 053327.1|	31.09	1.2
contig00008-orf00080	thiamine biosynthesis protein ThiS [Neisseria meningitidis MC58]	gi|15677892|ref|NP 275060.1|	93.75	1E-26
contig00008-orf00081	thiazole synthase [Neisseria meningitidis MC58]	gi|15677893|ref|NP 275061.1|	98.09	5E-145
contig00008-orf00083	DNA polymerase I [Neisseria meningitidis Z2491]	gi|15793464|ref|NP 283286.1|	92.21	0
contig00008-orf00086	hypothetical protein NMB2064 [Neisseria meningitidis MC58]	gi|15677886|ref|NP 275054.1|	81.61	0
contig00008-orf00087	hypothetical protein NMA0371 [Neisseria meningitidis Z2491]	gi|15793379|ref|NP 283201.1|	72	5E-23
contig00008-orf00090	hypothetical protein NMA0573 [Neisseria meningitidis Z2491]	gi|15793564|ref|NP 283386.1|	80.81	2E-42
contig00008-orf00091	protein-L-isoaspartate O-methyltransferase [Neisseria meningitidis Z2491]	gi|15793563|ref|NP 283385.1|	92.2	4E-108
contig00008-orf00094	hypothetical protein NMB1886 [Neisseria meningitidis MC58]	gi|15677721|ref|NP 274882.1|	95.71	4E-86
contig00008-orf00096	triosephosphate isomerase [Neisseria meningitidis MC58]	gi|15677722|ref|NP 274883.1|	97.25	7E-139
contig00008-orf00097	preprotein translocase subunit SecG [Neisseria meningitidis MC58]	gi|15677723|ref|NP 274884.1|	93.48	1E-15
contig00008-orf00098	putative prophage integrase [Escherichia coli CFT073]	gi|26250313|ref|NP 756353.1|	48.06	1E-29
contig00008-orf00100	hypothetical protein NMB2018 [Neisseria meningitidis MC58]	gi|15677843|ref|NP 275010.1|	70.35	1E-76
contig00008-orf00102	conserved hypothetical protein [Marinobacter aquaeolei VT8]	gi|77953576|ref|ZP 00817983.1|	52.2	2E-45
contig00008-orf00103	COG1434: Uncharacterized conserved protein [Magnetospirillum magnetotacticum MS-1]	gi|46202066|ref|ZP 00208367.1|	40.83	9E-18
contig00008-orf00104	#N/A	gi|19568856|gb|AAL91941.1|AF482013 1	91.67	0
contig00008-orf00106	CcsA-related protein [Neisseria meningitidis MC58]	gi|15676218|ref|NP 273350.1|	78.73	1E-102
contig00009-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	91.67	6E-37
contig00009-orf00003	hypothetical protein NMA0426A [Neisseria meningitidis Z2491]	gi|15793431|ref|NP 283253.1|	78.67	4E-24
contig00009-orf00004	hypothetical protein PBPRB0630 [Photobacterium profundum SS9]	gi|54302310|ref|YP 132303.1|	44.1	1E-100
contig00009-orf00005	hypothetical protein PBPRB0631 [Photobacterium profundum SS9]	gi|54302311|ref|YP 132304.1|	52.46	2E-133
contig00009-orf00006	HrpA [Neisseria gonorrhoeae FA 1090]	gi|59801559|ref|YP 208271.1|	93.42	0
contig00010-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676979|ref|NP 274130.1|	100	2E-19
contig00010-orf00003	hypothetical protein NMB1066 [Neisseria meningitidis MC58]	gi|15676950|ref|NP 274099.1|	62.22	1E-73
contig00010-orf00004	cell-division protein [Neisseria meningitidis Z2491]	gi|15794199|ref|NP 284021.1|	92.99	0
contig00010-orf00004	cell-division protein [Neisseria meningitidis Z2491]	gi|15794199|ref|NP 284021.1|	40.85	0.0002
contig00010-orf00007	hypothetical protein NGO0899 [Neisseria gonorrhoeae FA 1090]	gi|59801297|ref|YP 208009.1|	94.3	5E-63
contig00010-orf00009	polynucleotide phosphorylase/polyadenylase [Neisseria meningitidis Z2491]	gi|15793926|ref|NP 283748.1|	96.83	0
contig00010-orf00012	hypothetical protein NGO0532 [Neisseria gonorrhoeae FA 1090]	gi|59800970|ref|YP 207682.1|	61.11	4E-124

Query	NR Database Subject	Subject ID	% ID	E value
contig00010-orf00013	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794379|ref|NP 284201.1|	60.17	7E-115
contig00010-orf00015	polysaccharide modification protein [Neisseria meningitidis Z2491]	gi|15794378|ref|NP 284200.1|	75.94	0
contig00010-orf00018	COG0058: Glucan phosphorylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143802|ref|ZP 00133910.2|	64.66	0
contig00010-orf00020	pullulanase and related glycosidases [Actinobacillus succinogenes 130Z]	gi|75430352|ref|ZP 00732736.1|	50.9	0
contig00010-orf00021	PREDICTED: similar to Atrophin-1 (Dentatorubral-pallidoluysian atrophy protein) [Canis familiaris]	gi|73997728|ref|XP 854385.1|	39.39	3.7
contig00010-orf00022	AcrA protein [Mannheimia succiniciproducens MBEL55E]	gi|52425356|ref|YP 088493.1|	49.28	5E-69
contig00010-orf00024	DNA damage repair protein Mus42 [Aspergillus fumigatus Af293]	gi|70991795|ref|XP 750746.1|	35	3.7
contig00010-orf00025	anthranilate phosphoribosyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801562|ref|YP 208274.1|	88.01	5E-146
contig00010-orf00027	anthranilate synthase component II [Neisseria gonorrhoeae FA 1090]	gi|59801563|ref|YP 208275.1|	89.58	1E-97
contig00010-orf00030	prophage CP4-57 regulatory [Ralstonia eutropha JMP134]	gi|73542058|ref|YP 296578.1|	40.32	6E-08
contig00010-orf00032	hypothetical protein SAR11 0011 [Candidatus Pelagibacter ubique HTCC1062]	gi|71082720|ref|YP 265439.1|	38.53	1E-13
contig00010-orf00035	COG0270: Site-specific DNA methylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|53728781|ref|ZP 00135132.2|	61.54	5E-118
contig00010-orf00036	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801497|ref|YP 208209.1|	84.92	1E-155
contig00010-orf00038	imidazoleglycerol-phosphate dehydratase [Sulfolobus acidocaldarius DSM 639]	gi|70607313|ref|YP 256183.1|	32.84	0.96
contig00010-orf00039	single-stranded binding protein [Neisseria meningitidis MC58]	gi|15677316|ref|NP 274471.1|	60.47	5E-50
contig00010-orf00040	TonB-dependent receptor [Xanthomonas campestris pv. campestris str. ATCC 33913]	gi|77747725|ref|NP 635445.2|	33.96	0.57
contig00010-orf00041	surface protein C PspC [Streptococcus pneumoniae]	gi|4838563|gb|AAD31043.1|	23.63	0.024
contig00010-orf00042	Rac prophage; exonuclease VIII, 5' -> 3' specific dsDNA exonuclease [Escherichia coli str. K-12 substr. MG1655]	gi|16129311|ref|NP 415866.1|	37.27	3E-38
contig00010-orf00043	putative periplasmic protein [Dehalococcoides sp. CBDB1]	gi|73748881|ref|YP 308120.1|	30.16	4.8
contig00010-orf00045	putative Zn-dependent protease with chaperone function [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]	gi|62179503|ref|YP 215920.1|	32.43	0.12
contig00010-orf00047	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71651400|ref|XP 814379.1|	30.3	0.56
contig00010-orf00050	hypothetical protein [Plasmodium chabaudi chabaudi]	gi|70937411|ref|XP 739517.1|	28.7	0.43
contig00010-orf00051	hypothetical protein BL01431 [Bacillus licheniformis ATCC 14580]	gi|52080664|ref|YP 079455.1|	44.83	8.1
contig00010-orf00053	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801955|ref|YP 208667.1|	90.91	3E-65
contig00010-orf00055	putative CI protein [Haemophilus phage Aaphi23]	gi|31544010|ref|NP 852735.1|	61.9	3E-43
contig00010-orf00056	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800918|ref|YP 207630.1|	97.22	0.00007
contig00010-orf00057	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801960|ref|YP 208672.1|	79.03	5E-18
contig00010-orf00058	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800921|ref|YP 207633.1|	77.33	6E-27
contig00010-orf00059	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801963|ref|YP 208675.1|	65.28	5E-20
contig00010-orf00061	putative DNA replication protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801964|ref|YP 208676.1|	80.98	3E-83

Query	NR Database Subject	Subject ID	% ID	E value
contig00010-orf00062	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800924|ref|YP 207636.1|	56.52	1E-09
contig00010-orf00065	hypothetical protein CHGG 09668 [Chaetomium globosum CBS 148.51]	gi|116203569|ref|XP 001227595.1|	50	3.7
contig00010-orf00067	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800927|ref|YP 207639.1|	63.11	8E-32
contig00010-orf00068	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801470|ref|YP 208182.1|	41.98	4E-25
contig00010-orf00069	hypothetical protein Nmul A1530 [Nitrosospira multiformis ATCC 25196]	gi|82702659|ref|YP 412225.1|	32.73	0.085
contig00010-orf00071	COG2963: Transposase and inactivated derivatives [Escherichia coli HS]	gi|75194485|ref|ZP 00704555.1|	63.08	3E-45
contig00010-orf00072	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800933|ref|YP 207645.1|	90.49	0
contig00010-orf00073	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800934|ref|YP 207646.1|	88.66	0
contig00010-orf00074	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800935|ref|YP 207647.1|	83.96	9E-137
contig00010-orf00075	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800936|ref|YP 207648.1|	91.32	0
contig00010-orf00076	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800937|ref|YP 207649.1|	82.54	2E-22
contig00010-orf00077	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800938|ref|YP 207650.1|	72.73	7E-69
contig00010-orf00078	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800939|ref|YP 207651.1|	70	7E-38
contig00010-orf00079	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800940|ref|YP 207652.1|	89.44	3E-72
contig00010-orf00081	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800941|ref|YP 207653.1|	82.88	3E-120
contig00010-orf00082	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800942|ref|YP 207654.1|	85.26	1E-39
contig00010-orf00084	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800943|ref|YP 207655.1|	92.05	5E-43
contig00010-orf00085	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800944|ref|YP 207656.1|	92.96	8E-106
contig00010-orf00086	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800945|ref|YP 207657.1|	89.53	2E-74
contig00010-orf00086	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800945|ref|YP 207657.1|	71.01	3E-47
contig00010-orf00087	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800946|ref|YP 207658.1|	71.11	1E-54
contig00010-orf00088	DNA topoisomerase IV subunit A [Geobacillus kaustophilus HTA426]	gi|56420285|ref|YP 147603.1|	30.3	0.4
contig00010-orf00090	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800948|ref|YP 207660.1|	85.11	0
contig00010-orf00090	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800948|ref|YP 207660.1|	60.29	1E-72
contig00010-orf00091	hypothetical protein NGO0511 [Neisseria gonorrhoeae FA 1090]	gi|59800949|ref|YP 207661.1|	36.17	1E-10
contig00010-orf00092	putative tail length tape measure protein, putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800960|ref|YP 207672.1|	73.79	0
contig00010-orf00093	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800951|ref|YP 207663.1|	53.49	2E-35
contig00010-orf00095	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800952|ref|YP 207664.1|	52.13	1E-13
contig00010-orf00096	conserved hypothetical protein [Pseudomonas putida F1]	gi|82737966|ref|ZP 00900808.1|	39.13	0.0000005
contig00010-orf00097	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800957|ref|YP 207669.1|	53.1	3E-25
contig00010-orf00100	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801148|ref|YP 207860.1|	39.68	0.0007
contig00010-orf00101	PREDICTED: similar to Peripheral-type benzodiazepine receptor-associated protein 1 (PRAX-1) (Peripheral benzodiazepine receptor-interacting protein) (PBR-IP) (RIM-binding protein 1) (RIM-BP1) [Homo sapiens]	gi|89071856|ref|XP 947217.1|	25.88	0.11
contig00010-orf00102	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain containing protein [Tetrahymena thermophila SB210]	gi|89302248|gb|EAS00236.1|	35.37	0.25

Query	NR Database Subject	Subject ID	% ID	E value
contig00010-orf00103	prophage PSPPH01, site-specific recombinase phage integrase family protein [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71734594|ref|YP 272965.1|	42.34	2E-76
contig00010-orf00104	YALI0B01276p [Yarrowia lipolytica]	gi|50545681|ref|XP 500379.1|	29.69	0.56
contig00010-orf00106	conserved hypothetical protein [Polaribacter sp. MED152]	gi|86134350|ref|ZP 01052932.1|	45.74	2E-67
contig00010-orf00107	hypothetical protein CV 3590 [Chromobacterium violaceum ATCC 12472]	gi|34499045|ref|NP 903260.1|	45.65	0.008
contig00010-orf00109	hypothetical protein NGO0818 [Neisseria gonorrhoeae FA 1090]	gi|59801229|ref|YP 207941.1|	49.23	1E-09
contig00010-orf00111	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677112|ref|NP 274264.1|	97.6	0
contig00010-orf00113	superoxide dismutase [Neisseria meningitidis Z2491]	gi|15794051|ref|NP 283873.1|	98.45	3E-102
contig00010-orf00114	replicative DNA helicase [Neisseria meningitidis Z2491]	gi|15794052|ref|NP 283874.1|	94.23	0
contig00010-orf00115	hypothetical protein NMA1106 [Neisseria meningitidis Z2491]	gi|15794053|ref|NP 283875.1|	53.92	5E-61
contig00010-orf00116	putative type IV pilus assembly protein PilV [Neisseria meningitidis MC58]	gi|15676783|ref|NP 273928.1|	46.27	2E-30
contig00010-orf00117	membrane protein [Neisseria meningitidis Z2491]	gi|15794055|ref|NP 283877.1|	45.32	1E-69
contig00010-orf00120	putative type IV pilin-like protein [Neisseria gonorrhoeae FA 1090]	gi|59800895|ref|YP 207607.1|	47.71	8E-30
contig00010-orf00123	pantoate--beta-alanine ligase [Neisseria meningitidis MC58]	gi|15676767|ref|NP 273912.1|	85.2	7E-132
contig00010-orf00126	3-methyl-2-oxobutanoate hydroxymethyltransferase [Neisseria meningitidis Z2491]	gi|15794036|ref|NP 283858.1|	92.75	1E-115
contig00010-orf00127	spermidine synthase [Neisseria meningitidis MC58]	gi|15676765|ref|NP 273910.1|	88.21	1E-135
contig00010-orf00128	glutamyl-tRNA reductase [Neisseria gonorrhoeae FA 1090]	gi|59801748|ref|YP 208460.1|	84.82	0
contig00010-orf00129	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	90.24	9E-15
contig00010-orf00130	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	100	2E-23
contig00010-orf00130	IS1106A3 transposase [Neisseria meningitidis Z2491]	gi|15793461|ref|NP 283283.1|	90	2E-23
contig00010-orf00133	hypothetical protein Sden 1113 [Shewanella denitrificans OS217]	gi|91792473|ref|YP 562124.1|	35.44	2E-08
contig00010-orf00134	#N/A	gi|53732781|ref|ZP 00155061.2|	59.09	6.3
contig00010-orf00136	hypothetical protein TTHERM 00617800 [Tetrahymena thermophila SB210]	gi|89299669|gb|EAR97657.1|	30.91	0.49
contig00010-orf00137	hypothetical protein PnapDRAFT 4901 [Polaromonas naphthalenivorans CJ2]	gi|84710211|ref|ZP 01019146.1|	35.29	2E-15
contig00010-orf00137	hypothetical protein PnapDRAFT 4901 [Polaromonas naphthalenivorans CJ2]	gi|84710211|ref|ZP 01019146.1|	40.3	0.00001
contig00010-orf00138	hypothetical protein NTHI0420 [Haemophilus influenzae 86-028NP]	gi|68248909|ref|YP 248021.1|	41.43	2E-24
contig00010-orf00139	putative transposase [Neisseria meningitidis MC58]	gi|15677452|ref|NP 274608.1|	55.32	0.000003
contig00011-orf00001	cell wall biosynthesis glycosyltransferase-like protein [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]	gi|78355477|ref|YP 386926.1|	50	0.01
contig00011-orf00002	glycosyltransferase [Lactobacillus salivarius UCC118]	gi|90962544|ref|YP 536460.1|	27.54	7E-14
contig00011-orf00003	virulence factor MviN [Neisseria meningitidis MC58]	gi|15676201|ref|NP 273333.1|	93.04	1E-168
contig00011-orf00004	Virulence factor MVIN-like [Azotobacter vinelandii AvOP]	gi|67153816|ref|ZP 00415561.1|	74.23	5E-47
contig00011-orf00004	Virulence factor MVIN-like [Azotobacter vinelandii AvOP]	gi|67153816|ref|ZP 00415561.1|	63.41	5E-47
contig00011-orf00005	hypothetical protein NGO1718 [Neisseria gonorrhoeae FA 1090]	gi|59802039|ref|YP 208751.1|	94.44	0.43
contig00011-orf00008	thiol:disulfide interchange protein DsbA [Neisseria meningitidis MC58]	gi|15676202|ref|NP 273334.1|	84.65	1E-83
contig00011-orf00010	GTPase ObgE [Neisseria gonorrhoeae FA 1090]	gi|59802298|ref|YP 209010.1|	97.14	0

Query	NR Database Subject	Subject ID	% ID	E value
contig00011-orf00011	cysteinyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793358|ref|NP 283180.1|	97.46	0
contig00011-orf00012	putative acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802423|ref|YP 209135.1|	67.06	3E-55
contig00011-orf00014	50S ribosomal protein L31 [Neisseria meningitidis MC58]	gi|15677786|ref|NP 274950.1|	91.55	1E-34
contig00011-orf00015	hypothetical protein NGO2128 [Neisseria gonorrhoeae FA 1090]	gi|59802426|ref|YP 209138.1|	73.36	0
contig00011-orf00019	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793492|ref|NP 283314.1|	75.71	3E-58
contig00011-orf00020	hypothetical protein NMB1959 [Neisseria meningitidis MC58]	gi|15677789|ref|NP 274953.1|	60.63	3E-37
contig00011-orf00021	hypothetical protein NGO2122 [Neisseria gonorrhoeae FA 1090]	gi|59802420|ref|YP 209132.1|	95.83	5E-65
contig00011-orf00022	putative siderophore receptor [Neisseria meningitidis]	gi|6900452|emb|CAB72047.1|	90.49	9E-151
contig00011-orf00024	putative siderophore receptor [Neisseria meningitidis]	gi|6900458|emb|CAB72050.1|	93.53	0
contig00011-orf00026	phosphopantetheine adenylyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802386|ref|YP 209098.1|	77.64	2E-70
contig00011-orf00028	hypothetical protein NMB2020 [Neisseria meningitidis MC58]	gi|15677845|ref|NP 275012.1|	71.49	7E-79
contig00011-orf00030	hypothetical protein Aple02000468 [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|32033879|ref|ZP 00134150.1|	35.07	4E-10
contig00011-orf00031	orotate phosphoribosyltransferase [Neisseria meningitidis MC58]	gi|15677709|ref|NP 274870.1|	91.51	2E-98
contig00011-orf00033	hypothetical protein NGO0028 [Neisseria gonorrhoeae FA 1090]	gi|59800497|ref|YP 207209.1|	66.67	1E-26
contig00011-orf00034	N-acetylglutamate synthase [Neisseria meningitidis Z2491]	gi|15793571|ref|NP 283393.1|	64.02	8E-135
contig00011-orf00036	putative phage protein [Shewanella putrefaciens CN-32]	gi|77813731|ref|ZP 00813004.1|	43.17	5E-86
contig00011-orf00038	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA [Neisseria meningitidis Z2491]	gi|15793103|ref|NP 282925.1|	97.29	0
contig00011-orf00039	hypothetical protein R07G3.6 [Caenorhabditis elegans]	gi|17535559|ref|NP 495595.1|	39.53	2.1
contig00011-orf00041	uridylate kinase [Neisseria gonorrhoeae FA 1090]	gi|59802282|ref|YP 208994.1|	99.16	2E-115
contig00011-orf00043	elongation factor Ts [Neisseria meningitidis MC58]	gi|15677922|ref|NP 275090.1|	97.01	1E-134
contig00011-orf00045	30S ribosomal protein S2 [Neisseria meningitidis MC58]	gi|15677921|ref|NP 275089.1|	98.19	2E-120
contig00011-orf00047	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793341|ref|NP 283163.1|	84.85	6E-25
contig00011-orf00048	hypothetical protein NMA0330 [Neisseria meningitidis Z2491]	gi|15793342|ref|NP 283164.1|	87.56	4E-89
contig00011-orf00049	hypothetical protein NMA0331 [Neisseria meningitidis Z2491]	gi|15793343|ref|NP 283165.1|	71.35	6E-71
contig00011-orf00051	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	gi|15219480|ref|NP 177491.1|	40.48	6.3
contig00011-orf00052	malate:quinone oxidoreductase [Neisseria meningitidis Z2491]	gi|15793344|ref|NP 283166.1|	90.57	0
contig00011-orf00055	hypothetical protein NMA2208 [Neisseria meningitidis Z2491]	gi|15795077|ref|NP 284899.1|	88.32	1E-152
contig00011-orf00057	solvent tolerance protein [Neisseria meningitidis Z2491]	gi|15795076|ref|NP 284898.1|	62.17	0
contig00011-orf00058	peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58]	gi|15676205|ref|NP 273337.1|	67.2	1E-104
contig00011-orf00063	putative signalling protein [Xanthomonas campestris pv. vesicatoria str. 85-10]	gi|78048416|ref|YP 364591.1|	30.77	6.2
contig00011-orf00068	phosphoesterase, PA-phosphatase-related protein [Deinococcus geothermalis DSM 11300]	gi|94972215|ref|YP 594255.1|	58.33	1E-17
contig00011-orf00069	hypothetical protein NMB0276 [Neisseria meningitidis MC58]	gi|15676200|ref|NP 273332.1|	72.03	1E-118
contig00011-orf00070	putative protease [Neisseria meningitidis MC58]	gi|15677940|ref|NP 275112.1|	66.15	4E-103
contig00011-orf00072	dnaJ protein [Neisseria meningitidis MC58]	gi|15675997|ref|NP 273124.1|	81.75	8E-162

Query	NR Database Subject	Subject ID	% ID	E value
contig00011-orf00075	leucyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59800478|ref|YP 207190.1|	93.62	0
contig00011-orf00077	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.74	3E-14
contig00011-orf00078	type II restriction enzyme DpnI [Neisseria meningitidis MC58]	gi|15677728|ref|NP 274891.1|	95.51	1E-150
contig00011-orf00082	putative modification methylase [Neisseria gonorrhoeae FA 1090]	gi|59800480|ref|YP 207192.1|	88.07	1E-69
contig00011-orf00082	putative modification methylase [Neisseria gonorrhoeae FA 1090]	gi|59800480|ref|YP 207192.1|	94.74	1E-69
contig00011-orf00083	putative modification methylase [Neisseria gonorrhoeae FA 1090]	gi|59800480|ref|YP 207192.1|	90.24	2E-39
contig00011-orf00084	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15793483|ref|NP 283305.1|	59.17	4E-91
contig00011-orf00087	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603318|ref|NP 246392.1|	79.43	0
contig00011-orf00088	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	93.75	0.0002
contig00011-orf00088	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	68.75	0.0002
contig00011-orf00090	hypothetical protein NGO1889 [Neisseria gonorrhoeae FA 1090]	gi|59802206|ref|YP 208918.1|	56	1E-91
contig00011-orf00094	sodium/glutamate symport carrier protein [Neisseria meningitidis MC58]	gi|15676017|ref|NP 273147.1|	89.55	3E-177
contig00011-orf00095	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793077|ref|NP 282899.1|	84.44	2E-130
contig00011-orf00097	3-demethylubiquinone-9 3-methyltransferase [Neisseria meningitidis Z2491]	gi|15793415|ref|NP 283237.1|	78.02	7E-106
contig00011-orf00101	hypothetical protein MS1484 [Mannheimia succiniciproducens MBEL55E]	gi|52425539|ref|YP 088676.1|	65.68	2E-101
contig00011-orf00102	30S ribosomal protein S10 [Neisseria meningitidis MC58]	gi|15676068|ref|NP 273198.1|	99.03	3E-51
contig00012-orf00001	hypothetical protein NMA2164 [Neisseria meningitidis Z2491]	gi|15795035|ref|NP 284857.1|	90.61	0
contig00012-orf00002	hypothetical protein NMA2160 [Neisseria meningitidis Z2491]	gi|15795031|ref|NP 284853.1|	83.67	4E-65
contig00012-orf00003	octaprenyl-diphosphate synthase [Neisseria meningitidis MC58]	gi|15676243|ref|NP 273375.1|	89.51	5E-159
contig00012-orf00005	50S ribosomal protein L21 [Neisseria meningitidis MC58]	gi|15676242|ref|NP 273374.1|	99.02	4E-50
contig00012-orf00007	50S ribosomal protein L27 [Neisseria meningitidis MC58]	gi|15676241|ref|NP 273373.1|	98.89	1E-44
contig00012-orf00009	thiamine biosynthesis protein ThiC [Neisseria meningitidis Z2491]	gi|15793405|ref|NP 283227.1|	97.63	0
contig00012-orf00010	CcpR [Neisseria gonorrhoeae FA 1090]	gi|59802088|ref|YP 208800.1|	82.76	1E-179
contig00012-orf00012	glycerol-3-phosphate dehydrogenase [Neisseria meningitidis Z2491]	gi|15793383|ref|NP 283205.1|	91.79	5E-167
contig00012-orf00013	hypothetical protein NMB2059 [Neisseria meningitidis MC58]	gi|15677881|ref|NP 275049.1|	67.59	7E-31
contig00012-orf00015	hypothetical protein NGO2023 [Neisseria gonorrhoeae FA 1090]	gi|59802331|ref|YP 209043.1|	67	6E-30
contig00012-orf00017	50S ribosomal protein L13 [Neisseria meningitidis MC58]	gi|15677879|ref|NP 275047.1|	99.25	1E-71
contig00012-orf00018	30S ribosomal protein S9 [Neisseria gonorrhoeae FA 1090]	gi|59802333|ref|YP 209045.1|	97.69	3E-66
contig00012-orf00020	hypothetical protein NGO2162 [Neisseria gonorrhoeae FA 1090]	gi|59802456|ref|YP 209168.1|	64.6	4E-34
contig00012-orf00022	glutathione-regulated potassium-efflux system protein [Neisseria meningitidis MC58]	gi|15676136|ref|NP 273267.1|	83.99	0
contig00013-orf00001	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676806|ref|NP 273951.1|	75.76	0.000002
contig00013-orf00002	IS30 family transposase [Neisseria meningitidis MC58]	gi|15676806|ref|NP 273951.1|	85.37	4E-54
contig00013-orf00004	peptidyl-prolyl cis-trans isomerase A [Neisseria meningitidis Z2491]	gi|15794370|ref|NP 284192.1|	69.7	7E-60
contig00013-orf00006	hypothetical protein NMB1030 [Neisseria meningitidis MC58]	gi|15676917|ref|NP 274064.1|	91.62	5E-87
contig00013-orf00009	cell division protein FtsK [Neisseria meningitidis MC58]	gi|15677180|ref|NP 274333.1|	83.23	0

Query	NR Database Subject	Subject ID	% ID	E value
contig00013-orf00012	putative sodium-dependent transport protein [Neisseria gonorrhoeae FA 1090]	gi|59801034|ref|YP 207746.1|	94.69	0
contig00013-orf00013	FxsA [Neisseria meningitidis Z2491]	gi|15793898|ref|NP 283720.1|	59.59	3E-42
contig00013-orf00014	hypothetical protein NMB1369 [Neisseria meningitidis MC58]	gi|15677234|ref|NP 274387.1|	83.33	1E-46
contig00013-orf00016	hypothetical protein NMB1370 [Neisseria meningitidis MC58]	gi|15677235|ref|NP 274388.1|	62.2	4E-38
contig00014-orf00002	hypothetical protein pJS-B 08 [Neisseria meningitidis]	gi|30250501|ref|NP 842572.1|	82.58	3E-83
contig00014-orf00005	hypothetical protein pJS-B 06 [Neisseria meningitidis]	gi|30250500|ref|NP 842571.1|	46.25	6E-16
contig00015-orf00001	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677260|ref|NP 274413.1|	88.54	6E-96
contig00016-orf00001	hypothetical protein NGO2139 [Neisseria gonorrhoeae FA 1090]	gi|59802436|ref|YP 209148.1|	91.19	5E-118
contig00016-orf00003	transcriptional regulator CysB-like protein [Neisseria meningitidis Z2491]	gi|15794980|ref|NP 284802.1|	84.49	1E-152
contig00016-orf00004	Omp3 [Neisseria gonorrhoeae FA 1090]	gi|59801906|ref|YP 208618.1|	75	3E-83
contig00016-orf00006	seryl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15794826|ref|NP 284648.1|	94.2	0
contig00016-orf00007	30S ribosomal protein S6 [Neisseria meningitidis Z2491]	gi|15794430|ref|NP 284252.1|	96.81	1E-38
contig00016-orf00008	primosomal replication protein [Neisseria meningitidis MC58]	gi|15677188|ref|NP 274341.1|	75.36	4E-24
contig00016-orf00009	30S ribosomal protein S18 [Neisseria meningitidis MC58]	gi|15677187|ref|NP 274340.1|	97.37	5E-35
contig00016-orf00010	50S ribosomal protein L9 [Neisseria gonorrhoeae FA 1090]	gi|59801015|ref|YP 207727.1|	94.03	5E-58
contig00016-orf00013	putative murein hydrolase [Neisseria gonorrhoeae FA 1090]	gi|59801054|ref|YP 207766.1|	70.69	6E-141
contig00016-orf00015	aldose 1-epimerase [Salmonella typhimurium LT2]	gi|16764640|ref|NP 460255.1|	29.73	0.0000009
contig00016-orf00017	DNA polymerase III subunits gamma and tau [Neisseria gonorrhoeae FA 1090]	gi|59801160|ref|YP 207872.1|	71.76	0
contig00016-orf00019	hypothetical protein NMA1657 [Neisseria meningitidis Z2491]	gi|15794551|ref|NP 284373.1|	85.59	2E-49
contig00016-orf00021	#N/A	gi|6449094|gb|AAF08823.1|AF1940 79 10	72.31	2E-92
contig00016-orf00024	hypothetical protein NMB0541 [Neisseria meningitidis MC58]	gi|15676447|ref|NP 273586.1|	59.26	1E-51
contig00016-orf00025	hypothetical protein NMA0721 [Neisseria meningitidis Z2491]	gi|15793698|ref|NP 283520.1|	56.25	3E-18
contig00016-orf00026	(p)ppGpp synthetase [Streptococcus thermophilus CNRZ1066]	gi|55822133|ref|YP 140574.1|	29.33	2.1
contig00016-orf00029	hypothetical protein NGO1421 [Neisseria gonorrhoeae FA 1090]	gi|59801765|ref|YP 208477.1|	91.67	1E-13
contig00016-orf00030	thiamine biosynthesis lipoprotein ApbE [Neisseria meningitidis MC58]	gi|15676468|ref|NP 273607.1|	73.31	3E-133
contig00016-orf00033	S-adenosylmethionine synthetase [Neisseria gonorrhoeae FA 1090]	gi|59800567|ref|YP 207279.1|	98.16	0
contig00016-orf00035	#N/A	gi|12644548|sp|Q9RML6|PDXJ NEIMC	96.28	8E-128
contig00016-orf00038	holo-(acyl-carrier protein) synthase [Neisseria meningitidis Z2491]	gi|15794913|ref|NP 284735.1|	95.2	3E-53
contig00017-orf00002	methylenetetrahydrofolate dehydrogenase/cyclohydrolase [Neisseria meningitidis Z2491]	gi|15793364|ref|NP 283186.1|	85.87	1E-136
contig00017-orf00006	isochorismatase hydrolase [Desulfuromonas acetoxidans DSM 684]	gi|95929044|ref|ZP 01311789.1|	42.94	1E-32
contig00017-orf00007	GCN5-related N-acetyltransferase [Psychrobacter cryohalolentis K5]	gi|93006865|ref|YP 581302.1|	47.73	4E-41
contig00017-orf00008	ClpXP protease specificity-enhancing factor [Neisseria meningitidis Z2491]	gi|15793498|ref|NP 283320.1|	66.34	7E-30
contig00017-orf00009	stringent starvation protein A [Neisseria meningitidis MC58]	gi|15677783|ref|NP 274947.1|	94.03	7E-107

Query	NR Database Subject	Subject ID	% ID	E value
contig00017-orf00011	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Neisseria meningitidis Z2491]	gi|15795024|ref|NP 284846.1|	98.53	1E-139
contig00017-orf00012	unnamed protein product [Tetraodon nigroviridis]	gi|47228428|emb|CAG05248.1|	36.54	4.8
contig00017-orf00016	glutamate-ammonia-ligase adenylyltransferase [Neisseria meningitidis Z2491]	gi|15793067|ref|NP 282889.1|	96.75	0
contig00017-orf00019	lipid A biosynthesis lauroyl acyltransferase [Neisseria meningitidis MC58]	gi|15677639|ref|NP 274798.1|	72.5	2E-110
contig00017-orf00021	ArsR family transcriptional regulator [Neisseria meningitidis MC58]	gi|15676312|ref|NP 273447.1|	68.82	1E-28
contig00017-orf00024	exodeoxyribonuclease III [Neisseria meningitidis MC58]	gi|15676313|ref|NP 273448.1|	89.8	9E-136
contig00018-orf00002	hypothetical protein NMA0256 [Neisseria meningitidis Z2491]	gi|15793274|ref|NP 283096.1|	92.68	2E-36
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	24.91	3E-121
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	25.36	3E-118
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	24.67	1E-77
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	23.4	3E-74
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	24.59	7E-72
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	24.12	2E-64
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	22.89	5E-46
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	25.91	2E-35
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	23.79	1E-34
contig00018-orf00010	hypothetical protein AsucDRAFT 1054 [Actinobacillus succinogenes 130Z]	gi|75429524|ref|ZP 00732297.1|	22.91	1E-30
contig00019-orf00001	hypothetical protein MS0981 [Mannheimia succiniciproducens MBEL55E]	gi|52425036|ref|YP 088173.1|	81.32	1E-81
contig00020-orf00001	phosphoribosylaminoimidazole-succinocarboxamide synthase [Neisseria gonorrhoeae FA 1090]	gi|59800779|ref|YP 207491.1|	89.9	4E-149
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	46.41	1E-31
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	39.83	2E-30
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	38.74	4E-27
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	45.13	1E-26
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	42.67	2E-20
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	44	2E-09
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	46.67	0.0000001
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	26.24	0.000003
contig00020-orf00005	hypothetical protein alr7304 [Nostoc sp. PCC 7120]	gi|17233320|ref|NP 490410.1|	45.45	0.0001
contig00020-orf00006	orf189 2 [Paramecium aurelia]	gi|8928620|ref|NP 059425.1|	38.78	8
contig00020-orf00007	putative reductase [Neisseria gonorrhoeae FA 1090]	gi|59800778|ref|YP 207490.1|	70.63	2E-106
contig00020-orf00009	hypothetical protein NMB0753 [Neisseria meningitidis MC58]	gi|15676651|ref|NP 273795.1|	78.95	2E-31
contig00020-orf00010	putative bacterioferritin-associated ferredoxin [Neisseria meningitidis MC58]	gi|15676650|ref|NP 273794.1|	80.3	1E-25
contig00021-orf00001	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	97.14	2E-13
contig00021-orf00003	hypothetical protein NMA0184 [Neisseria meningitidis Z2491]	gi|15793212|ref|NP 283034.1|	47.85	3E-94
contig00021-orf00004	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793875|ref|NP 283697.1|	78.34	1E-95

Query	NR Database Subject	Subject ID	% ID	E value
contig00021-orf00005	ribonuclease HII [Neisseria meningitidis MC58]	gi|15676119|ref|NP 273250.1|	82.81	3E-84
contig00021-orf00009	lipid-A-disaccharide synthase [Neisseria meningitidis Z2491]	gi|15793098|ref|NP 282920.1|	82.01	4E-168
contig00021-orf00010	hypothetical protein NGO2121 [Neisseria gonorrhoeae FA 1090]	gi|59802419|ref|YP 209131.1|	73.26	3E-111
contig00021-orf00011	hypothetical protein NMA0489 [Neisseria meningitidis Z2491]	gi|15793488|ref|NP 283310.1|	83.33	3E-35
contig00021-orf00014	periplasmic transport protein [Neisseria meningitidis Z2491]	gi|15793487|ref|NP 283309.1|	93.37	6E-77
contig00021-orf00016	hypothetical protein NGO2118 [Neisseria gonorrhoeae FA 1090]	gi|59802416|ref|YP 209128.1|	85.11	6E-73
contig00021-orf00019	hypothetical protein NMB1965 [Neisseria meningitidis MC58]	gi|15677795|ref|NP 274959.1|	98.06	2E-125
contig00021-orf00022	ABC transport ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793484|ref|NP 283306.1|	98.12	6E-144
contig00021-orf00026	hypothetical protein NGO1701 [Neisseria gonorrhoeae FA 1090]	gi|59802022|ref|YP 208734.1|	62.91	3E-30
contig00021-orf00027	cell division protein FtsZ [Neisseria meningitidis MC58]	gi|15676339|ref|NP 273475.1|	81.41	3E-157
contig00021-orf00028	cell division protein [Neisseria meningitidis MC58]	gi|15676338|ref|NP 273474.1|	73.67	7E-170
contig00021-orf00030	cell division protein [Neisseria meningitidis Z2491]	gi|15794937|ref|NP 284759.1|	60.33	1E-71
contig00021-orf00032	D-alanine--D-alanine ligase [Neisseria meningitidis MC58]	gi|15676336|ref|NP 273472.1|	93.09	6E-153
contig00021-orf00035	#N/A	gi|25008815|sp|Q9JSZ8|MURC NEIMA	94.67	0
contig00021-orf00037	TcmP [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603187|ref|NP 246260.1|	55.15	5E-83
contig00021-orf00040	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentape pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Neisseria meningitidis Z2491]	gi|15794940|ref|NP 284762.1|	95.49	2E-180
contig00021-orf00042	cell division protein [Neisseria meningitidis MC58]	gi|15676333|ref|NP 273469.1|	61.63	3E-123
contig00021-orf00045	periplasmic sensor hybrid histidine kinase [Rhodobacter sphaeroides 2.4.1]	gi|77462965|ref|YP 352469.1|	38.78	1.6
contig00021-orf00047	6-aminohexanoate-cyclic-dimer hydrolase [Deinococcus radiodurans R1]	gi|15805271|ref|NP 293959.1|	40.51	3E-56
contig00021-orf00049	hypothetical protein BLi00325 [Bacillus licheniformis ATCC 14580]	gi|52784148|ref|YP 089977.1|	40.79	2E-09
contig00021-orf00051	PREDICTED: similar to hypothetical protein FLJ22104 [Gallus gallus]	gi|50731193|ref|XP 417208.1|	38	2.1
contig00021-orf00052	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [Neisseria meningitidis MC58]	gi|15676332|ref|NP 273468.1|	97.08	0
contig00021-orf00054	hypothetical protein NMB0419 [Neisseria meningitidis MC58]	gi|15676331|ref|NP 273467.1|	74.47	6E-79
contig00021-orf00055	hypothetical protein Daro 1997 [Dechloromonas aromatica RCB]	gi|71907626|ref|YP 285213.1|	50.82	1E-30
contig00022-orf00001	50S ribosomal protein L33 [Neisseria meningitidis MC58]	gi|15676239|ref|NP 273371.1|	98.04	3E-22
contig00022-orf00002	50S ribosomal protein L28 [Neisseria meningitidis MC58]	gi|15676238|ref|NP 273370.1|	100	1E-17
contig00022-orf00005	multidrug resistance translocase [Neisseria meningitidis Z2491]	gi|15795039|ref|NP 284861.1|	81.4	0
contig00022-orf00007	fatty acid efflux system protein [Neisseria meningitidis MC58]	gi|15676235|ref|NP 273367.1|	64.38	7E-111
contig00022-orf00009	acetate kinase [Neisseria meningitidis MC58]	gi|15676347|ref|NP 273483.1|	94.49	0
contig00022-orf00011	hypothetical protein NMA2051 [Neisseria meningitidis Z2491]	gi|15794929|ref|NP 284751.1|	96.14	0
contig00022-orf00013	aconitate hydratase [Neisseria meningitidis Z2491]	gi|15794930|ref|NP 284752.1|	96.38	0
contig00022-orf00014	aconitate hydratase [Neisseria meningitidis MC58]	gi|15676345|ref|NP 273481.1|	97.83	2E-132
contig00022-orf00014	aconitate hydratase [Neisseria meningitidis MC58]	gi|15676345|ref|NP 273481.1|	95.18	2E-132
contig00022-orf00016	hypothetical protein PFL 2353 [Pseudomonas fluorescens Pf-5]	gi|70729721|ref|YP 259460.1|	42.66	4E-38

Query	NR Database Subject	Subject ID	% ID	E value
contig00022-orf00019	hypothetical protein NMB0432 [Neisseria meningitidis MC58]	gi|15676344|ref|NP 273480.1|	98.85	3E-101
contig00022-orf00020	hypothetical protein OG2516 18480 [Oceanicola granulosus HTCC2516]	gi|89068366|ref|ZP 01155769.1|	35.71	0.63
contig00022-orf00021	methylcitrate synthase [Neisseria gonorrhoeae FA 1090]	gi|59801861|ref|YP 208573.1|	94.01	0
contig00022-orf00025	2-methylisocitrate lyase [Neisseria meningitidis MC58]	gi|15676342|ref|NP 273478.1|	97.37	2E-143
contig00022-orf00031	drug-export protein [Bacillus licheniformis ATCC 14580]	gi|52080543|ref|YP 079334.1|	38.81	2E-81
contig00023-orf00001	putative phosphate acetyltransferase Pta [Neisseria meningitidis MC58]	gi|15676533|ref|NP 273674.1|	85.4	0
contig00023-orf00003	amino-acid transport protein [Neisseria meningitidis Z2491]	gi|15793414|ref|NP 283236.1|	92.49	0
contig00023-orf00004	carbonate dehydratase [Cytophaga hutchinsonii ATCC 33406]	gi|110636727|ref|YP 676934.1|	61.02	3E-15
contig00023-orf00005	hypothetical protein [Neurospora crassa OR74A]	gi|85093349|ref|XP 959676.1|	67.15	3E-49
contig00023-orf00007	COG0659: Sulfate permease and related transporters (MFS superfamily) [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|32033895|ref|ZP 00134166.1|	58.55	4E-118
contig00023-orf00008	hypothetical protein NGO1163 [Neisseria gonorrhoeae FA 1090]	gi|59801529|ref|YP 208241.1|	57.14	0.56
contig00023-orf00013	dTDP-4-keto-6-deoxy-D-glucose-3,6-epimerase [Neisseria meningitidis MC58]	gi|15676014|ref|NP 273144.1|	93.3	4E-89
contig00023-orf00014	diaminopimelate decarboxylase [Neisseria meningitidis Z2491]	gi|15793470|ref|NP 283292.1|	94.58	0
contig00023-orf00015	hypothetical protein NMB1977 [Neisseria meningitidis MC58]	gi|15677806|ref|NP 274970.1|	83.33	1E-12
contig00023-orf00016	frataxin-like protein [Neisseria gonorrhoeae FA 1090]	gi|59802401|ref|YP 209113.1|	95.33	6E-54
contig00023-orf00018	S-ribosylhomocysteinase [Neisseria meningitidis Z2491]	gi|15793465|ref|NP 283287.1|	95.83	3E-89
contig00023-orf00019	rarD protein [Psychrobacter cryohalolentis K5]	gi|93005188|ref|YP 579625.1|	46.67	5E-60
contig00023-orf00020	sugar-phosphate nucleotidyl transferase [Neisseria meningitidis Z2491]	gi|15793605|ref|NP 283427.1|	68.83	1E-83
contig00023-orf00022	putative 4-hydroxyphenylacetate 3-hydroxylase, small subunit [Neisseria meningitidis MC58]	gi|15677678|ref|NP 274839.1|	77.48	1E-66
contig00023-orf00023	MarR family transcriptional regulator [Neisseria meningitidis MC58]	gi|15677679|ref|NP 274840.1|	93.39	8E-58
contig00023-orf00025	thioredoxin [Neisseria meningitidis MC58]	gi|15677681|ref|NP 274842.1|	50	1E-45
contig00023-orf00026	glyceraldehyde 3-phosphate dehydrogenase [Neisseria gonorrhoeae]	gi|27573095|gb|AAO19947.1|	88.86	9E-175
contig00023-orf00029	hypothetical protein NMA1951 [Neisseria meningitidis Z2491]	gi|15794834|ref|NP 284656.1|	50.79	0
contig00023-orf00030	chorismate mutase-related protein [Neisseria meningitidis MC58]	gi|15677540|ref|NP 274696.1|	50.41	9E-61
contig00023-orf00034	#N/A	gi|4887081|gb|AAD32176.1|AF125563 1	97.79	0
contig00023-orf00036	ATP-dependent protease ATP-binding subunit [Neisseria meningitidis MC58]	gi|15677237|ref|NP 274390.1|	87.17	0
contig00023-orf00040	putative D-alanyl-D-alanine-endopeptidase [Neisseria gonorrhoeae FA 1090]	gi|59800773|ref|YP 207485.1|	80.36	3E-117
contig00023-orf00041	hypothetical protein NMA0562 [Neisseria meningitidis Z2491]	gi|15793554|ref|NP 283376.1|	50.59	4E-65
contig00024-orf00005	isoleucyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677669|ref|NP 274830.1|	94.52	0
contig00024-orf00007	putative heme degradation protein [Hahella chejuensis KCTC 2396]	gi|83648114|ref|YP 436549.1|	44.83	0.000002
contig00024-orf00010	hypothetical protein PM1078 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602943|ref|NP 246015.1|	48.97	6E-68
contig00024-orf00012	hypothetical protein PM1079 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602944|ref|NP 246016.1|	61.69	4E-79
contig00024-orf00014	hypothetical protein PM1080 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602945|ref|NP 246017.1|	46.55	7E-50
contig00024-orf00016	thermoresistant gluconokinase [Neisseria meningitidis MC58]	gi|15677853|ref|NP 275020.1|	84.3	3E-82

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contig00024-orf00019	gluconate permease [Neisseria meningitidis Z2491]	gi|15793418|ref|NP 283240.1|	87.64	2E-173
contig00024-orf00021	sigma-54 modulation protein [Chromobacterium violaceum ATCC 12472]	gi|34498788|ref|NP 903003.1|	56.7	5E-27
contig00024-orf00023	RNA polymerase factor sigma-54 [Dechloromonas aromatica RCB]	gi|71909758|ref|YP 287345.1|	40.07	8E-46
contig00024-orf00024	putative RNA polymerase sigma-54 factor RpoN [Neisseria meningitidis MC58]	gi|15676143|ref|NP 273274.1|	75.25	2E-48
contig00024-orf00024	putative RNA polymerase sigma-54 factor RpoN [Neisseria meningitidis MC58]	gi|15676143|ref|NP 273274.1|	75.38	2E-48
contig00024-orf00026	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676271|ref|NP 273405.1|	94.26	4E-124
contig00024-orf00028	hypothetical protein NGO1606 [Neisseria gonorrhoeae FA 1090]	gi|59801934|ref|YP 208646.1|	80.11	2E-61
contig00024-orf00029	hypothetical protein NMB0354 [Neisseria meningitidis MC58]	gi|15676269|ref|NP 273403.1|	75.56	2E-76
contig00024-orf00031	hypothetical protein NMA2134 [Neisseria meningitidis Z2491]	gi|15795005|ref|NP 284827.1|	93.26	1E-90
contig00024-orf00032	transcriptional activator protein METR [Neisseria meningitidis Z2491]	gi|15793389|ref|NP 283211.1|	91.5	3E-153
contig00024-orf00033	hypothetical protein NGO2028 [Neisseria gonorrhoeae FA 1090]	gi|59802336|ref|YP 209048.1|	72.29	2E-105
contig00024-orf00034	ubiquinol-cytochrome c reductase iron-sulfur subunit [Neisseria meningitidis MC58]	gi|15677875|ref|NP 275043.1|	91.19	9E-91
contig00024-orf00035	PetB [Neisseria gonorrhoeae FA 1090]	gi|59802338|ref|YP 209050.1|	96.66	0
contig00024-orf00036	cytochrome C1 precursor [Neisseria meningitidis MC58]	gi|15677873|ref|NP 275041.1|	94.74	2E-148
contig00024-orf00037	hypothetical protein NGO2019 [Neisseria gonorrhoeae FA 1090]	gi|59802327|ref|YP 209039.1|	70.08	5E-78
contig00024-orf00040	iron(III) ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15677818|ref|NP 274982.1|	86.11	7E-112
contig00024-orf00042	iron(III) ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15677819|ref|NP 274983.1|	88.36	1E-125
contig00024-orf00043	lipopolysaccharide modification acyltransferase [Neisseria meningitidis Z2491]	gi|15793609|ref|NP 283431.1|	37.95	3E-94
contig00024-orf00044	hypothetical protein NMB1992 [Neisseria meningitidis MC58]	gi|15677820|ref|NP 274984.1|	85.1	6E-90
contig00024-orf00045	iron(III) ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677821|ref|NP 274985.1|	83.73	8E-118
contig00024-orf00047	hypothetical protein NMB1785 [Neisseria meningitidis MC58]	gi|15677625|ref|NP 274784.1|	84	2E-30
contig00024-orf00049	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Neisseria meningitidis MC58]	gi|15677694|ref|NP 274855.1|	89.18	2E-175
contig00024-orf00051	hypothetical protein NMA0611 [Neisseria meningitidis Z2491]	gi|15793601|ref|NP 283423.1|	82.73	2E-160
contig00025-orf00003	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	96.64	0
contig00025-orf00003	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	47.83	0.0000001
contig00026-orf00001	hypothetical protein NGO1291 [Neisseria gonorrhoeae FA 1090]	gi|59801645|ref|YP 208357.1|	97.93	1E-123
contig00026-orf00003	periplasmic binding protein MntC [Neisseria gonorrhoeae]	gi|11139295|gb|AAG30300.1|	82.24	4E-130
contig00026-orf00005	hypothetical protein NMB0863 [Neisseria meningitidis MC58]	gi|15676759|ref|NP 273904.1|	74.07	0.0002
contig00026-orf00008	hypothetical protein NMB0863 [Neisseria meningitidis MC58]	gi|15676759|ref|NP 273904.1|	80	0.000001
contig00026-orf00008	hypothetical protein NMB0863 [Neisseria meningitidis MC58]	gi|15676759|ref|NP 273904.1|	76.47	0.000001
contig00026-orf00011	hypothetical protein NMA1072 [Neisseria meningitidis Z2491]	gi|15794020|ref|NP 283842.1|	91.89	4E-35
contig00026-orf00011	hypothetical protein NMA1072 [Neisseria meningitidis Z2491]	gi|15794020|ref|NP 283842.1|	100	4E-35
contig00026-orf00012	hypothetical protein NGO0162 [Neisseria gonorrhoeae FA 1090]	gi|59800618|ref|YP 207330.1|	89.74	2E-34
contig00026-orf00014	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794015|ref|NP 283837.1|	86.7	4E-102

Query	NR Database Subject	Subject ID	% ID	E value
contig00026-orf00016	electron transfer flavoprotein-ubiquinone oxidoreductase [Neisseria meningitidis MC58]	gi|15676486|ref|NP 273625.1|	96.93	0
contig00026-orf00019	oxidoreductase [Neisseria meningitidis Z2491]	gi|15794150|ref|NP 283972.1|	96.95	0
contig00026-orf00020	xylose transporter [Robiginitalea biformata HTCC2501]	gi|88803966|ref|ZP 01119486.1|	59.26	2E-09
contig00026-orf00021	D-lactate dehydrogenase [Neisseria meningitidis MC58]	gi|15676888|ref|NP 274033.1|	96.8	0
contig00026-orf00023	macrophage infectivity potentiator-related protein [Neisseria meningitidis MC58]	gi|15676886|ref|NP 274031.1|	68.42	6.3
contig00026-orf00024	macrophage infectivity potentiator-related protein [Neisseria meningitidis MC58]	gi|15676886|ref|NP 274031.1|	92.31	1E-89
contig00026-orf00026	acyl-CoA dehydrogenase family protein [Neisseria meningitidis MC58]	gi|15676885|ref|NP 274030.1|	87.02	6E-172
contig00026-orf00029	putative rubredoxin [Neisseria gonorrhoeae FA 1090]	gi|59801284|ref|YP 207996.1|	98.21	6E-30
contig00026-orf00030	hypothetical protein NMB1701 [Neisseria meningitidis MC58]	gi|15677549|ref|NP 274705.1|	58.95	2E-26
contig00026-orf00031	putative acyltransferase [Neisseria meningitidis MC58]	gi|15677546|ref|NP 274702.1|	63.86	1E-23
contig00026-orf00032	acyl carrier protein [Neisseria meningitidis MC58]	gi|15677544|ref|NP 274700.1|	82.5	8E-29
contig00026-orf00034	hypothetical protein ACIAD2340 [Acinetobacter sp. ADP1]	gi|50085431|ref|YP 046941.1|	41.03	0.0000005
contig00027-orf00001	hypothetical protein NMB0484 [Neisseria meningitidis MC58]	gi|15676395|ref|NP 273531.1|	100	5E-31
contig00027-orf00002	hypothetical protein NMA1168 [Neisseria meningitidis Z2491]	gi|15794113|ref|NP 283935.1|	97.92	3E-48
contig00027-orf00003	hypothetical protein NMA1167 [Neisseria meningitidis Z2491]	gi|15794112|ref|NP 283934.1|	95.35	0
contig00027-orf00005	outer membrane lipoprotein carrier protein [Neisseria meningitidis MC58]	gi|15676525|ref|NP 273666.1|	87.92	2E-94
contig00027-orf00008	hypothetical protein NMB0621 [Neisseria meningitidis MC58]	gi|15676524|ref|NP 273665.1|	92	3E-143
contig00027-orf00011	potassium/proton-divalent cation antiporter [Bacillus subtilis subsp. subtilis str. 168]	gi|16079718|ref|NP 390542.1|	57.48	4E-100
contig00027-orf00014	phosphoglycolate phosphatase [Neisseria meningitidis MC58]	gi|15676523|ref|NP 273664.1|	88.84	8E-91
contig00027-orf00015	malate oxidoreductase (NAD) [Neisseria meningitidis MC58]	gi|15676569|ref|NP 273713.1|	97.18	0
contig00027-orf00016	thymidylate kinase [Neisseria meningitidis Z2491]	gi|15793838|ref|NP 283660.1|	84.39	6E-94
contig00027-orf00018	hypothetical protein Pcryo 1832 [Psychrobacter cryohalolentis K5]	gi|93006656|ref|YP 581093.1|	30.38	0.0000001
contig00027-orf00019	pili assembly chaperone [Xanthomonas campestris pv. vesicatoria str. 85-10]	gi|78047039|ref|YP 363214.1|	40.26	5E-38
contig00027-orf00020	outer membrane usher protein FasD [Xanthomonas campestris pv. campestris str. ATCC 33913]	gi|77747802|ref|NP 636753.2|	33.38	3E-103
contig00027-orf00023	hypothetical protein Pcryo 1832 [Psychrobacter cryohalolentis K5]	gi|93006656|ref|YP 581093.1|	34.48	5E-13
contig00027-orf00024	hypothetical protein NMA1773 [Neisseria meningitidis Z2491]	gi|15794666|ref|NP 284488.1|	84.83	3E-135
contig00027-orf00026	hypothetical protein OA2633 09589 [Oceanicaulis alexandrii HTCC2633]	gi|83944871|ref|ZP 00957237.1|	26.69	1E-14
contig00027-orf00027	hypothetical protein NMA1086 [Neisseria meningitidis Z2491]	gi|15794034|ref|NP 283856.1|	84.83	6E-100
contig00027-orf00031	DNA topoisomerase IV subunit B [Neisseria meningitidis Z2491]	gi|15794824|ref|NP 284646.1|	97.73	0
contig00027-orf00033	dinucleoside polyphosphate hydrolase [Neisseria meningitidis MC58]	gi|15677531|ref|NP 274687.1|	92.53	4E-96
contig00027-orf00035	COG2116: Formate/nitrite family of transporters [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143738|ref|ZP 00204560.1|	70	5E-100
contig00027-orf00036	conserved hypothetical protein [Actinobacillus succinogenes 130Z]	gi|75434759|ref|ZP 00733251.1|	51.32	3E-124
contig00027-orf00038	putative sodium/alanine symporter [Neisseria meningitidis MC58]	gi|15676104|ref|NP 273235.1|	91.14	0

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contig00027-orf00039	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15794381|ref|NP 284203.1|	93.77	3E-176
contig00027-orf00040	hypothetical protein NMB1100 [Neisseria meningitidis MC58]	gi|15676980|ref|NP 274131.1|	85.71	0.087
contig00028-orf00001	#N/A	gi|13517946|gb|AAK29066.1|AF345 899 2	55.46	3E-27
contig00028-orf00002	preprotein translocase subunit SecB [Neisseria gonorrhoeae FA 1090]	gi|59800576|ref|YP 207288.1|	89.58	4E-68
contig00028-orf00003	glutaredoxin [Neisseria meningitidis Z2491]	gi|15793656|ref|NP 283478.1|	82.35	5E-35
contig00028-orf00006	putative ribonuclease G / cytoplasmic axial filament protein [Neisseria gonorrhoeae FA 1090]	gi|59800573|ref|YP 207285.1|	94.57	0
contig00028-orf00008	#N/A	gi|10880475|gb|AAG24269.1|AF139 614 1	80.28	7E-83
contig00028-orf00011	#N/A	gi|10880470|gb|AAG24266.1|AF139 612 3	61	3E-125
contig00028-orf00013	3-ketoacyl-(acyl-carrier-protein) reductase [Neisseria meningitidis MC58]	gi|15677752|ref|NP 274915.1|	96.37	1E-119
contig00028-orf00014	hypothetical protein Psyc 1209 [Psychrobacter arcticus 273-4]	gi|71065767|ref|YP 264494.1|	36.73	2E-57
contig00028-orf00015	hypothetical protein Psyc 1209 [Psychrobacter arcticus 273-4]	gi|71065767|ref|YP 264494.1|	35.17	1E-47
contig00028-orf00017	glycosyl transferase [Pyrococcus abyssi GE5]	gi|14521365|ref|NP 126841.1|	28.7	4E-13
contig00028-orf00018	putative glycosyl transferase [Burkholderia thailandensis E264]	gi|83721331|ref|YP 442023.1|	30.86	9E-23
contig00028-orf00019	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793530|ref|NP 283352.1|	77.74	0
contig00028-orf00020	acyl-carrier-protein S-malonyltransferase [Neisseria meningitidis Z2491]	gi|15793531|ref|NP 283353.1|	90.91	7E-141
contig00028-orf00023	cold shock DNA-binding domain-containing protein [Nitrosomonas europaea ATCC 19718]	gi|30248726|ref|NP 840796.1|	34.2	1E-21
contig00028-orf00027	3-oxoacyl-(acyl carrier protein) synthase III [Neisseria meningitidis Z2491]	gi|15793533|ref|NP 283355.1|	87.19	5E-158
contig00028-orf00029	hypothetical protein NMB1925 [Neisseria meningitidis MC58]	gi|15677755|ref|NP 274919.1|	72.5	1E-87
contig00028-orf00030	hypothetical protein NMA0529 [Neisseria meningitidis Z2491]	gi|15793526|ref|NP 283348.1|	88.08	7E-123
contig00028-orf00033	glutathione S-transferase [Rhodobacter sphaeroides 2.4.1]	gi|77464476|ref|YP 353980.1|	43.01	4E-35
contig00028-orf00035	hypothetical protein lpl2094 [Legionella pneumophila str. Lens]	gi|54295014|ref|YP 127429.1|	47.58	2E-45
contig00028-orf00037	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Neisseria meningitidis Z2491]	gi|15794127|ref|NP 283949.1|	96.04	0
contig00028-orf00040	hypothetical protein NMB1126 [Neisseria meningitidis MC58]	gi|15677003|ref|NP 274155.1|	79.02	1E-93
contig00028-orf00041	hypothetical protein NMB1125 [Neisseria meningitidis MC58]	gi|15677002|ref|NP 274154.1|	52.58	4E-21
contig00028-orf00042	COG4380: Uncharacterized protein conserved in bacteria [Pseudomonas aeruginosa C3719]	gi|84318263|ref|ZP 00966689.1|	75	0.000002
contig00028-orf00043	COG4380: Uncharacterized protein conserved in bacteria [Yersinia pseudotuberculosis IP 31758]	gi|77629741|ref|ZP 00792327.1|	63.04	2E-41
contig00028-orf00044	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.29	2E-12
contig00028-orf00045	hypothetical protein NGO1512 [Neisseria gonorrhoeae FA 1090]	gi|59801850|ref|YP 208562.1|	73.14	5E-103
contig00028-orf00047	factor-for-inversion-stimulation protein [Neisseria meningitidis MC58]	gi|15677279|ref|NP 274432.1|	83.54	1E-34

Query	NR Database Subject	Subject ID	% ID	E value
contig00028-orf00050	hypothetical protein NMA1633 [Neisseria meningitidis Z2491]	gi|15794527|ref|NP 284349.1|	90.36	2E-174
contig00028-orf00052	hypothetical protein NMB1731 [Neisseria meningitidis MC58]	gi|15677577|ref|NP 274734.1|	65.57	2E-69
contig00028-orf00055	DNA polymerase III subunit delta [Neisseria meningitidis MC58]	gi|15676606|ref|NP 273750.1|	80.18	1E-138
contig00028-orf00056	hypothetical protein NGO0282 [Neisseria gonorrhoeae FA 1090]	gi|59800731|ref|YP 207443.1|	59.49	6E-49
contig00028-orf00057	PREDICTED: similar to hypothetical protein 4933429F08 [Gallus gallus]	gi|50754730|ref|XP 414480.1|	40.82	4.7
contig00028-orf00058	proline iminopeptidase [Neisseria gonorrhoeae FA 1090]	gi|59801340|ref|YP 208052.1|	81.49	3E-149
contig00028-orf00059	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	69.57	5E-11
contig00028-orf00060	hypothetical protein NMB0709 [Neisseria meningitidis MC58]	gi|15676607|ref|NP 273751.1|	92.09	4E-53
contig00028-orf00062	hypothetical protein NGO0285 [Neisseria gonorrhoeae FA 1090]	gi|59800734|ref|YP 207446.1|	68.42	3E-55
contig00028-orf00066	proline dehydrogenase [Neisseria meningitidis Z2491]	gi|15794959|ref|NP 284781.1|	92.51	0
contig00028-orf00067	putative sodium/proline symporter, proline permease [Neisseria gonorrhoeae FA 1090]	gi|59801888|ref|YP 208600.1|	91.29	0
contig00028-orf00070	putative ubiquinone biosynthesis protein UbiB [Neisseria meningitidis MC58]	gi|15676464|ref|NP 273603.1|	92.71	0
contig00028-orf00075	hypothetical protein NGO1551 [Neisseria gonorrhoeae FA 1090]	gi|59801887|ref|YP 208599.1|	92.06	2E-25
contig00028-orf00079	chelatase [Neisseria meningitidis Z2491]	gi|15794956|ref|NP 284778.1|	93.98	0
contig00028-orf00082	IS1016C2 transposase [Neisseria meningitidis MC58]	gi|15677271|ref|NP 274424.1|	100	2E-40
contig00028-orf00086	hypothetical protein NMB0406 [Neisseria meningitidis MC58]	gi|15676319|ref|NP 273455.1|	52.85	1E-20
contig00028-orf00086	hypothetical protein NMB0406 [Neisseria meningitidis MC58]	gi|15676319|ref|NP 273455.1|	60.71	3.3
contig00028-orf00087	thiol:disulfide interchange protein DsbA [Neisseria meningitidis MC58]	gi|15676320|ref|NP 273456.1|	66.32	4E-62
contig00028-orf00089	#N/A	gi|29468174|gb|AAO85431.1|AF469 607 1	76.47	9E-111
contig00028-orf00091	hypothetical protein NMB1908 [Neisseria meningitidis MC58]	gi|15677739|ref|NP 274902.1|	88.14	2E-111
contig00028-orf00092	Maf-like protein [Neisseria gonorrhoeae FA 1090]	gi|59802468|ref|YP 209180.1|	71.43	2E-76
contig00028-orf00093	hypothetical protein NMA0545 [Neisseria meningitidis Z2491]	gi|15793539|ref|NP 283361.1|	84.43	3E-76
contig00028-orf00094	50S ribosomal protein L32 [Neisseria meningitidis MC58]	gi|15677742|ref|NP 274905.1|	96.61	1E-26
contig00028-orf00095	hypothetical protein NMA0543 [Neisseria meningitidis Z2491]	gi|15793537|ref|NP 283359.1|	91.95	8E-92
contig00028-orf00098	putative glycerol-3-phosphate acyltransferase PlsX [Neisseria meningitidis Z2491]	gi|15793536|ref|NP 283358.1|	84.38	1E-158
contig00028-orf00101	glycyl-tRNA synthetase subunit beta [Neisseria meningitidis MC58]	gi|15677760|ref|NP 274924.1|	85.73	0
contig00028-orf00102	glycyl-tRNA synthetase subunit alpha [Neisseria meningitidis MC58]	gi|15677762|ref|NP 274926.1|	98.99	5E-174
contig00028-orf00105	hypothetical protein NMB1417 [Neisseria meningitidis MC58]	gi|15677276|ref|NP 274429.1|	85.55	9E-137
contig00029-orf00003	hypothetical protein NGO1387 [Neisseria gonorrhoeae FA 1090]	gi|59801735|ref|YP 208447.1|	97.22	2E-36
contig00029-orf00006	hypothetical protein NMB0372 [Neisseria meningitidis MC58]	gi|15676286|ref|NP 273421.1|	89.58	1E-73
contig00029-orf00010	hypothetical protein NMB0050 [Neisseria meningitidis MC58]	gi|15675988|ref|NP 273115.1|	77.01	0
contig00029-orf00011	hypothetical protein NMB0508 [Neisseria meningitidis MC58]	gi|15676417|ref|NP 273554.1|	93.88	7E-23
contig00029-orf00014	aspartate carbamoyltransferase catalytic subunit [Neisseria meningitidis MC58]	gi|15676034|ref|NP 273164.1|	91.83	5E-150
contig00029-orf00016	aspartate carbamoyltransferase regulatory subunit [Neisseria meningitidis Z2491]	gi|15793194|ref|NP 283016.1|	89.47	1E-74

Query	NR Database Subject	Subject ID	% ID	E value
contig00029-orf00018	hypothetical protein NMA0178 [Neisseria meningitidis Z2491]	gi|15793206|ref|NP 283028.1|	75.11	0
contig00029-orf00020	NADH dehydrogenase subunit H [Ralstonia metallidurans CH34]	gi|94309879|ref|YP 583089.1|	32.56	2.2
contig00029-orf00021	hypothetical protein NGO1694 [Neisseria gonorrhoeae FA 1090]	gi|59802018|ref|YP 208730.1|	68.94	4E-51
contig00029-orf00023	hypothetical protein MED121 17144 [Marinomonas sp. MED121]	gi|87118774|ref|ZP 01074673.1|	42	2.8
contig00029-orf00025	hypothetical protein PAM 636 [Onion yellows phytoplasma OY-M]	gi|39939122|ref|NP 950888.1|	26.79	1E-17
contig00029-orf00028	peptide chain release factor 2 [Neisseria meningitidis MC58]	gi|15677951|ref|NP 275123.1|	98.91	0
contig00029-orf00032	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Neisseria meningitidis Z2491]	gi|15793276|ref|NP 283098.1|	89.93	0
contig00029-orf00035	putative acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59802241|ref|YP 208953.1|	64.47	5E-53
contig00029-orf00037	methionyl-tRNA synthetase [Neisseria meningitidis Z2491]	gi|15793293|ref|NP 283115.1|	97.11	3E-90
contig00030-orf00002	DNA helicase II [Neisseria meningitidis Z2491]	gi|15793060|ref|NP 282882.1|	96.19	0
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	46.81	1E-20
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	43.33	2E-18
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	49.17	3E-17
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	43.45	4E-17
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	42.74	4E-13
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	43.96	5E-10
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	38.58	2E-09
contig00030-orf00008	hypothetical protein MA1892 [Methanosarcina acetivorans C2A]	gi|20090742|ref|NP 616817.1|	40.43	0.00004
contig00030-orf00011	iron-sulfur cluster binding protein [Carboxydothermus hydrogenoformans Z-2901]	gi|78044449|ref|YP 360062.1|	34.29	4.7
contig00031-orf00002	#N/A	gi|4887082|gb|AAD32177.1|AF125563 2	94.26	4E-169
contig00031-orf00005	arginyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15677359|ref|NP 274514.1|	96.96	0
contig00031-orf00007	hypothetical protein NGO0585 [Neisseria gonorrhoeae FA 1090]	gi|59801016|ref|YP 207728.1|	72.76	4E-96
contig00031-orf00010	CDP-diacylglycerol--serine O-phosphatidyltransferse [Neisseria meningitidis MC58]	gi|15677184|ref|NP 274337.1|	89.3	1E-107
contig00031-orf00011	hypothetical protein NMB1917 [Neisseria meningitidis MC58]	gi|15677748|ref|NP 274911.1|	66.67	1E-09
contig00031-orf00014	exodeoxyribonuclease VII large subunit [Neisseria meningitidis MC58]	gi|15677228|ref|NP 274381.1|	87.53	0
contig00031-orf00016	PREDICTED: similar to sortilin-related receptor containing LDLR class A repeats preproprotein [Canis familiaris]	gi|73954998|ref|XP 536545.2|	36.59	1.2
contig00031-orf00023	tetraacyldisaccharide 4'-kinase [Neisseria meningitidis Z2491]	gi|15793841|ref|NP 283663.1|	68.25	1E-38
contig00032-orf00002	MFS family transporter [Acinetobacter sp. ADP1]	gi|50083512|ref|YP 045022.1|	64.76	1E-148
contig00032-orf00005	ABC transporter [Enterococcus faecium DO]	gi|69249959|ref|ZP 00605070.1|	57.92	1E-81
contig00032-orf00006	hypothetical protein RB2501 01620 [Robiginitalea biformata HTCC2501]	gi|88806964|ref|ZP 01122479.1|	37.04	6.2
contig00032-orf00008	Hmp protein [Mannheimia succiniciproducens MBEL55E]	gi|52424735|ref|YP 087872.1|	41	1E-75
contig00032-orf00009	LysR protein [Mannheimia succiniciproducens MBEL55E]	gi|52425458|ref|YP 088595.1|	67.68	4E-35

Query	NR Database Subject	Subject ID	% ID	E value
contig00032-orf00011	helicase, putative [Geobacter sulfurreducens PCA]	gi|39995869|ref|NP 951820.1|	46.98	0
contig00032-orf00012	potassium-tellurite ethidium and proflavin transporter [Neisseria meningitidis MC58]	gi|15677453|ref|NP 274609.1|	63.45	2E-19
contig00032-orf00013	potassium-tellurite ethidium and proflavin transporter [Neisseria meningitidis MC58]	gi|15677453|ref|NP 274609.1|	71.17	6E-52
contig00032-orf00016	similar to Methylase involved in ubiquinone/menaquinone biosynthesis [Rhodobacter sphaeroides ATCC 17025]	gi|83368656|ref|ZP 00913518.1|	34.21	3E-16
contig00033-orf00003	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	91.22	0
contig00033-orf00007	putative transposase [Neisseria meningitidis MC58]	gi|15677452|ref|NP 274608.1|	85.71	0.0000007
contig00033-orf00010	putative hemolysin activation protein HecB [Neisseria meningitidis MC58]	gi|15677604|ref|NP 274762.1|	85.59	0
contig00036-orf00002	PA2459 [synthetic construct]	gi|49082746|gb|AAT50773.1|	37.37	1E-33
contig00036-orf00005	hypothetical protein NGO1062 [Neisseria gonorrhoeae FA 1090]	gi|59801432|ref|YP 208144.1|	98.17	1E-57
contig00036-orf00006	short chain dehydrogenase [Neisseria meningitidis MC58]	gi|15677004|ref|NP 274156.1|	92.05	3E-123
contig00036-orf00008	hypothetical protein NMB1128 [Neisseria meningitidis MC58]	gi|15677005|ref|NP 274157.1|	72.16	9E-179
contig00036-orf00010	putative phytoene synthase [Neisseria meningitidis MC58]	gi|15677007|ref|NP 274159.1|	89.77	3E-136
contig00036-orf00011	chaperone protein HscA [Neisseria gonorrhoeae FA 1090]	gi|59801239|ref|YP 207951.1|	89.84	0
contig00036-orf00013	conserved hypothetical protein [Enterococcus faecium DO]	gi|69244302|ref|ZP 00602770.1|	61.67	3E-39
contig00036-orf00014	putative ferredoxin [Neisseria gonorrhoeae FA 1090]	gi|59801235|ref|YP 207947.1|	93.81	4E-48
contig00036-orf00015	hypothetical protein NMA1345 [Neisseria meningitidis Z2491]	gi|15794268|ref|NP 284090.1|	38.31	3E-27
contig00036-orf00016	hypothetical protein NMB1137 [Neisseria meningitidis MC58]	gi|15677014|ref|NP 274166.1|	92.31	1E-29
contig00036-orf00018	5,10-methylenetetrahydrofolate reductase [Neisseria meningitidis Z2491]	gi|15794085|ref|NP 283907.1|	98.63	1E-164
contig00036-orf00020	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Neisseria meningitidis Z2491]	gi|15794086|ref|NP 283908.1|	98.11	0
contig00036-orf00022	5'-methylthioadenosine phosphorylase [Chromobacterium violaceum ATCC 12472]	gi|34499349|ref|NP 903564.1|	49.77	4E-58
contig00036-orf00025	integral membrane protein [Neisseria meningitidis Z2491]	gi|15794302|ref|NP 284124.1|	72.88	8E-110
contig00036-orf00026	phosphoribosylaminoimidazole synthetase [Neisseria meningitidis Z2491]	gi|15794333|ref|NP 284155.1|	92.73	0
contig00037-orf00002	hypothetical protein MM 0503 [Methanosarcina mazei Go1]	gi|21226605|ref|NP 632527.1|	31.93	5E-26
contig00037-orf00003	menaquinone biosynthesis methyltransferase (2-heptaprenyl-1, 4-naphthoquinone methyltransferase) [Alkaliphilus metalliredigenes QYMF]	gi|77684925|ref|ZP 00800341.1|	53.85	0.000003
contig00037-orf00004	hypothetical protein CV 4086 [Chromobacterium violaceum ATCC 12472]	gi|34499541|ref|NP 903756.1|	78.26	0.006
contig00037-orf00006	hypothetical protein CV 4086 [Chromobacterium violaceum ATCC 12472]	gi|34499541|ref|NP 903756.1|	89.29	0.000002
contig00037-orf00008	amino acid carrier protein [Psychrobacter cryohalolentis K5]	gi|93006043|ref|YP 580480.1|	69.71	5E-165
contig00037-orf00009	aldehyde dehydrogenase [Psychrobacter cryohalolentis K5]	gi|93006044|ref|YP 580481.1|	66.6	6E-179
contig00037-orf00012	dihydrodipicolinate synthetase [Psychrobacter cryohalolentis K5]	gi|93006045|ref|YP 580482.1|	67.7	2E-111
contig00037-orf00013	FAD dependent oxidoreductase [Psychrobacter cryohalolentis K5]	gi|93006046|ref|YP 580483.1|	52.46	3E-118
contig00037-orf00014	COG3938: Proline racemase [Pseudomonas aeruginosa C3719]	gi|84321952|ref|ZP 00970302.1|	63.43	7E-108

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contig00037-orf00016	hypothetical protein plu2244 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37526157|ref|NP 929501.1|	46.9	1E-56
contig00038-orf00001	phosphoribosyltransferase [Trichodesmium erythraeum IMS101]	gi|113474287|ref|YP 720348.1|	48.15	2.8
contig00039-orf00001	hypothetical protein AsucDRAFT 0181 [Actinobacillus succinogenes 130Z]	gi|75431019|ref|ZP 00732913.1|	40.76	1E-15
contig00039-orf00004	hypothetical protein NMA2173 [Neisseria meningitidis Z2491]	gi|15795044|ref|NP 284866.1|	50.15	8E-96
contig00039-orf00007	hypothetical protein NGO1686 [Neisseria gonorrhoeae FA 1090]	gi|59802011|ref|YP 208723.1|	61.26	8E-146
contig00039-orf00010	hypothetical protein NMB0316 [Neisseria meningitidis MC58]	gi|15676233|ref|NP 273365.1|	95.92	1E-105
contig00039-orf00011	7-cyano-7-deazaguanine reductase [Neisseria meningitidis Z2491]	gi|15795041|ref|NP 284863.1|	98.73	8E-89
contig00039-orf00012	MarR family transcriptional regulator [Chromobacterium violaceum ATCC	gi|34496224|ref|NP 900439.1|	39.04	4E-25
contig00039-orf00013	outer membrane multidrug resistance lipoprotein [Chromobacterium violaceum ATCC 12472]	gi|34496223|ref|NP 900438.1|	37.84	3E-80
contig00039-orf00014	#N/A	gi|14548177|sp|O87626|PBPA NEIFL	85.44	0
contig00039-orf00014	#N/A	gi|14548177|sp|O87626|PBPA NEIFL	84.62	0.006
contig00039-orf00015	pilM protein [Neisseria meningitidis MC58]	gi|15677646|ref|NP 274805.1|	61.48	2E-116
contig00039-orf00016	pilN protein [Neisseria meningitidis MC58]	gi|15678015|ref|NP 274806.1|	55.93	2E-31
contig00039-orf00018	pilP protein [Neisseria meningitidis MC58]	gi|15677648|ref|NP 274808.1|	53.66	2E-19
contig00039-orf00019	hypothetical protein NGO0094 [Neisseria gonorrhoeae FA 1090]	gi|59800555|ref|YP 207267.1|	62.09	0
contig00039-orf00021	3-dehydroquinate synthase [Neisseria meningitidis MC58]	gi|15677650|ref|NP 274811.1|	81.62	2E-170
contig00039-orf00023	N-acetyl-gamma-glutamyl-phosphate reductase [Neisseria meningitidis MC58]	gi|15677627|ref|NP 274786.1|	77.52	3E-156
contig00039-orf00024	hypothetical protein NGO1484 [Neisseria gonorrhoeae FA 1090]	gi|59801822|ref|YP 208534.1|	69.93	9E-103
contig00039-orf00026	23S rRNA 5-methyluridine methyltransferase [Nitrosospira multiformis ATCC 25196]	gi|82703334|ref|YP 412900.1|	47.13	8E-104
contig00039-orf00028	hypothetical protein NMA2010 [Neisseria meningitidis Z2491]	gi|15794890|ref|NP 284712.1|	58.37	2E-141
contig00039-orf00029	hypothetical protein NMB0476 [Neisseria meningitidis MC58]	gi|15676387|ref|NP 273523.1|	61.2	7E-123
contig00039-orf00030	hypothetical protein NMB0477 [Neisseria meningitidis MC58]	gi|15676388|ref|NP 273524.1|	84.5	2E-58
contig00039-orf00031	hypothetical protein NMB0478 [Neisseria meningitidis MC58]	gi|15676389|ref|NP 273525.1|	78.57	3E-12
contig00039-orf00032	hypothetical protein NMB0479 [Neisseria meningitidis MC58]	gi|15676390|ref|NP 273526.1|	81.51	8E-48
contig00039-orf00034	HemK protein [Neisseria meningitidis Z2491]	gi|15793377|ref|NP 283199.1|	72.68	1E-76
contig00039-orf00036	hemagglutinin precursor [Influenza B virus]	gi|325296|gb|AAA43777.1|	41.67	2.8
contig00040-orf00001	Holliday junction DNA helicase B [Neisseria gonorrhoeae FA 1090]	gi|59801175|ref|YP 207887.1|	94.46	0
contig00040-orf00003	hypothetical protein NMB1242 [Neisseria meningitidis MC58]	gi|15677114|ref|NP 274266.1|	94.12	1E-42
contig00040-orf00005	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase [Neisseria meningitidis MC58]	gi|15677113|ref|NP 274265.1|	92.57	0
contig00040-orf00006	#N/A	gi|7228883|gb|AAF42675.1|AF2265 27 1	90.4	1E-150

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contig00040-orf00008	hypothetical protein NMB1221 [Neisseria meningitidis MC58]	gi|15677094|ref|NP 274246.1|	53.79	3E-27
contig00040-orf00011	conserved hypothetical protein [Congregibacter litoralis KT71]	gi|88706105|ref|ZP 01103813.1|	53.76	1E-126
contig00040-orf00012	ABC-type long-chain fatty acid transport system, fused permease and ATPase components [Actinobacillus succinogenes 130Z]	gi|75431181|ref|ZP 00732953.1|	50.26	4E-170
contig00040-orf00014	TonB-dependent receptor protein [Neisseria meningitidis Z2491]	gi|15794451|ref|NP 284273.1|	79.92	0
contig00040-orf00015	ferredoxin--NADP reductase [Neisseria meningitidis MC58]	gi|15676930|ref|NP 274078.1|	98.84	2E-147
contig00041-orf00001	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	84.85	9E-10
contig00041-orf00004	hypothetical protein NMB0350 [Neisseria meningitidis MC58]	gi|15676265|ref|NP 273399.1|	100	8E-22
contig00041-orf00006	hypothetical protein YmolA 01003827 [Yersinia mollaretii ATCC 43969]	gi|77959848|ref|ZP 00823794.1|	51.49	5E-27
contig00041-orf00007	hypothetical protein NMA0482 [Neisseria meningitidis Z2491]	gi|15793482|ref|NP 283304.1|	100	5E-20
contig00041-orf00010	hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	gi|15676403|ref|NP 273539.1|	80.5	0
contig00042-orf00001	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801511|ref|YP 208223.1|	95.52	7E-31
contig00042-orf00002	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801512|ref|YP 208224.1|	94.44	1E-42
contig00042-orf00004	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59801513|ref|YP 208225.1|	90.85	1E-176
contig00042-orf00006	hypothetical protein NGO1147 [Neisseria gonorrhoeae FA 1090]	gi|59801514|ref|YP 208226.1|	81.08	2E-26
contig00042-orf00007	putative peptide transporter [Neisseria gonorrhoeae FA 1090]	gi|59802265|ref|YP 208977.1|	77.11	0
contig00042-orf00009	hypothetical protein NMB0043 [Neisseria meningitidis MC58]	gi|15675983|ref|NP 273109.1|	74.83	2E-51
contig00042-orf00013	hypothetical protein [Neisseria meningitidis]	gi|14140110|emb|CAC38866.1|	95.08	0
contig00042-orf00014	hypothetical protein NMB1116 [Neisseria meningitidis MC58]	gi|15676995|ref|NP 274146.1|	55.81	0.0005
contig00042-orf00014	hypothetical protein NMB1116 [Neisseria meningitidis MC58]	gi|15676995|ref|NP 274146.1|	55	0.15
contig00042-orf00016	DNA ligase [Neisseria meningitidis Z2491]	gi|15793396|ref|NP 283218.1|	91.39	3E-142
contig00042-orf00017	hydrolase [Neisseria meningitidis Z2491]	gi|15793395|ref|NP 283217.1|	80	5E-98
contig00042-orf00020	lipoprotein [Neisseria meningitidis]	gi|577422|gb|AAA85675.1|	71.83	1E-51
contig00042-orf00022	periplasmic protein [Neisseria meningitidis Z2491]	gi|15793550|ref|NP 283372.1|	66.19	1E-47
contig00044-orf00001	outer membrane protein; transferrin-binding protein [Actinobacillus pleuropneumoniae]	gi|577529|emb|CAA86730.1|	27.1	2E-10
contig00044-orf00001	outer membrane protein; transferrin-binding protein [Actinobacillus pleuropneumoniae]	gi|577529|emb|CAA86730.1|	24.49	0.0003
contig00044-orf00003	exodeoxyribonuclease small subunit [Neisseria meningitidis MC58]	gi|15676186|ref|NP 273318.1|	84.93	1E-25
contig00044-orf00006	geranyltranstransferase [Neisseria meningitidis Z2491]	gi|15795095|ref|NP 284917.1|	82.47	6E-119
contig00044-orf00008	hypothetical protein Bcen 5302 [Burkholderia cenocepacia AU 1054]	gi|107027638|ref|YP 625149.1|	50.78	3E-30
contig00044-orf00010	#N/A	gi|24418598|sp|Q9K1R0|PGK NEIMB	97.96	0
contig00044-orf00013	tRNA modification GTPase TrmE [Neisseria meningitidis MC58]	gi|15677815|ref|NP 274979.1|	79.07	0
contig00044-orf00016	Holliday junction DNA helicase motor protein [Neisseria gonorrhoeae FA 1090]	gi|59802051|ref|YP 208763.1|	86.6	3E-92
contig00044-orf00018	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794004|ref|NP 283826.1|	53.66	5E-13
contig00044-orf00020	ParA family protein [Neisseria meningitidis MC58]	gi|15676118|ref|NP 273249.1|	85.06	6E-105

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contig00044-orf00021	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	87.5	4E-09
contig00044-orf00022	methionine aminopeptidase [Neisseria meningitidis MC58]	gi|15677913|ref|NP 275081.1|	95.92	3E-139
contig00044-orf00024	#N/A	gi|66815395|ref|XP 641714.1|	29.7	0.012
contig00044-orf00026	putative hemolysin [Neisseria meningitidis MC58]	gi|15677911|ref|NP 275079.1|	83.54	2E-74
contig00044-orf00028	phosphoheptose isomerase [Neisseria gonorrhoeae FA 1090]	gi|59802294|ref|YP 209006.1|	95.94	6E-103
contig00044-orf00030	hypothetical protein NGO1987 [Neisseria gonorrhoeae FA 1090]	gi|59802295|ref|YP 209007.1|	88.7	3E-54
contig00044-orf00031	hypothetical protein NGO1988 [Neisseria gonorrhoeae FA 1090]	gi|59802296|ref|YP 209008.1|	85.12	1E-132
contig00044-orf00033	hypothetical protein MS1522 [Mannheimia succiniciproducens MBEL55E]	gi|52425577|ref|YP 088714.1|	53.72	2E-30
contig00044-orf00037	exodeoxyribonuclease [Neisseria meningitidis MC58]	gi|15677903|ref|NP 275071.1|	95.37	8E-148
contig00044-orf00038	hypothetical protein NGO1995 [Neisseria gonorrhoeae FA 1090]	gi|59802303|ref|YP 209015.1|	76.32	2E-50
contig00044-orf00040	hypothetical protein NGO1996 [Neisseria gonorrhoeae FA 1090]	gi|59802304|ref|YP 209016.1|	73.3	1E-72
contig00044-orf00042	zinc transporter ZupT [Neisseria meningitidis MC58]	gi|15676102|ref|NP 273233.1|	88.48	2E-114
contig00044-orf00044	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793107|ref|NP 282929.1|	49.69	1E-18
contig00044-orf00046	XRE family transcriptional regulator [Nitrosospira multiformis ATCC 25196]	gi|82703063|ref|YP 412629.1|	73.12	6E-35
contig00044-orf00048	valyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15676101|ref|NP 273232.1|	92.17	0
contig00044-orf00050	indole-3-glycerol-phosphate synthase [Neisseria meningitidis MC58]	gi|15676199|ref|NP 273331.1|	83.08	2E-106
contig00044-orf00051	membrane protein [Neisseria meningitidis Z2491]	gi|15794573|ref|NP 284395.1|	47.92	0.006
contig00044-orf00052	Phage integrase [Dechloromonas aromatica RCB]	gi|71906676|ref|YP 284263.1|	52.36	3E-59
contig00044-orf00053	#N/A	gi|46133055|ref|ZP 00156525.2|	54.76	0.00008
contig00044-orf00054	hypothetical protein Cag 1180 [Chlorobium chlorochromatii CaD3]	gi|78189147|ref|YP 379485.1|	35.14	8.3
contig00045-orf00002	hypothetical protein NMA0245 [Neisseria meningitidis Z2491]	gi|15793263|ref|NP 283085.1|	92.79	1E-116
contig00045-orf00005	putative pyrazinamidase/nicotinamidase PncA [Neisseria meningitidis MC58]	gi|15677970|ref|NP 275142.1|	94.79	1E-117
contig00045-orf00006	1,5 heptosyltransferase I [Neisseria meningitidis]	gi|1173888|gb|AAA86622.1|	96.27	1E-179
contig00045-orf00008	electron transfer flavoprotein, beta subunit [Neisseria meningitidis MC58]	gi|15677968|ref|NP 275140.1|	97.07	4E-101
contig00045-orf00009	electron transfer flavoprotein subunit alpha [Neisseria meningitidis MC58]	gi|15677967|ref|NP 275139.1|	95.18	2E-160
contig00045-orf00010	hypothetical protein NMA0240 [Neisseria meningitidis Z2491]	gi|15793258|ref|NP 283080.1|	97.04	2E-104
contig00045-orf00011	hypothetical protein NMB2152 [Neisseria meningitidis MC58]	gi|15677965|ref|NP 275137.1|	93.27	6E-54
contig00045-orf00012	phosphoribosylamine--glycine ligase [Neisseria gonorrhoeae FA 1090]	gi|59802251|ref|YP 208963.1|	95.27	0
contig00045-orf00013	hypothetical protein NMA0237 [Neisseria meningitidis Z2491]	gi|15793255|ref|NP 283077.1|	81.22	6E-84
contig00045-orf00014	hypothetical protein NGO1942 [Neisseria gonorrhoeae FA 1090]	gi|59802254|ref|YP 208966.1|	61.54	8E-40
contig00045-orf00017	ATP-dependent DNA helicase [Neisseria meningitidis MC58]	gi|15676198|ref|NP 273330.1|	78.1	0
contig00045-orf00017	ATP-dependent DNA helicase [Neisseria meningitidis MC58]	gi|15676198|ref|NP 273330.1|	33.54	7E-16
contig00045-orf00017	ATP-dependent DNA helicase [Neisseria meningitidis MC58]	gi|15676198|ref|NP 273330.1|	35.14	0.0008
contig00045-orf00018	methyltransferase, type III DNA modification enzyme [Actinobacillus succinogenes 130Z]	gi|75428982|ref|ZP 00732021.1|	72.88	5E-16
contig00045-orf00019	type III restriction system methylase [Desulfotomaculum reducens MI-1]	gi|88946117|ref|ZP 01149205.1|	54.9	0.0000004
contig00045-orf00020	ribonuclease II-related protein [Neisseria meningitidis MC58]	gi|15676206|ref|NP 273338.1|	95.15	0

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contig00045-orf00025	acyl-CoA dehydrogenase [Chromobacterium violaceum ATCC 12472]	gi|34499271|ref|NP 903486.1|	58.11	1E-137
contig00045-orf00028	ATP-dependent DNA helicase DinG [Neisseria meningitidis MC58]	gi|15676210|ref|NP 273342.1|	92.04	0
contig00045-orf00030	hypothetical protein Daro 3801 [Dechloromonas aromatica RCB]	gi|71909412|ref|YP 286999.1|	66.67	1E-17
contig00045-orf00032	RNA polymerase sigma factor [Neisseria meningitidis MC58]	gi|15677957|ref|NP 275129.1|	74.6	7E-80
contig00045-orf00033	hypothetical protein NMB2145 [Neisseria meningitidis MC58]	gi|15677958|ref|NP 275130.1|	54.55	5E-08
contig00045-orf00036	cytochrome c5 [Neisseria meningitidis MC58]	gi|15677525|ref|NP 274681.1|	78.05	3E-34
contig00045-orf00036	cytochrome c5 [Neisseria meningitidis MC58]	gi|15677525|ref|NP 274681.1|	52.44	7E-19
contig00045-orf00038	phnA protein [Neisseria meningitidis MC58]	gi|15675977|ref|NP 273103.1|	84.55	2E-48
contig00045-orf00039	periplasmic protein [Neisseria meningitidis Z2491]	gi|15795088|ref|NP 284910.1|	79.61	6E-86
contig00045-orf00042	RNA methyltransferase [Neisseria meningitidis MC58]	gi|15676192|ref|NP 273324.1|	88.96	3E-76
contig00045-orf00044	hypothetical protein NGO1726 [Neisseria gonorrhoeae FA 1090]	gi|59802047|ref|YP 208759.1|	73.89	6E-85
contig00045-orf00046	hydrolase [Neisseria meningitidis Z2491]	gi|15795085|ref|NP 284907.1|	74.6	9E-92
contig00045-orf00048	anion transporter [Rhodoferax ferrireducens T118]	gi|89899730|ref|YP 522201.1|	68.47	0
contig00045-orf00051	hypothetical protein NGO1724 [Neisseria gonorrhoeae FA 1090]	gi|59802045|ref|YP 208757.1|	70.11	2E-94
contig00045-orf00054	trifunctional thioredoxin/methionine sulfoxide reductase A/B protein [Neisseria meningitidis Z2491]	gi|15793307|ref|NP 283129.1|	94.64	0
contig00045-orf00057	signal recognition particle protein [Neisseria meningitidis MC58]	gi|15675985|ref|NP 273111.1|	98.68	7E-164
contig00045-orf00057	signal recognition particle protein [Neisseria meningitidis MC58]	gi|15675985|ref|NP 273111.1|	86.36	0.068
contig00045-orf00060	hypothetical protein NMA0229 [Neisseria meningitidis Z2491]	gi|15793251|ref|NP 283073.1|	68.58	6E-85
contig00045-orf00061	hypothetical protein NGO1946 [Neisseria gonorrhoeae FA 1090]	gi|59802258|ref|YP 208970.1|	96.79	4E-156
contig00045-orf00065	hypothetical protein NMB2140 [Neisseria meningitidis MC58]	gi|15677953|ref|NP 275125.1|	84.96	1E-34
contig00045-orf00066	ribosome-associated GTPase [Neisseria meningitidis Z2491]	gi|15795093|ref|NP 284915.1|	87.41	4E-120
contig00045-orf00068	hypothetical protein CV 0778 [Chromobacterium violaceum ATCC 12472]	gi|34496233|ref|NP 900448.1|	65.71	2E-74
contig00045-orf00069	tRNA pseudouridine synthase C [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602344|ref|NP 245416.1|	62.98	1E-78
contig00045-orf00075	adenylosuccinate lyase [Neisseria meningitidis MC58]	gi|15676208|ref|NP 273340.1|	93.86	0
contig00045-orf00076	hypothetical protein STH2030 [Symbiobacterium thermophilum IAM 14863]	gi|51893168|ref|YP 075859.1|	34.81	1E-13
contig00045-orf00077	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	55.56	0.0005
contig00045-orf00079	serine/threonine transporter SstT [Neisseria meningitidis MC58]	gi|15677946|ref|NP 275118.1|	74.32	2E-137
contig00045-orf00081	hypothetical protein NGO1956 [Neisseria gonorrhoeae FA 1090]	gi|59802267|ref|YP 208979.1|	76.33	0
contig00045-orf00083	hypothetical protein NGO2057 [Neisseria gonorrhoeae FA 1090]	gi|59802364|ref|YP 209076.1|	73.23	3E-29
contig00045-orf00086	Protein of unknown function DUF336 [Rhodopseudomonas palustris BisB18]	gi|78492503|ref|ZP 00844739.1|	57.24	1E-28
contig00045-orf00089	hypothetical protein NMB2135 [Neisseria meningitidis MC58]	gi|15677948|ref|NP 275120.1|	65.19	0
contig00045-orf00090	hypothetical protein NMA2201 [Neisseria meningitidis Z2491]	gi|15795070|ref|NP 284892.1|	67.49	7E-50
contig00045-orf00091	NADH dehydrogenase I chain A [Neisseria meningitidis Z2491]	gi|15793053|ref|NP 282875.1|	94.07	9E-60
contig00045-orf00092	NADH dehydrogenase subunit B [Neisseria meningitidis MC58]	gi|15676166|ref|NP 273298.1|	99.38	8E-78
contig00045-orf00093	NADH dehydrogenase subunit C [Neisseria meningitidis MC58]	gi|15676167|ref|NP 273299.1|	96.95	3E-109

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contig00045-orf00095	NADH dehydrogenase subunit D [Neisseria meningitidis Z2491]	gi|15793050|ref|NP 282872.1|	99.04	0
contig00045-orf00096	NADH dehydrogenase subunit E [Neisseria meningitidis MC58]	gi|15676169|ref|NP 273301.1|	96.82	1E-83
contig00045-orf00097	NADH dehydrogenase I chain F [Neisseria meningitidis MC58]	gi|15676170|ref|NP 273302.1|	98.15	0
contig00045-orf00098	hypothetical protein [Plasmodium berghei strain ANKA]	gi|68070831|ref|XP 677329.1|	36.84	0.55
contig00045-orf00099	hypothetical protein NMA0012 [Neisseria meningitidis Z2491]	gi|15793046|ref|NP 282868.1|	81.08	1E-10
contig00045-orf00101	hypothetical protein NMA0011 [Neisseria meningitidis Z2491]	gi|15793045|ref|NP 282867.1|	96.63	2E-47
contig00045-orf00104	NADH dehydrogenase subunit G [Neisseria meningitidis Z2491]	gi|15793044|ref|NP 282866.1|	96.15	0
contig00045-orf00105	NADH dehydrogenase I chain H [Neisseria meningitidis MC58]	gi|15676174|ref|NP 273306.1|	98.6	0
contig00045-orf00108	NADH dehydrogenase subunit I [Neisseria meningitidis MC58]	gi|15676175|ref|NP 273307.1|	98.74	1E-79
contig00045-orf00109	NADH dehydrogenase I chain J [Neisseria meningitidis MC58]	gi|15676177|ref|NP 273309.1|	95.07	9E-75
contig00045-orf00110	NADH dehydrogenase subunit K [Neisseria meningitidis MC58]	gi|15676178|ref|NP 273310.1|	100	2E-40
contig00045-orf00113	cell filamentation protein Fic-related protein [Neisseria meningitidis MC58]	gi|15676179|ref|NP 273311.1|	98.43	1E-91
contig00045-orf00117	NADH dehydrogenase subunit L [Neisseria meningitidis Z2491]	gi|15793036|ref|NP 282858.1|	97.63	0
contig00045-orf00120	hypothetical protein STER 1555 [Streptococcus thermophilus LMD-9]	gi|116628284|ref|YP 820903.1|	61.36	1E-21
contig00045-orf00121	hypothetical protein NMA0001 [Neisseria meningitidis Z2491]	gi|15793035|ref|NP 282857.1|	92.45	8E-53
contig00045-orf00123	NADH dehydrogenase subunit M [Neisseria meningitidis Z2491]	gi|15795098|ref|NP 284920.1|	93.17	0
contig00045-orf00125	NADH dehydrogenase subunit N [Neisseria meningitidis MC58]	gi|15676183|ref|NP 273315.1|	81.87	0
contig00045-orf00127	hypothetical protein NMB0260 [Neisseria meningitidis MC58]	gi|15676184|ref|NP 273316.1|	85.71	0.0003
contig00045-orf00128	hypothetical protein NMA2227 [Neisseria meningitidis Z2491]	gi|15795096|ref|NP 284918.1|	87.34	8E-37
contig00045-orf00130	gamma-glutamyl kinase [Methylobacillus flagellatus KT]	gi|91776568|ref|YP 546324.1|	62.74	1E-115
contig00045-orf00133	deoxyribodopyrimidine photolyase [Neisseria meningitidis Z2491]	gi|15795067|ref|NP 284889.1|	48	2E-100
contig00045-orf00137	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793108|ref|NP 282930.1|	86.33	2E-148
contig00045-orf00138	hypothetical protein NMB0013 [Neisseria meningitidis MC58]	gi|15675961|ref|NP 273079.1|	83.22	9E-58
contig00045-orf00140	hypothetical protein NMB0012 [Neisseria meningitidis MC58]	gi|15675960|ref|NP 273078.1|	75	5E-34
contig00045-orf00140	hypothetical protein NMB0012 [Neisseria meningitidis MC58]	gi|15675960|ref|NP 273078.1|	88.46	5E-34
contig00045-orf00141	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793277|ref|NP 283099.1|	82.11	2E-100
contig00045-orf00145	Rrf [Neisseria gonorrhoeae FA 1090]	gi|59802114|ref|YP 208826.1|	97.3	1E-94
contig00045-orf00146	undecaprenyl pyrophosphate synthetase [Neisseria meningitidis MC58]	gi|15676113|ref|NP 273244.1|	95.95	9E-136
contig00045-orf00148	phosphatidate cytidylyltransferase [Neisseria meningitidis Z2491]	gi|15793111|ref|NP 282933.1|	84.79	7E-136
contig00045-orf00151	1-deoxy-D-xylulose 5-phosphate reductoisomerase [Neisseria meningitidis Z2491]	gi|15793112|ref|NP 282934.1|	93.91	0
contig00045-orf00154	hypothetical protein NGO1800 [Neisseria gonorrhoeae FA 1090]	gi|59802118|ref|YP 208830.1|	77.13	0
contig00045-orf00157	outer membrane protein OMP85 [Neisseria meningitidis Z2491]	gi|15793114|ref|NP 282936.1|	83.25	0
contig00045-orf00159	hypothetical protein NMA0086 [Neisseria meningitidis Z2491]	gi|15793115|ref|NP 282937.1|	68.06	5E-50
contig00045-orf00160	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Neisseria meningitidis MC58]	gi|15676107|ref|NP 273238.1|	93.64	7E-172
contig00045-orf00162	(3R)-hydroxymyristoyl-ACP dehydratase [Neisseria meningitidis MC58]	gi|15676106|ref|NP 273237.1|	96.64	8E-77

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contig00045-orf00164	hypothetical protein NMA0089 [Neisseria meningitidis Z2491]	gi|15793118|ref|NP 282940.1|	94.69	4E-114
contig00045-orf00165	UDP-N-acetylglucosamine acyltransferase [Neisseria meningitidis Z2491]	gi|15793119|ref|NP 282941.1|	96.12	8E-145
contig00045-orf00170	#N/A	gi|20139201|sp|Q9K1F9|PDXA NEIMB	76.22	3E-124
contig00045-orf00172	hypothetical protein NGO1925 [Neisseria gonorrhoeae FA 1090]	gi|59802238|ref|YP 208950.1|	74.05	9E-69
contig00045-orf00172	hypothetical protein NGO1925 [Neisseria gonorrhoeae FA 1090]	gi|59802238|ref|YP 208950.1|	55.17	9E-69
contig00045-orf00174	ArsC [Neisseria gonorrhoeae FA 1090]	gi|59802237|ref|YP 208949.1|	76.72	7E-44
contig00045-orf00178	putative thioredoxin [Neisseria gonorrhoeae FA 1090]	gi|59802236|ref|YP 208948.1|	80	5E-68
contig00045-orf00180	ABC transporter ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793272|ref|NP 283094.1|	96.3	7E-114
contig00045-orf00181	ABC transporter integral membrane protein [Neisseria meningitidis Z2491]	gi|15793273|ref|NP 283095.1|	89.51	1E-141
contig00045-orf00184	DNA mismatch repair protein [Neisseria gonorrhoeae FA 1090]	gi|59802243|ref|YP 208955.1|	85.25	0
contig00045-orf00185	hypothetical protein NMB0507 [Neisseria meningitidis MC58]	gi|15676416|ref|NP 273553.1|	98.44	4E-31
contig00045-orf00186	hypothetical protein NMB1433 [Neisseria meningitidis MC58]	gi|15678009|ref|NP 274445.1|	82.72	3E-73
contig00045-orf00189	hypothetical protein Aple02002088 [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143279|ref|ZP 00135556.2|	36.53	3E-19
contig00045-orf00193	hypothetical protein NMA1494 [Neisseria meningitidis Z2491]	gi|15794394|ref|NP 284216.1|	50.37	2E-30
contig00045-orf00196	putative twitching motility - like protein [Neisseria gonorrhoeae FA 1090]	gi|59802223|ref|YP 208935.1|	68.69	5E-157
contig00045-orf00197	putative glycine-rich protein [Oryza sativa Japonica Group]	gi|52075614|dbj|BAD44785.1|	44.74	6.2
contig00045-orf00199	twitching motility protein PilT [Neisseria meningitidis MC58]	gi|15675990|ref|NP 273117.1|	89.06	1E-158
contig00045-orf00201	hypothetical protein NMA0217 [Neisseria meningitidis Z2491]	gi|15793240|ref|NP 283062.1|	80.62	1E-99
contig00045-orf00202	lipoprotein [Neisseria meningitidis Z2491]	gi|15793239|ref|NP 283061.1|	65.77	6E-35
contig00045-orf00203	pyrroline-5-carboxylate reductase [Neisseria meningitidis Z2491]	gi|15793238|ref|NP 283060.1|	81.75	2E-103
contig00045-orf00204	hypothetical protein Daro 3886 [Dechloromonas aromatica RCB]	gi|71909497|ref|YP 287084.1|	26.53	0.003
contig00045-orf00206	DnaK suppressor protein [Neisseria meningitidis MC58]	gi|15675994|ref|NP 273121.1|	93.48	2E-69
contig00046-orf00003	Histidine kinase, HAMP region:Bacterial chemotaxis sensory transducer [Geobacter uraniumreducens Rf4]	gi|88935071|ref|ZP 01140708.1|	27.87	2.1
contig00046-orf00006	aldehyde dehydrogenase A [Neisseria meningitidis MC58]	gi|15677798|ref|NP 274962.1|	98.32	0
contig00046-orf00010	lysyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59801795|ref|YP 208507.1|	98.41	0
contig00046-orf00012	septum formation inhibitor [Neisseria gonorrhoeae FA 1090]	gi|59802133|ref|YP 208845.1|	66.06	3E-75
contig00046-orf00013	septum site-determining protein [Neisseria meningitidis MC58]	gi|15676098|ref|NP 273229.1|	94.58	7E-123
contig00046-orf00015	hypothetical protein NGO1814 [Neisseria gonorrhoeae FA 1090]	gi|59802132|ref|YP 208844.1|	92.5	2E-34
contig00046-orf00017	hydrogen peroxide-inducible genes activator [Neisseria meningitidis Z2491]	gi|15793126|ref|NP 282948.1|	90.52	4E-155
contig00046-orf00021	dihydrodipicolinate reductase [Neisseria gonorrhoeae FA 1090]	gi|59802100|ref|YP 208812.1|	94.78	2E-141
contig00046-orf00022	lipoprotein [Neisseria meningitidis Z2491]	gi|15793094|ref|NP 282916.1|	78.45	3E-47
contig00046-orf00023	#N/A	gi|60416380|sp|P0A0S9|FUR NEIMC	96.53	8E-77
contig00046-orf00027	leucyl/phenylalanyl-tRNA--protein transferase [Neisseria gonorrhoeae FA 1090]	gi|59802097|ref|YP 208809.1|	73.73	1E-101

Query	NR Database Subject	Subject ID	% ID	E value
contig00046-orf00029	D-tyrosyl-tRNA deacylase [Neisseria gonorrhoeae FA 1090]	gi|59801981|ref|YP 208693.1|	75.84	9E-60
contig00046-orf00031	putative cell-binding factor [Neisseria meningitidis MC58]	gi|15676260|ref|NP 273394.1|	59.14	2E-80
contig00046-orf00032	hypothetical protein NGO1657 [Neisseria gonorrhoeae FA 1090]	gi|59801984|ref|YP 208696.1|	66.27	1E-15
contig00046-orf00033	YciI-like protein [Neisseria gonorrhoeae FA 1090]	gi|59801985|ref|YP 208697.1|	81.25	7E-39
contig00046-orf00034	intracellular septation protein A [Neisseria meningitidis MC58]	gi|15676257|ref|NP 273391.1|	77.27	4E-76
contig00046-orf00037	tspA protein [Neisseria meningitidis MC58]	gi|15676256|ref|NP 273390.1|	43.08	6E-33
contig00046-orf00037	tspA protein [Neisseria meningitidis MC58]	gi|15676256|ref|NP 273390.1|	27.62	9E-22
contig00046-orf00039	tRNA pseudouridine synthase A [Neisseria meningitidis MC58]	gi|15677859|ref|NP 275027.1|	77.12	1E-103
contig00046-orf00040	#N/A	gi|266700|sp|P30692|OMPB NEISI	79.22	1E-163
contig00046-orf00042	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	46.34	0.004
contig00046-orf00043	YALI0F01628p [Yarrowia lipolytica]	gi|50554921|ref|XP 504869.1|	43.14	0.003
contig00046-orf00052	DNA gyrase subunit B [Neisseria gonorrhoeae FA 1090]	gi|59802091|ref|YP 208803.1|	96.73	0
contig00046-orf00055	L-serine dehydratase [Neisseria meningitidis Z2491]	gi|15793088|ref|NP 282910.1|	95.42	2E-150
contig00046-orf00058	L-serine dehydratase [Neisseria meningitidis MC58]	gi|15676137|ref|NP 273268.1|	79.77	3E-74
contig00046-orf00060	putative site-specific recombinase [Neisseria gonorrhoeae FA 1090]	gi|59800504|ref|YP 207216.1|	68.75	1E-107
contig00046-orf00061	esterase [Alkalilimnicola ehrlichii MLHE-1]	gi|114320612|ref|YP 742295.1|	44.27	4E-28
contig00046-orf00063	fructose-1,6-bisphosphate aldolase [Neisseria meningitidis Z2491]	gi|15793578|ref|NP 283400.1|	96.89	0
contig00046-orf00067	two-component system, regulatory protein [Chromobacterium violaceum ATCC 12472]	gi|34495662|ref|NP 899877.1|	43.46	8E-40
contig00046-orf00068	glutamyl-Q tRNA(Asp) synthetase [Neisseria meningitidis Z2491]	gi|15795009|ref|NP 284831.1|	76.45	4E-123
contig00046-orf00069	PREDICTED: similar to Enah/Vasp-like isoform 1 [Bos taurus]	gi|76647836|ref|XP 582618.2|	45.16	4.8
contig00046-orf00070	hypothetical protein NGO0032 [Neisseria gonorrhoeae FA 1090]	gi|59800501|ref|YP 207213.1|	72.77	2E-89
contig00046-orf00071	acetyltransferase [Neisseria meningitidis Z2491]	gi|15793575|ref|NP 283397.1|	59.18	6E-41
contig00046-orf00072	hypothetical protein NMA0583 [Neisseria meningitidis Z2491]	gi|15793574|ref|NP 283396.1|	43.01	3E-49
contig00046-orf00077	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein [Neisseria meningitidis MC58]	gi|15677833|ref|NP 274997.1|	86.95	0
contig00046-orf00080	hypothetical protein NMB2003 [Neisseria meningitidis MC58]	gi|15677831|ref|NP 274995.1|	83.78	7E-42
contig00046-orf00081	hypothetical protein NMB2004 [Neisseria meningitidis MC58]	gi|15677832|ref|NP 274996.1|	90.31	7E-81
contig00047-orf00001	hypothetical protein NMB1828 [Neisseria meningitidis MC58]	gi|15677664|ref|NP 274825.1|	55.3	1E-75
contig00047-orf00003	TonB-dependent receptor [Neisseria meningitidis MC58]	gi|15677665|ref|NP 274826.1|	81.7	0
contig00047-orf00005	sugar transporter [Leeuwenhoekiella blandensis MED217]	gi|86140748|ref|ZP 01059307.1|	47.89	2E-112
contig00047-orf00007	transcriptional regulator, LacI family protein [Oceanicola granulosus	gi|89068785|ref|ZP 01156171.1|	53.04	1E-93
contig00047-orf00008	glucose-6-phosphate isomerase 2 [Neisseria gonorrhoeae]	gi|27573133|gb|AAO19966.1|	73.37	0
contig00047-orf00012	hypothetical protein NGO1195 [Neisseria gonorrhoeae FA 1090]	gi|59801555|ref|YP 208267.1|	79.54	4E-177
contig00047-orf00013	phosphoenolpyruvate carboxylase [Neisseria gonorrhoeae FA 1090]	gi|59802328|ref|YP 209040.1|	92.68	2E-27
contig00047-orf00015	phosphoenolpyruvate carboxylase [Neisseria meningitidis Z2491]	gi|15793382|ref|NP 283204.1|	89.29	0
contig00047-orf00015	phosphoenolpyruvate carboxylase [Neisseria meningitidis Z2491]	gi|15793382|ref|NP 283204.1|	92.86	2E-76

Query	NR Database Subject	Subject ID	% ID	E value
contig00047-orf00019	molybdenum cofactor biosynthesis protein C [Campylobacter jejuni subsp. jejuni NCTC 11168]	gi|15791623|ref|NP 281446.1|	39.85	3E-20
contig00047-orf00021	hypothetical protein NGO1370 [Neisseria gonorrhoeae FA 1090]	gi|59801718|ref|YP 208430.1|	80.61	0
contig00047-orf00023	putative transferase [Neisseria gonorrhoeae FA 1090]	gi|59802308|ref|YP 209020.1|	88.41	1E-74
contig00047-orf00027	bifunctional biotin--[acetyl-CoA-carboxylase] ligase/pantothenate kinase [Neisseria meningitidis MC58]	gi|15677897|ref|NP 275065.1|	71.57	0
contig00047-orf00030	hypothetical protein NMB2074 [Neisseria meningitidis MC58]	gi|15677896|ref|NP 275064.1|	53.55	1E-39
contig00047-orf00030	hypothetical protein NMB2074 [Neisseria meningitidis MC58]	gi|15677896|ref|NP 275064.1|	43.48	0.25
contig00047-orf00032	hypothetical protein BURPS1710b 0503 [Burkholderia pseudomallei 1710b]	gi|76810922|ref|YP 331917.1|	28.21	1E-12
contig00047-orf00033	TPR repeat-containing protein [Clostridium tetani E88]	gi|28211870|ref|NP 782814.1|	44.44	1.2
contig00047-orf00034	transmembrane transport protein [Neisseria meningitidis Z2491]	gi|15793692|ref|NP 283514.1|	93.21	0
contig00047-orf00035	hypothetical protein NMB1796 [Neisseria meningitidis MC58]	gi|15677635|ref|NP 274794.1|	84.57	4E-88
contig00047-orf00037	PnuC protein [Mannheimia succiniciproducens MBEL55E]	gi|52424248|ref|YP 087385.1|	74.03	8E-93
contig00047-orf00041	radical SAM family protein [Psychrobacter cryohalolentis K5]	gi|93005656|ref|YP 580093.1|	65.39	2E-154
contig00047-orf00042	hypothetical protein Pcryo 0825 [Psychrobacter cryohalolentis K5]	gi|93005655|ref|YP 580092.1|	42.47	1E-52
contig00048-orf00001	elongation factor G [Neisseria meningitidis Z2491]	gi|15793163|ref|NP 282985.1|	98.43	0
contig00048-orf00003	30S ribosomal protein S7 [Neisseria gonorrhoeae FA 1090]	gi|59802165|ref|YP 208877.1|	99.31	4E-75
contig00048-orf00004	30S ribosomal protein S12 [Chromobacterium violaceum ATCC 12472]	gi|34499646|ref|NP 903861.1|	100	8E-37
contig00048-orf00007	DNA-directed RNA polymerase subunit beta' [Neisseria meningitidis Z2491]	gi|15793169|ref|NP 282991.1|	98.49	0
contig00048-orf00010	DNA-directed RNA polymerase subunit beta [Neisseria meningitidis Z2491]	gi|15793170|ref|NP 282992.1|	97.63	0
contig00048-orf00011	#N/A	gi|14195171|sp|Q9F5M1|RL7 NEIPE	100	2E-46
contig00048-orf00012	50S ribosomal protein L10 [Neisseria gonorrhoeae FA 1090]	gi|59802174|ref|YP 208886.1|	98.68	5E-27
contig00048-orf00013	50S ribosomal protein L1 [Neisseria meningitidis MC58]	gi|15676056|ref|NP 273186.1|	97.84	3E-110
contig00048-orf00014	50S ribosomal protein L11 [Neisseria meningitidis Z2491]	gi|15793174|ref|NP 282996.1|	99.31	1E-74
contig00048-orf00015	transcription antitermination protein NusG [Neisseria meningitidis MC58]	gi|15676054|ref|NP 273184.1|	88.82	2E-82
contig00048-orf00016	preprotein translocase subunit SecE [Neisseria gonorrhoeae FA 1090]	gi|59802178|ref|YP 208890.1|	73.53	1E-08
contig00049-orf00001	integral membrane ion transporter [Neisseria meningitidis Z2491]	gi|15794844|ref|NP 284666.1|	86.52	0
contig00049-orf00003	NosX accesory protein [Sinorhizobium meliloti 1021]	gi|16263101|ref|NP 435894.1|	46.24	4E-57
contig00049-orf00005	peptide chain release factor 1 [Neisseria meningitidis MC58]	gi|15677534|ref|NP 274690.1|	98.88	5E-171
contig00049-orf00006	putative ABC transporter, permease protein [Neisseria gonorrhoeae FA 1090]	gi|59802435|ref|YP 209147.1|	95.18	2E-93
contig00049-orf00008	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15677778|ref|NP 274942.1|	97.55	4E-122
contig00049-orf00009	hypothetical protein NMB0087 [Neisseria meningitidis MC58]	gi|15676019|ref|NP 273149.1|	40.38	0.00005
contig00049-orf00010	coproporphyrinogen III oxidase [Neisseria gonorrhoeae FA 1090]	gi|59801909|ref|YP 208621.1|	93.95	0
contig00049-orf00011	coproporphyrinogen III oxidase [Neisseria gonorrhoeae FA 1090]	gi|59801909|ref|YP 208621.1|	84.09	2E-15
contig00049-orf00012	Crp/FNR family transcriptional regulator [Neisseria meningitidis MC58]	gi|15676294|ref|NP 273429.1|	91.8	2E-116
contig00049-orf00014	cell division inhibitor SULA [Bdellovibrio bacteriovorus HD100]	gi|42523666|ref|NP 969046.1|	30.28	1E-08

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contig00049-orf00016	hypothetical protein MED121 16609 [Marinomonas sp. MED121]	gi|87118667|ref|ZP 01074566.1|	39.66	1E-15
contig00049-orf00021	DNA ligase [Neisseria meningitidis Z2491]	gi|15793834|ref|NP 283656.1|	91.06	0
contig00049-orf00022	hypothetical protein NMB0667 [Neisseria meningitidis MC58]	gi|15676565|ref|NP 273709.1|	69.16	4E-162
contig00049-orf00023	N-acetyl-anhydromuranmyl-L-alanine amidase [Neisseria meningitidis Z2491]	gi|15793836|ref|NP 283658.1|	77.09	2E-79
contig00049-orf00024	hypothetical protein NMB0669 [Neisseria meningitidis MC58]	gi|15676567|ref|NP 273711.1|	79.76	4E-136
contig00049-orf00026	single-stranded-DNA-specific exonuclease RecJ [Neisseria meningitidis MC58]	gi|15676738|ref|NP 273883.1|	93.99	0
contig00049-orf00028	Fe-S protein [Photobacterium profundum SS9]	gi|54308726|ref|YP 129746.1|	52.33	2E-17
contig00049-orf00031	component protein of adhesin complex [Eikenella corrodens]	gi|1817528|dbj|BAA11228.1|	34.75	4E-16
contig00049-orf00031	component protein of adhesin complex [Eikenella corrodens]	gi|1817528|dbj|BAA11228.1|	25.51	0.00006
contig00049-orf00035	hypothetical protein NGO1455 [Neisseria gonorrhoeae FA 1090]	gi|59801796|ref|YP 208508.1|	89.5	0
contig00049-orf00036	hypothetical protein NMA1703 [Neisseria meningitidis Z2491]	gi|15794596|ref|NP 284418.1|	94.16	1E-75
contig00049-orf00039	hypothetical protein NGO0960 [Neisseria gonorrhoeae FA 1090]	gi|59801349|ref|YP 208061.1|	88.37	2E-121
contig00049-orf00041	ABC transporter, permease protein [Streptococcus pneumoniae TIGR4]	gi|15900033|ref|NP 344637.1|	26.53	0.11
contig00049-orf00043	segregation and condensation protein A [Neisseria meningitidis MC58]	gi|15677357|ref|NP 274512.1|	89.73	7E-122
contig00049-orf00046	BraB [Bacillus sp. NRRL B-14911]	gi|89100086|ref|ZP 01172955.1|	46.97	8E-114
contig00049-orf00049	nicotinate phosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15794599|ref|NP 284421.1|	90.84	0
contig00050-orf00001	hypothetical protein SG1155 [Sodalis glossinidius str. 'morsitans']	gi|85059133|ref|YP 454835.1|	63.29	2E-23
contig00050-orf00002	#N/A	gi|2499099|sp|Q50939|UVRB NEIGO	98.51	0
contig00050-orf00003	putative thioredoxin I [Neisseria gonorrhoeae FA 1090]	gi|59801079|ref|YP 207791.1|	90.91	4E-52
contig00050-orf00006	ABC transporter related [Polaromonas sp. JS666]	gi|91788288|ref|YP 549240.1|	50.94	2E-140
contig00050-orf00008	acyl-CoA synthetase [Neisseria meningitidis Z2491]	gi|15794382|ref|NP 284204.1|	85.6	0
contig00050-orf00011	ABC peptide transporter, inner membrane subunit [Burkholderia xenovorans LB400]	gi|91784163|ref|YP 559369.1|	63.72	1E-93
contig00050-orf00013	Hypothetical protein CBG18879 [Caenorhabditis briggsae]	gi|39583059|emb|CAE71838.1|	38.46	0.73
contig00050-orf00014	binding-protein dependent transport system inner membrane protein [Ralstonia eutropha JMP134]	gi|73541816|ref|YP 296336.1|	69.94	2E-118
contig00050-orf00016	hypothetical protein Neut 1890 [Nitrosomonas eutropha C91]	gi|114331865|ref|YP 748087.1|	55.56	3E-47
contig00050-orf00017	hypothetical protein NGO1755 [Neisseria gonorrhoeae FA 1090]	gi|59802076|ref|YP 208788.1|	92.86	8.1
contig00050-orf00019	hypothetical protein VEx2w 02000813 [Vibrio sp. Ex25]	gi|116186656|ref|ZP 01476549.1|	71.43	9E-20
contig00050-orf00022	hypothetical protein NGO0543 [Neisseria gonorrhoeae FA 1090]	gi|59800977|ref|YP 207689.1|	97.08	7E-173
contig00050-orf00023	cation uptake regulator [Neisseria meningitidis Z2491]	gi|15794372|ref|NP 284194.1|	94.3	7E-66
contig00050-orf00025	hypothetical protein BL1634 [Bifidobacterium longum NCC2705]	gi|23466183|ref|NP 696786.1|	44.44	4.7
contig00050-orf00028	hypothetical protein NMB1048 [Neisseria meningitidis MC58]	gi|15676934|ref|NP 274082.1|	80.41	0
contig00050-orf00031	hypothetical protein Psyc 0269 [Psychrobacter arcticus 273-4]	gi|71064846|ref|YP 263573.1|	65.63	4E-153
contig00050-orf00035	hypothetical protein Rmet 3395 [Ralstonia metallidurans CH34]	gi|94312326|ref|YP 585536.1|	46.69	3E-63
contig00050-orf00035	hypothetical protein Rmet 3395 [Ralstonia metallidurans CH34]	gi|94312326|ref|YP 585536.1|	24.3	1.3

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contig00050-orf00037	hypothetical protein TTHERM 00564150 [Tetrahymena thermophila SB210]	gi|89303781|gb|EAS01769.1|	17.16	0.1
contig00050-orf00038	PREDICTED: similar to CG5362-PA, partial [Apis mellifera]	gi|66557775|ref|XP 624954.1|	70.59	7E-106
contig00050-orf00041	hypothetical protein NGO0984 [Neisseria gonorrhoeae FA 1090]	gi|59801370|ref|YP 208082.1|	75.16	0
contig00050-orf00045	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Neisseria meningitidis MC58]	gi|15677375|ref|NP 274530.1|	87.76	2E-70
contig00050-orf00049	#N/A	gi|34098748|sp|Q9RQI5|GLGB NEIDE	77.02	0
contig00051-orf00001	PilT protein, N-terminal [Paracoccus denitrificans PD1222]	gi|69938574|ref|ZP 00633015.1|	57.41	6E-13
contig00051-orf00004	TraS protein [Plasmid pSB102]	gi|15919970|ref|NP 361030.1|	41.58	3E-44
contig00051-orf00005	hypothetical protein pIPO2T p12 [Plasmid pIPO2T]	gi|16751952|ref|NP 444536.1|	33.99	6E-12
contig00051-orf00007	hypothetical protein LSL 1826 [Lactobacillus salivarius UCC118]	gi|90962799|ref|YP 536714.1|	34.78	0.00004
contig00051-orf00008	similar to Uncharacterized protein conserved in bacteria [Burkholderia vietnamiensis G4]	gi|67544959|ref|ZP 00422884.1|	36.13	3E-48
contig00051-orf00009	TRAG protein [Xylella fastidiosa Ann-1]	gi|71900565|ref|ZP 00682693.1|	36.65	1E-87
contig00051-orf00010	putative single-stranded DNA binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801407|ref|YP 208119.1|	39.77	3E-12
contig00051-orf00011	hypothetical protein Psyc 0997 [Psychrobacter arcticus 273-4]	gi|71065557|ref|YP 264284.1|	26.5	0.19
contig00051-orf00012	transporter [Arabidopsis thaliana]	gi|30696701|ref|NP 200427.2|	39.13	3.7
contig00051-orf00014	type II secretion system protein E [Xylella fastidiosa Ann-1]	gi|71900564|ref|ZP 00682692.1|	44.85	1E-74
contig00051-orf00015	TraL protein [Plasmid pSB102]	gi|15919980|ref|NP 361040.1|	46.64	1E-53
contig00051-orf00017	Conjugal transfer protein TrbG/VirB9/CagX [Xylella fastidiosa Ann-1]	gi|71900562|ref|ZP 00682690.1|	37.01	9E-39
contig00051-orf00018	VirB8 [Xylella fastidiosa Ann-1]	gi|71900561|ref|ZP 00682689.1|	35.65	8E-36
contig00051-orf00020	hypothetical protein NAP1 02340 [Erythrobacter sp. NAP1]	gi|85708037|ref|ZP 01039103.1|	32.73	1.3
contig00051-orf00021	putative periplasmic transport system [Pseudomonas aeruginosa UCBPP-PA14]	gi|116054182|ref|YP 788626.1|	36.11	0.067
contig00051-orf00022	hypothetical protein R46 015 [IncN plasmid R46]	gi|17530595|ref|NP 511193.1|	25.68	3E-15
contig00051-orf00023	hypothetical protein CbeiDRAFT 4011 [Clostridium beijerincki NCIMB 8052]	gi|82745222|ref|ZP 00907735.1|	36.11	3.6
contig00051-orf00024	TraF protein [Plasmid pSB102]	gi|15919987|ref|NP 361047.1|	32.18	2E-16
contig00051-orf00026	CagE, TrbE, VirB component of type IV transporter system [Xylella fastidiosa Ann-1]	gi|71900558|ref|ZP 00682686.1|	39.4	9E-151
contig00051-orf00028	hypothetical protein TTHERM 00589950 [Tetrahymena thermophila SB210]	gi|89301670|gb|EAR99658.1|	34.69	0.74
contig00051-orf00034	pilus retraction protein [Neisseria meningitidis Z2491]	gi|15793936|ref|NP 283758.1|	84.55	0
contig00051-orf00038	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase [Neisseria meningitidis Z2491]	gi|15793935|ref|NP 283757.1|	88.84	1E-94
contig00051-orf00040	GTP-binding protein LepA [Neisseria meningitidis MC58]	gi|15676664|ref|NP 273808.1|	99.5	0
contig00051-orf00041	signal peptidase I [Neisseria meningitidis MC58]	gi|15676663|ref|NP 273807.1|	69.53	2E-139
contig00051-orf00044	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793932|ref|NP 283754.1|	72.28	6E-98
contig00051-orf00045	hypothetical protein NGO1432 [Neisseria gonorrhoeae FA 1090]	gi|59801775|ref|YP 208487.1|	95.08	4E-175
contig00051-orf00046	Clr6 histone deacetylase complex subunit Pst2 [Schizosaccharomyces pombe]	gi|19114558|ref|NP 593646.1|	25.17	3.3

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contig00051-orf00049	putative ABC transporter, permease protein [Neisseria gonorrhoeae FA 1090]	gi|59801776|ref|YP 208488.1|	93.99	1E-105
contig00051-orf00051	putative ABC transporter, ATP-binding protein [Neisseria gonorrhoeae FA 1090]	gi|59801777|ref|YP 208489.1|	94.55	2E-94
contig00051-orf00053	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793708|ref|NP 283530.1|	93.56	3E-152
contig00051-orf00054	putative acyl-CoA hydrolase [Neisseria gonorrhoeae FA 1090]	gi|59801445|ref|YP 208157.1|	86.9	2E-56
contig00051-orf00056	hypothetical protein NMB0706 [Neisseria meningitidis MC58]	gi|15676604|ref|NP 273748.1|	86.27	5E-127
contig00051-orf00060	ribosomal large subunit pseudouridine synthase D [Neisseria meningitidis MC58]	gi|15676602|ref|NP 273746.1|	90.65	4E-176
contig00051-orf00061	ComL [Neisseria gonorrhoeae FA 1090]	gi|59800727|ref|YP 207439.1|	85.83	2E-124
contig00051-orf00063	threonine dehydratase [Neisseria meningitidis Z2491]	gi|15794044|ref|NP 283866.1|	86.05	1E-155
contig00051-orf00064	threonine dehydratase [Neisseria gonorrhoeae FA 1090]	gi|59800885|ref|YP 207597.1|	88.11	1E-65
contig00051-orf00067	D-ala-D-ala-carboxypeptidase [Chromobacterium violaceum ATCC 12472]	gi|34498549|ref|NP 902764.1|	60.7	5E-106
contig00051-orf00068	hypothetical protein NMB1071 [Neisseria meningitidis MC58]	gi|15676955|ref|NP 274104.1|	70.87	1E-81
contig00051-orf00070	hypothetical protein NMB0932 [Neisseria meningitidis MC58]	gi|15676826|ref|NP 273971.1|	58.45	8E-34
contig00051-orf00071	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	82.22	2E-14
contig00051-orf00073	hypothetical protein NMB1023 [Neisseria meningitidis MC58]	gi|15676911|ref|NP 274057.1|	96.24	4E-177
contig00051-orf00075	cation transporter E1-E2 family ATPase [Neisseria meningitidis MC58]	gi|15677191|ref|NP 274344.1|	94.59	0
contig00051-orf00078	putative mercury transport periplasmic protein [Neisseria meningitidis MC58]	gi|15677139|ref|NP 274292.1|	72.46	5E-21
contig00051-orf00079	heavy metal dependent transcriptional regulator [Haemophilus influenzae 86-028NP]	gi|68248895|ref|YP 248007.1|	65.87	1E-34
contig00051-orf00080	conserved hypothetical protein [Desulfotomaculum reducens MI-1]	gi|88945618|ref|ZP 01148786.1|	37.38	2E-14
contig00051-orf00081	similar to thioredoxin [Enterococcus faecium DO]	gi|69245899|ref|ZP 00603692.1|	46.55	0.00001
contig00051-orf00083	ArsR family transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59801545|ref|YP 208257.1|	96.12	5E-51
contig00051-orf00084	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	92.65	2E-104
contig00051-orf00084	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	83.95	7E-29
contig00051-orf00085	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	92.41	7E-37
contig00051-orf00085	hypothetical protein NGO1184 [Neisseria gonorrhoeae FA 1090]	gi|59801544|ref|YP 208256.1|	73.33	7E-37
contig00051-orf00087	malate dehydrogenase [Propionibacterium acnes KPA171202]	gi|50841800|ref|YP 055027.1|	71.06	0
contig00051-orf00088	#N/A	gi|46133014|ref|ZP 00156449.2|	94.19	3E-127
contig00051-orf00090	ARA1 protein [Mannheimia succiniciproducens MBEL55E]	gi|52425264|ref|YP 088401.1|	71.59	1E-40
contig00051-orf00090	ARA1 protein [Mannheimia succiniciproducens MBEL55E]	gi|52425264|ref|YP 088401.1|	70	1E-40
contig00051-orf00091	morphine 6-dehydrogenase [Listeria monocytogenes str. 4b F2365]	gi|46908764|ref|YP 015153.1|	61.83	3E-41
contig00051-orf00092	hypothetical protein MS0141 [Mannheimia succiniciproducens MBEL55E]	gi|52424196|ref|YP 087333.1|	62.55	5E-95
contig00051-orf00093	dihydroorotate dehydrogenase 1A [Streptococcus pneumoniae TIGR4]	gi|15900658|ref|NP 345262.1|	81.94	3E-150
contig00051-orf00095	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.59	6E-14
contig00051-orf00096	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein [Neisseria meningitidis MC58]	gi|15677236|ref|NP 274389.1|	82.95	0
contig00051-orf00099	hypothetical protein NGO0448 [Neisseria gonorrhoeae FA 1090]	gi|59800888|ref|YP 207600.1|	75.76	3E-24
contig00051-orf00100	#N/A	gi|85108197|ref|XP 962527.1|	48.28	1.6

Query	NR Database Subject	Subject ID	% ID	E value
contig00051-orf00102	phosphatidylserine decarboxylase [Neisseria gonorrhoeae FA 1090]	gi|59801565|ref|YP 208277.1|	78.28	9E-107
contig00051-orf00106	excinuclease ABC subunit A [Neisseria meningitidis MC58]	gi|15676855|ref|NP 274000.1|	97.18	0
contig00051-orf00107	SMC family chromosome segregation protein [Candidatus Pelagibacter ubique HTCC1062]	gi|71082822|ref|YP 265541.1|	27.27	0.12
contig00051-orf00107	SMC family chromosome segregation protein [Candidatus Pelagibacter ubique HTCC1062]	gi|71082822|ref|YP 265541.1|	24.64	1.7
contig00052-orf00001	glyceraldehyde 3-phosphate dehydrogenase C [Neisseria meningitidis Z2491]	gi|15793264|ref|NP 283086.1|	97.31	0
contig00052-orf00005	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Neisseria meningitidis Z2491]	gi|15793281|ref|NP 283103.1|	96.68	1E-157
contig00052-orf00008	hypothetical protein BSU12680 [Bacillus subtilis subsp. subtilis str. 168]	gi|16078333|ref|NP 389150.1|	30.61	8.1
contig00052-orf00010	gamma-glutamyltranspeptidase [Neisseria meningitidis MC58]	gi|15676942|ref|NP 274091.1|	65.47	0
contig00052-orf00013	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]	gi|27573069|gb|AAO19934.1|	90.66	0
contig00052-orf00018	glycerate dehydrogenase [Neisseria meningitidis MC58]	gi|15675969|ref|NP 273095.1|	76.27	7E-137
contig00052-orf00019	hypothetical protein NMB0028 [Neisseria meningitidis MC58]	gi|15675968|ref|NP 273094.1|	71.83	3E-23
contig00052-orf00022	regulatory protein, TetR:Tetracyclin repressor, C-terminal [Frankia sp. EAN1pec]	gi|68233000|ref|ZP 00572133.1|	48.39	8.2
contig00052-orf00023	peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58]	gi|15675967|ref|NP 273093.1|	92.66	7E-54
contig00052-orf00025	periplasmic type I secretion system protein [Neisseria meningitidis Z2491]	gi|15794874|ref|NP 284696.1|	43.36	2E-91
contig00052-orf00026	putative tape measure protein [Lactobacillus phage Lc-Nu]	gi|78000025|ref|YP 358771.1|	38.46	0.56
contig00052-orf00027	#N/A	gi|66818877|ref|XP 643098.1|	34.43	0.017
contig00052-orf00028	MFS transport protein AraJ [Escherichia coli CFT073]	gi|26246399|ref|NP 752438.1|	31.91	1.7
contig00052-orf00030	HECT domain and RCC1-like domain protein 3 [Tetrahymena thermophila SB210]	gi|89305267|gb|EAS03255.1|	50	8.3
contig00052-orf00031	NADH dehydrogenase subunit 3 [Paramecium aurelia]	gi|8928621|ref|NP 059426.1|	34.04	2.8
contig00052-orf00036	putative secretion protein [Neisseria gonorrhoeae FA 1090]	gi|59800583|ref|YP 207295.1|	51.18	9E-117
contig00052-orf00037	hypothetical protein plu0852 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37524849|ref|NP 928193.1|	54.63	6E-37
contig00052-orf00037	hypothetical protein plu0852 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37524849|ref|NP 928193.1|	56.86	6E-37
contig00052-orf00039	unknown [Moraxella catarrhalis]	gi|7406836|gb|AAF61810.1|	55.68	3E-162
contig00052-orf00041	glutamyl-tRNA synthetase [Neisseria gonorrhoeae FA 1090]	gi|59802239|ref|YP 208951.1|	100	2E-31
contig00052-orf00043	putative periplasmic iron/siderophore binding protein [Actinobacillus succinogenes 130Z]	gi|75430074|ref|ZP 00732613.1|	72.62	5E-148
contig00052-orf00046	glutamyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15675951|ref|NP 273069.1|	96.12	0
contig00052-orf00047	peptidase M16-like [Nitrosospira multiformis ATCC 25196]	gi|82703849|ref|YP 413415.1|	48.68	9E-43
contig00052-orf00049	putative zinc protease [Aromatoleum aromaticum EbN1]	gi|56476191|ref|YP 157780.1|	37.18	2E-33
contig00052-orf00053	ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676188|ref|NP 273320.1|	89	0
contig00052-orf00057	hypothetical protein NMA0169 [Neisseria meningitidis Z2491]	gi|15793196|ref|NP 283018.1|	83.93	9E-129

Query	NR Database Subject	Subject ID	% ID	E value
contig00052-orf00058	enolase [Bradyrhizobium japonicum USDA 110]	gi|27379905|ref|NP 771434.1|	41.67	1.3
contig00052-orf00062	hypothetical protein NGO2032 [Neisseria gonorrhoeae FA 1090]	gi|59802340|ref|YP 209052.1|	74.09	3E-165
contig00052-orf00062	hypothetical protein NGO2032 [Neisseria gonorrhoeae FA 1090]	gi|59802340|ref|YP 209052.1|	33.06	1E-20
contig00052-orf00070	ABC transporter ATP-binding protein [Neisseria meningitidis MC58]	gi|15677865|ref|NP 275033.1|	63.46	1E-105
contig00052-orf00074	hypothetical protein NMA0394 [Neisseria meningitidis Z2491]	gi|15793402|ref|NP 283224.1|	64.21	3E-106
contig00052-orf00076	putative carbonic anhydrase [Neisseria gonorrhoeae FA 1090]	gi|59802380|ref|YP 209092.1|	84.86	7E-86
contig00052-orf00078	hypothetical protein NMB2024 [Neisseria meningitidis MC58]	gi|15677849|ref|NP 275016.1|	79	1E-90
contig00052-orf00080	hypothetical protein NGO2081 [Neisseria gonorrhoeae FA 1090]	gi|59802382|ref|YP 209094.1|	93.75	7E-63
contig00052-orf00082	SPOUT methyltransferase superfamily protein [Neisseria meningitidis MC58]	gi|15677847|ref|NP 275014.1|	97.44	1E-82
contig00052-orf00085	hypothetical protein NMB0311 [Neisseria meningitidis MC58]	gi|15676229|ref|NP 273361.1|	40.51	4E-15
contig00052-orf00088	hypothetical protein NMB0310 [Neisseria meningitidis MC58]	gi|15676228|ref|NP 273360.1|	68.18	5E-37
contig00052-orf00090	hypothetical protein NGO1693 [Neisseria gonorrhoeae FA 1090]	gi|59802017|ref|YP 208729.1|	70.13	2E-61
contig00052-orf00092	hypothetical protein UM00456.1 [Ustilago maydis 521]	gi|71003874|ref|XP 756603.1|	48.48	8.3
contig00052-orf00094	#N/A	gi|7274446|gb|AAF44778.1|AF235144 1	92.47	6E-46
contig00052-orf00095	#N/A	gi|7228614|gb|AAF42541.1|AF226392 1	77.2	4E-131
contig00052-orf00095	#N/A	gi|7228614|gb|AAF42541.1|AF226392 1	85	2E-11
contig00052-orf00096	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793297|ref|NP 283119.1|	89.96	7E-130
contig00052-orf00097	hypothetical protein NMB0035 [Neisseria meningitidis MC58]	gi|15675975|ref|NP 273101.1|	83.76	9E-177
contig00052-orf00101	hypothetical protein NMA0282 [Neisseria meningitidis Z2491]	gi|15793299|ref|NP 283121.1|	84.34	0
contig00053-orf00002	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit [Neisseria gonorrhoeae FA 1090]	gi|59800512|ref|YP 207224.1|	89.36	1E-13
contig00053-orf00006	hypothetical protein NMA1806 [Neisseria meningitidis Z2491]	gi|15794696|ref|NP 284518.1|	64.74	3E-70
contig00053-orf00006	hypothetical protein NMA1806 [Neisseria meningitidis Z2491]	gi|15794696|ref|NP 284518.1|	73.68	3E-70
contig00053-orf00010	formate--tetrahydrofolate ligase [Neisseria gonorrhoeae FA 1090]	gi|59800526|ref|YP 207238.1|	98.16	0
contig00053-orf00011	polyphosphate kinase [Neisseria meningitidis Z2491]	gi|15793549|ref|NP 283371.1|	86.11	0
contig00053-orf00016	magnesium transporter [Neisseria meningitidis MC58]	gi|15677827|ref|NP 274991.1|	93.39	0
contig00053-orf00021	putative sugar transporter [Neisseria meningitidis MC58]	gi|15676302|ref|NP 273437.1|	96	0
contig00053-orf00025	maltose phosphorylase [Neisseria meningitidis Z2491]	gi|15794973|ref|NP 284795.1|	97.46	0
contig00053-orf00028	beta-phosphoglucomutase [Neisseria meningitidis Z2491]	gi|15794972|ref|NP 284794.1|	96.83	2E-96
contig00053-orf00030	hypothetical protein NMB1840 [Neisseria meningitidis MC58]	gi|15677676|ref|NP 274837.1|	96.06	1E-57
contig00053-orf00032	fimbrial assembly protein [Neisseria meningitidis Z2491]	gi|15794588|ref|NP 284410.1|	66.8	8E-85
contig00053-orf00034	hypothetical protein NMB0436 [Neisseria meningitidis MC58]	gi|15676348|ref|NP 273484.1|	89.05	4E-99
contig00053-orf00036	hypothetical protein NGO1410 [Neisseria gonorrhoeae FA 1090]	gi|59801754|ref|YP 208466.1|	75.63	3E-49
contig00053-orf00038	hypothetical protein NMB0572 [Neisseria meningitidis MC58]	gi|15676477|ref|NP 273616.1|	85.19	1E-90

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contig00053-orf00039	Hypothetical protein CBG01056 [Caenorhabditis briggsae]	gi|39589260|emb|CAE57993.1|	28.57	6.3
contig00053-orf00040	polyamine permease substrate-binding protein [Neisseria meningitidis Z2491]	gi|15793802|ref|NP 283624.1|	78.63	4E-170
contig00053-orf00041	IS1106 transposase [Neisseria meningitidis MC58]	gi|15677391|ref|NP 274546.1|	100	3E-22
contig00055-orf00001	hypothetical protein NMA0028 [Neisseria meningitidis Z2491]	gi|15793061|ref|NP 282883.1|	98.14	5E-119
contig00055-orf00003	hypothetical protein NMA0029 [Neisseria meningitidis Z2491]	gi|15793062|ref|NP 282884.1|	98.71	8E-162
contig00055-orf00005	hypothetical protein NMB0228 [Neisseria meningitidis MC58]	gi|15676154|ref|NP 273285.1|	98.78	1E-117
contig00055-orf00007	hypothetical protein NMB0227 [Neisseria meningitidis MC58]	gi|15676153|ref|NP 273284.1|	99.75	0
contig00055-orf00008	hypothetical protein NMB0226 [Neisseria meningitidis MC58]	gi|15676152|ref|NP 273283.1|	96.52	2E-131
contig00055-orf00010	Hypothetical membrane spanning protein [Ralstonia solanacearum UW551]	gi|83747068|ref|ZP 00944112.1|	38.02	6E-52
contig00055-orf00013	#N/A	gi|6449096|gb|AAF08825.1|AF1940 79 12	79.22	8E-150
contig00055-orf00014	hypothetical protein ELI 07200 [Erythrobacter litoralis HTCC2594]	gi|85374267|ref|YP 458329.1|	40.91	2E-10
contig00055-orf00016	D,D-heptose 1,7-bisphosphate phosphatase [Neisseria meningitidis Z2491]	gi|15793412|ref|NP 283234.1|	81.82	2E-84
contig00055-orf00018	NlaB [Neisseria gonorrhoeae FA 1090]	gi|59802370|ref|YP 209082.1|	81.74	8E-109
contig00055-orf00021	chaperonin GroEL [Neisseria meningitidis Z2491]	gi|15793474|ref|NP 283296.1|	98.5	0
contig00055-orf00023	co-chaperonin GroES [Neisseria meningitidis MC58]	gi|15677803|ref|NP 274967.1|	98.95	4E-46
contig00055-orf00026	outer membrane protein 64 [Actinobacillus actinomycetemcomitans]	gi|19911158|dbj|BAB86907.1|	51.51	1E-163
contig00055-orf00028	iron(III) ABC transporter, periplasmic binding protein [Neisseria meningitidis MC58]	gi|15677817|ref|NP 274981.1|	94.33	5E-141
contig00055-orf00029	phosphoglyceromutase [Neisseria gonorrhoeae FA 1090]	gi|59801617|ref|YP 208329.1|	95.15	1E-105
contig00055-orf00032	aromatic acid decarboxylase [Neisseria gonorrhoeae FA 1090]	gi|59802437|ref|YP 209149.1|	78.49	1E-79
contig00055-orf00033	valine--pyruvate transaminase [Neisseria meningitidis MC58]	gi|15677659|ref|NP 274820.1|	91.36	0
contig00055-orf00035	KatA [Neisseria gonorrhoeae FA 1090]	gi|59802086|ref|YP 208798.1|	94.11	0
contig00055-orf00037	D-fructose-6-phosphate amidotransferase [Neisseria meningitidis Z2491]	gi|15793294|ref|NP 283116.1|	89.54	0
contig00055-orf00039	diaminohydroxyphosphoribosylaminopyrimidine deaminase/phosphoribosylamino)uracil reductase [Neisseria meningitidis Z2491]	gi|15793630|ref|NP 283452.1|	74.73	3E-149
contig00055-orf00040	tegument protein US11 [Papiine herpesvirus 2]	gi|83722640|ref|YP 443918.1|	36.96	0.85
contig00055-orf00040	tegument protein US11 [Papiine herpesvirus 2]	gi|83722640|ref|YP 443918.1|	38.89	4.2
contig00055-orf00042	transcriptional regulator NrdR [Chromobacterium violaceum ATCC 12472]	gi|34496742|ref|NP 900957.1|	57.6	5E-32
contig00055-orf00044	2-dehydro-3-deoxyphosphooctonate aldolase [Neisseria meningitidis MC58]	gi|15677150|ref|NP 274303.1|	82.42	6E-123
contig00055-orf00045	aspartate alpha-decarboxylase [Neisseria meningitidis MC58]	gi|15677149|ref|NP 274302.1|	92.13	5E-61
contig00055-orf00047	hypothetical protein WS1043 [Wolinella succinogenes DSM 1740]	gi|34557428|ref|NP 907243.1|	42.42	2E-12
contig00055-orf00047	hypothetical protein WS1043 [Wolinella succinogenes DSM 1740]	gi|34557428|ref|NP 907243.1|	43.24	2E-12
contig00055-orf00049	TonB [Neisseria gonorrhoeae FA 1090]	gi|59801727|ref|YP 208439.1|	32.93	0.01
contig00055-orf00052	hypothetical protein NMB1075 [Neisseria meningitidis MC58]	gi|15676959|ref|NP 274108.1|	94.14	6E-122
contig00055-orf00053	hypothetical protein NGO0841 [Neisseria gonorrhoeae FA 1090]	gi|59801246|ref|YP 207958.1|	89.19	5E-112
contig00055-orf00055	hypothetical protein NGO0869 [Neisseria gonorrhoeae FA 1090]	gi|59801270|ref|YP 207982.1|	77.25	1E-86

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contig00055-orf00058	hypothetical protein V12B01 03578 [Vibrio splendidus 12B01]	gi|84394029|ref|ZP 00992767.1|	67.92	4E-42
contig00055-orf00060	hypothetical protein NMB1610 [Neisseria meningitidis MC58]	gi|15677460|ref|NP 274616.1|	53.08	2E-65
contig00055-orf00061	hypothetical protein NMA1810 [Neisseria meningitidis Z2491]	gi|15794700|ref|NP 284522.1|	89.02	2E-34
contig00055-orf00062	histidine-binding periplasmic protein [Neisseria meningitidis Z2491]	gi|15794701|ref|NP 284523.1|	86.49	2E-107
contig00055-orf00065	respiratory nitrate reductase alpha chain [Chromobacterium violaceum ATCC 12472]	gi|34497998|ref|NP 902213.1|	78.15	0
contig00055-orf00066	COG0521: Molybdopterin biosynthesis enzymes [Rubrivivax gelatinosus PM1]	gi|47574364|ref|ZP 00244400.1|	63.3	5E-61
contig00055-orf00068	transposase (fragment) [Neisseria meningitidis Z2491]	gi|15795054|ref|NP 284876.1|	89.66	5E-15
contig00055-orf00068	transposase (fragment) [Neisseria meningitidis Z2491]	gi|15795054|ref|NP 284876.1|	100	5E-15
contig00055-orf00069	putative transposase [Neisseria meningitidis]	gi|6900417|emb|CAB72028.1|	79.41	3E-08
contig00055-orf00070	hypothetical protein NMB0428 [Neisseria meningitidis MC58]	gi|15676340|ref|NP 273476.1|	87.5	9E-10
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	25.41	2E-127
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	25.07	1E-108
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	25.34	3E-103
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	24.49	1E-100
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	23.44	3E-88
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	22.65	5E-74
contig00056-orf00005	hypothetical protein MS0748 [Mannheimia succiniciproducens MBEL55E]	gi|52424803|ref|YP 087940.1|	23.99	2E-18
contig00056-orf00008	serine/arginine repetitive matrix 1 [Danio rerio]	gi|47087423|ref|NP 998607.1|	30.66	0.0002
contig00056-orf00008	serine/arginine repetitive matrix 1 [Danio rerio]	gi|47087423|ref|NP 998607.1|	22.11	3.6
contig00056-orf00009	hypothetical protein NGO1598 [Neisseria gonorrhoeae FA 1090]	gi|59801926|ref|YP 208638.1|	67.86	9E-28
contig00056-orf00011	probable transcriptional regulator [Actinobacillus succinogenes 130Z]	gi|75429391|ref|ZP 00732213.1|	39.19	1E-44
contig00056-orf00012	NAD-dependent epimerase/dehydratase [Polaromonas sp. JS666]	gi|91790410|ref|YP 551362.1|	49.54	6E-39
contig00056-orf00013	COG4922: Uncharacterized protein conserved in bacteria [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|32033902|ref|ZP 00134173.1|	74.65	2E-24
contig00056-orf00014	hypothetical protein [Plasmodium berghei strain ANKA]	gi|68067690|ref|XP 675787.1|	32.61	6.2
contig00056-orf00015	WblA protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37528609|ref|NP 931954.1|	74.83	0
contig00056-orf00018	hypothetical protein NGO0088 [Neisseria gonorrhoeae FA 1090]	gi|59800549|ref|YP 207261.1|	47.83	2E-91
contig00056-orf00020	hypothetical protein MS1493 [Mannheimia succiniciproducens MBEL55E]	gi|52425548|ref|YP 088685.1|	34.34	7E-35
contig00056-orf00023	hypothetical protein NGO0087 [Neisseria gonorrhoeae FA 1090]	gi|59800548|ref|YP 207260.1|	78.31	3E-165
contig00056-orf00025	hypothetical protein NGO0086 [Neisseria gonorrhoeae FA 1090]	gi|59800547|ref|YP 207259.1|	88.97	0
contig00056-orf00026	pilin glycosylation protein PglB [Neisseria meningitidis MC58]	gi|15677656|ref|NP 274817.1|	87.88	3E-98
contig00056-orf00028	putative carbamoyl phosphate synthase large subunit [Vibrio parahaemolyticus RIMD 2210633]	gi|28897006|ref|NP 796611.1|	51.79	1E-88
contig00056-orf00029	hypothetical protein VP0233 [Vibrio parahaemolyticus RIMD 2210633]	gi|28897007|ref|NP 796612.1|	41.86	9E-38
contig00056-orf00030	methionyl-tRNA formyltransferase [Chlorobium tepidum TLS]	gi|21674274|ref|NP 662339.1|	37.7	4E-12
contig00056-orf00031	pilin glycosylation protein [Neisseria meningitidis Z2491]	gi|15793626|ref|NP 283448.1|	94.86	0

Query	NR Database Subject	Subject ID	% ID	E value
contig00056-orf00034	pilin glycosylation protein [Neisseria meningitidis MC58]	gi|15677658|ref|NP 274819.1|	74.33	0
contig00056-orf00037	putative polysaccharide export protein [Pectobacterium atrosepticum SCRI1043]	gi|50120356|ref|YP 049523.1|	46.77	1E-91
contig00056-orf00039	putative protein-tyrosine-phosphatase [Marinomonas sp. MED121]	gi|87120045|ref|ZP 01075941.1|	53.52	1E-37
contig00056-orf00040	tyrosine kinase [Pectobacterium atrosepticum SCRI1043]	gi|50120358|ref|YP 049525.1|	42.17	1E-156
contig00056-orf00041	hypothetical protein ACIAD1673 [Acinetobacter sp. ADP1]	gi|50084830|ref|YP 046340.1|	53.04	4E-58
contig00056-orf00042	putative transporter [Acinetobacter sp. ADP1]	gi|50084831|ref|YP 046341.1|	38.71	3E-16
contig00056-orf00043	LysR family transcriptional regulator [Acinetobacter sp. ADP1]	gi|50084832|ref|YP 046342.1|	52.24	7E-11
contig00056-orf00043	LysR family transcriptional regulator [Acinetobacter sp. ADP1]	gi|50084832|ref|YP 046342.1|	50	0.02
contig00056-orf00043	LysR family transcriptional regulator [Acinetobacter sp. ADP1]	gi|50084832|ref|YP 046342.1|	40	0.02
contig00056-orf00045	WblB protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37528610|ref|NP 931955.1|	73.28	5E-151
contig00056-orf00046	#N/A	gi|42629388|ref|ZP 00154935.1|	58.99	5E-70
contig00056-orf00048	phospho-N-acetylmuramoyl-pentapeptide-transferase [Neisseria meningitidis Z2491]	gi|15794944|ref|NP 284766.1|	94.17	1E-166
contig00056-orf00049	hypothetical protein NMB0417 [Neisseria meningitidis MC58]	gi|15676329|ref|NP 273465.1|	85.19	0.0000007
contig00056-orf00050	UDP-MurNAc-pentapeptide synthetase [Neisseria meningitidis MC58]	gi|15676328|ref|NP 273464.1|	91.43	0
contig00056-orf00052	hypothetical protein TTC0921 [Thermus thermophilus HB27]	gi|46199225|ref|YP 004892.1|	22.84	8E-11
contig00056-orf00054	peptidase M23B [Deinococcus geothermalis DSM 11300]	gi|94986326|ref|YP 605690.1|	56.74	8E-41
contig00056-orf00057	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase [Neisseria gonorrhoeae FA 1090]	gi|59801877|ref|YP 208589.1|	93.28	0
contig00056-orf00059	penicillin binding protein 2 [Neisseria gonorrhoeae]	gi|24559775|gb|AAN61107.1|	82.3	0
contig00056-orf00061	cell division protein FtsL-related protein [Neisseria meningitidis MC58]	gi|15676325|ref|NP 273461.1|	65.52	4E-17
contig00056-orf00062	S-adenosyl-methyltransferase MraW [Neisseria meningitidis Z2491]	gi|15794950|ref|NP 284772.1|	85.22	6E-149
contig00056-orf00063	cell division protein MraZ [Neisseria gonorrhoeae FA 1090]	gi|59801881|ref|YP 208593.1|	78.47	8E-61
contig00056-orf00064	hypothetical protein NGO1546 [Neisseria gonorrhoeae FA 1090]	gi|59801882|ref|YP 208594.1|	71.76	8E-142
contig00056-orf00067	dihydroorotate dehydrogenase 2 [Neisseria meningitidis MC58]	gi|15676147|ref|NP 273278.1|	90.39	1E-162
contig00056-orf00068	putative phosphoglycolate phosphatase [Neisseria meningitidis MC58]	gi|15677666|ref|NP 274827.1|	63.38	3E-72
contig00056-orf00070	conserved hypothetical protein [Actinobacillus succinogenes 130Z]	gi|75430081|ref|ZP 00732620.1|	50.55	2E-75
contig00056-orf00071	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143632|ref|ZP 00134825.2|	72.62	2E-147
contig00056-orf00074	Fe(III) dicitrate ABC transporter, permease [Actinobacillus succinogenes 130Z]	gi|75430078|ref|ZP 00732617.1|	78.9	1E-107
contig00056-orf00077	COG1120: ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143630|ref|ZP 00134823.2|	71.15	3E-100
contig00056-orf00078	COG3794: Plastocyanin [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|32034684|ref|ZP 00134822.1|	58.74	6E-45
contig00056-orf00080	putative transcriptional regulator [Neisseria meningitidis MC58]	gi|15676212|ref|NP 273344.1|	74.92	1E-123
contig00056-orf00082	hypothetical protein NMB0291 [Neisseria meningitidis MC58]	gi|15676213|ref|NP 273345.1|	76.69	1E-44
contig00056-orf00083	hypothetical protein NMA2195 [Neisseria meningitidis Z2491]	gi|15795064|ref|NP 284886.1|	85.57	7E-97
contig00056-orf00085	hypothetical protein NMB2021 [Neisseria meningitidis MC58]	gi|15677846|ref|NP 275013.1|	95.4	1E-42

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contig00056-orf00086	pathogenicity island-encoded protein D [Photobacterium sp. SKA34]	gi|89076044|ref|ZP 01162407.1|	44.12	1.7
contig00056-orf00087	hypothetical protein plu3515 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527388|ref|NP 930732.1|	41.92	4E-31
contig00056-orf00088	hypothetical protein plu3514 [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527387|ref|NP 930731.1|	34.45	3E-75
contig00056-orf00091	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793314|ref|NP 283136.1|	91.55	5E-31
contig00056-orf00092	hypothetical protein NMB2130 [Neisseria meningitidis MC58]	gi|15677943|ref|NP 275115.1|	83.1	2E-26
contig00056-orf00093	argininosuccinate synthase [Neisseria meningitidis Z2491]	gi|15793316|ref|NP 283138.1|	98.21	0
contig00056-orf00094	PREDICTED: similar to polycystin 1-like 2 [Danio rerio]	gi|68431741|ref|XP 691431.1|	22.02	0.15
contig00056-orf00096	CinA-related protein [Neisseria meningitidis MC58]	gi|15677941|ref|NP 275113.1|	85.77	5E-130
contig00057-orf00001	hypothetical protein NMB1853 [Neisseria meningitidis MC58]	gi|15677688|ref|NP 274849.1|	76.32	0.023
contig00057-orf00004	#N/A	gi|66811648|ref|XP 640003.1|	39.39	0.73
contig00057-orf00008	carbamoyl phosphate synthase large subunit [Neisseria meningitidis Z2491]	gi|15793592|ref|NP 283414.1|	96.36	0
contig00057-orf00009	hypothetical protein NMB1486 [Neisseria meningitidis MC58]	gi|15677339|ref|NP 274494.1|	75	0.43
contig00057-orf00010	hypothetical protein NMB1485 [Neisseria meningitidis MC58]	gi|15677338|ref|NP 274493.1|	91.51	0
contig00057-orf00011	beta-hexosaminidase [Neisseria meningitidis Z2491]	gi|15793686|ref|NP 283508.1|	81.44	3E-161
contig00057-orf00015	integral membrane protein [Neisseria meningitidis Z2491]	gi|15793687|ref|NP 283509.1|	89.44	0
contig00057-orf00018	protease DO [Neisseria meningitidis MC58]	gi|15677994|ref|NP 273577.1|	73.95	0
contig00057-orf00021	endonuclease III [Neisseria meningitidis MC58]	gi|15676439|ref|NP 273578.1|	94.71	6E-112
contig00057-orf00026	primosome assembly protein PriA [Neisseria meningitidis MC58]	gi|15676457|ref|NP 273596.1|	95.2	0
contig00057-orf00027	thiol:disulfide interchange protein DsbC [Neisseria meningitidis MC58]	gi|15676456|ref|NP 273595.1|	78.6	2E-106
contig00057-orf00029	hypothetical protein NMA0716 [Neisseria meningitidis Z2491]	gi|15793693|ref|NP 283515.1|	91.97	3E-139
contig00057-orf00031	hypothetical protein NMB0538 [Neisseria meningitidis MC58]	gi|15676444|ref|NP 273583.1|	86.39	7E-72
contig00057-orf00034	variant surface glycoprotein [Trypanosoma brucei TREU927]	gi|74026464|ref|XP 829798.1|	32.22	0.56
contig00057-orf00035	porphobilinogen deaminase [Neisseria gonorrhoeae FA 1090]	gi|59800604|ref|YP 207316.1|	91.29	7E-142
contig00057-orf00037	O-succinylhomoserine sulfhydrolase [Neisseria meningitidis Z2491]	gi|15794698|ref|NP 284520.1|	97.43	0
contig00057-orf00038	hypothetical protein NGO1148 [Neisseria gonorrhoeae FA 1090]	gi|59801515|ref|YP 208227.1|	85.07	5E-15
contig00057-orf00040	deoxyguanosinetriphosphate triphosphohydrolase-like protein [Chromobacterium violaceum ATCC 12472]	gi|34498665|ref|NP 902880.1|	62.08	6E-149
contig00057-orf00041	ribonuclease HI [Neisseria meningitidis Z2491]	gi|15794707|ref|NP 284529.1|	84.03	1E-71
contig00057-orf00044	tellurite resistance protein TehB [Neisseria gonorrhoeae FA 1090]	gi|59801527|ref|YP 208239.1|	71.68	2E-104
contig00057-orf00045	Irg1 [Neisseria gonorrhoeae FA 1090]	gi|59801187|ref|YP 207899.1|	64.38	6E-114
contig00058-orf00002	homoserine kinase [Neisseria meningitidis MC58]	gi|15678023|ref|NP 275021.1|	74.67	6E-132
contig00058-orf00003	#N/A	gi|13959357|sp|Q9K0C7|ERA NEIMB	83.17	6E-127
contig00058-orf00005	ribonuclease III [Neisseria meningitidis Z2491]	gi|15793857|ref|NP 283679.1|	85.77	3E-105
contig00058-orf00006	hypothetical protein NGO0258 [Neisseria gonorrhoeae FA 1090]	gi|59800709|ref|YP 207421.1|	81.31	5E-48

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contig00058-orf00008	riboflavin synthase subunit beta [Neisseria meningitidis MC58]	gi|15676582|ref|NP 273726.1|	84.81	1E-61
contig00058-orf00011	transcription antitermination protein NusB [Neisseria meningitidis Z2491]	gi|15793854|ref|NP 283676.1|	87.86	1E-65
contig00058-orf00012	leucine-responsive regulatory protein [Neisseria meningitidis MC58]	gi|15677499|ref|NP 274655.1|	86.33	7E-64
contig00058-orf00013	D-amino acid dehydrogenase small subunit [Neisseria meningitidis MC58]	gi|15676103|ref|NP 273234.1|	78.12	0
contig00058-orf00016	hypothetical protein NMB1644 [Neisseria meningitidis MC58]	gi|15677493|ref|NP 274649.1|	86.97	0
contig00058-orf00019	hypothetical protein NMB1645 [Neisseria meningitidis MC58]	gi|15677494|ref|NP 274650.1|	87.44	0
contig00058-orf00020	hypothetical protein TTHERM 00071100 [Tetrahymena thermophila SB210]	gi|89289615|gb|EAR87603.1|	36.17	6.2
contig00058-orf00023	isocitrate dehydrogenase, NADP-dependent, monomeric type [Neisseria meningitidis MC58]	gi|15676815|ref|NP 273960.1|	96.12	0
contig00058-orf00024	isocitrate dehydrogenase, NADP-dependent, monomeric type [Neisseria meningitidis MC58]	gi|15676815|ref|NP 273960.1|	86.44	2E-78
contig00058-orf00024	isocitrate dehydrogenase, NADP-dependent, monomeric type [Neisseria meningitidis MC58]	gi|15676815|ref|NP 273960.1|	82.19	1E-26
contig00058-orf00026	dmpR [Pseudomonas sp.]	gi|483552|emb|CAA48174.1|	53.15	4E-131
contig00058-orf00027	DMS oxygenase component [Acinetobacter sp.]	gi|2605608|dbj|BAA23330.1|	47.37	0.005
contig00058-orf00028	#N/A	gi|39931049|sp|Q7WTJ6|DMPL ACICA	60	1E-109
contig00058-orf00029	DMS oxygenase component [Acinetobacter sp.]	gi|2605610|dbj|BAA23332.1|	68.54	1E-31
contig00058-orf00031	DMS oxygenase component [Acinetobacter sp.]	gi|2605611|dbj|BAA23333.1|	87.73	0
contig00058-orf00032	DMS oxygenase component [Acinetobacter sp.]	gi|2605612|dbj|BAA23334.1|	47.5	7E-28
contig00058-orf00033	#N/A	gi|39931048|sp|Q7WTJ2|DMPP ACICA	74.41	2E-148
contig00058-orf00034	acetaldehyde dehydrogenase [Pseudomonas stutzeri]	gi|4104770|gb|AAD02152.1|	81.13	5E-136
contig00058-orf00035	4-hydroxy-2-ketovalerate aldolase [Pseudomonas putida]	gi|32469924|ref|NP 863098.1|	81.12	1E-156
contig00058-orf00036	4-oxalocrotonate decarboxylase [Acinetobacter sp. YAA]	gi|2627158|dbj|BAA23561.1|	79.92	1E-118
contig00058-orf00038	#N/A	gi|45593119|sp|Q9ZI54|4OT PSEST	67.86	4E-14
contig00058-orf00039	#N/A	gi|18767665|gb|AAK08203.2|AF320 981 2	54.93	0.00001
contig00058-orf00040	catechol 2,3-dioxygenase [Acinetobacter sp. YAA]	gi|2627152|dbj|BAA23555.1|	73.2	7E-127
contig00058-orf00041	hydroxymuconic semialdehyde dehydrogenase [Pseudomonas stutzeri]	gi|4104767|gb|AAD02149.1|	74.07	0
contig00058-orf00042	2-oxypent-4-pentenoate hydratase [Pseudomonas sp. KB35B]	gi|82393830|gb|ABB72211.1|	74.33	1E-105
contig00058-orf00043	cell division initiation protein [Thermoanaerobacter tengcongensis MB4]	gi|20808025|ref|NP 623196.1|	32.63	0.05
contig00058-orf00044	amidophosphoribosyltransferase [Neisseria meningitidis Z2491]	gi|15793861|ref|NP 283683.1|	96.32	0
contig00058-orf00045	spermidine synthase [Ralstonia eutropha JMP134]	gi|73542987|ref|YP 297507.1|	63.07	2E-155
contig00058-orf00047	sulfite reductase subunit beta [Escherichia coli CFT073]	gi|26249161|ref|NP 755201.1|	70.25	0
contig00058-orf00050	hypothetical protein NGO1063 [Neisseria gonorrhoeae FA 1090]	gi|59801433|ref|YP 208145.1|	66.22	1E-21
contig00058-orf00051	50S ribosomal protein L31 type B [Neisseria meningitidis MC58]	gi|15676835|ref|NP 273980.1|	94.51	3E-46

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contig00058-orf00052	hypothetical protein NGO1299 [Neisseria gonorrhoeae FA 1090]	gi|59801653|ref|YP 208365.1|	71.33	1E-60
contig00058-orf00053	hypothetical protein NGO1299 [Neisseria gonorrhoeae FA 1090]	gi|59801653|ref|YP 208365.1|	65.31	9E-31
contig00058-orf00055	hypothetical protein NGO0306 [Neisseria gonorrhoeae FA 1090]	gi|59800753|ref|YP 207465.1|	58.65	2E-27
contig00058-orf00056	IfhA [Neisseria gonorrhoeae FA 1090]	gi|59800752|ref|YP 207464.1|	99	9E-50
contig00058-orf00058	phenylalanyl-tRNA synthetase subunit beta [Neisseria meningitidis MC58]	gi|15676626|ref|NP 273770.1|	93.9	0
contig00058-orf00059	type II restriction enzyme HpaII (endonuclease HpaII) [Bacillus thuringiensis serovar konkukian str. 97-27]	gi|49476999|ref|YP 035185.1|	32.59	2E-53
contig00058-orf00061	methylase [Neisseria lactamica]	gi|27497145|gb|AAO17336.1|	93.36	9E-128
contig00058-orf00062	methylase [Neisseria lactamica]	gi|27497145|gb|AAO17336.1|	81.15	3E-50
contig00058-orf00063	putative very short patch repair endonuclease [Neisseria lactamica]	gi|27497144|gb|AAO17335.1|	95.74	3E-75
contig00058-orf00065	phenylalanyl-tRNA synthetase alpha subunit [Neisseria gonorrhoeae FA 1090]	gi|59800747|ref|YP 207459.1|	97.87	5E-149
contig00058-orf00067	50S ribosomal protein L20 [Neisseria meningitidis Z2491]	gi|15793891|ref|NP 283713.1|	99.1	3E-47
contig00058-orf00068	50S ribosomal protein L35 [Neisseria meningitidis MC58]	gi|15676620|ref|NP 273764.1|	100	1E-29
contig00058-orf00069	translation initiation factor IF-3 [Neisseria meningitidis MC58]	gi|15676619|ref|NP 273763.1|	99.25	3E-70
contig00058-orf00070	threonyl-tRNA synthetase [Neisseria meningitidis MC58]	gi|15676618|ref|NP 273762.1|	97.33	0
contig00058-orf00073	queuine tRNA-ribosyltransferase [Neisseria meningitidis Z2491]	gi|15793887|ref|NP 283709.1|	95.96	0
contig00058-orf00074	ferrochelatase [Neisseria meningitidis Z2491]	gi|15793886|ref|NP 283708.1|	78.92	2E-146
contig00058-orf00075	putative cytochrome [Neisseria meningitidis MC58]	gi|15676615|ref|NP 273759.1|	71.97	9E-52
contig00058-orf00078	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase [Neisseria meningitidis MC58]	gi|15677504|ref|NP 274660.1|	90.27	2E-155
contig00058-orf00079	hypothetical protein NMB1494 [Neisseria meningitidis MC58]	gi|15677347|ref|NP 274502.1|	90	1E-20
contig00058-orf00081	carbon starvation protein A [Neisseria meningitidis MC58]	gi|15677346|ref|NP 274501.1|	96.68	0
contig00058-orf00085	alcohol dehydrogenase, zinc-containing [Neisseria meningitidis MC58]	gi|15677256|ref|NP 274409.1|	97.4	0
contig00058-orf00086	adenine glycosylase [Neisseria meningitidis Z2491]	gi|15794508|ref|NP 284330.1|	84.62	4E-173
contig00058-orf00089	COG0397: Uncharacterized conserved protein [Burkholderia dolosa AUO158]	gi|84361981|ref|ZP 00986618.1|	50.6	2E-126
contig00058-orf00090	amino acid ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15677362|ref|NP 274517.1|	91.53	2E-103
contig00058-orf00093	putative protease [Neisseria meningitidis MC58]	gi|15677513|ref|NP 274669.1|	96.88	0
contig00058-orf00096	COG3237: Uncharacterized protein conserved in bacteria [Rubrivivax gelatinosus PM1]	gi|47574292|ref|ZP 00244328.1|	72.13	1E-19
contig00058-orf00102	glycine dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801676|ref|YP 208388.1|	93.47	0
contig00058-orf00105	DNA-3-methyladenine glycosylase I [Neisseria meningitidis MC58]	gi|15677522|ref|NP 274678.1|	79.78	9E-84
contig00058-orf00107	glycine cleavage system protein H [Neisseria gonorrhoeae FA 1090]	gi|59801749|ref|YP 208461.1|	96.88	8E-67
contig00058-orf00109	glycine cleavage system aminomethyltransferase T [Neisseria meningitidis	gi|15676479|ref|NP 273618.1|	98.91	0
contig00058-orf00111	transcription regulator AsnC [Neisseria meningitidis Z2491]	gi|15793731|ref|NP 283553.1|	87.97	2E-74
contig00058-orf00112	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	80	6.2
contig00058-orf00114	putative ATP-dependent RNA helicase [Neisseria gonorrhoeae FA 1090]	gi|59800607|ref|YP 207319.1|	80.64	0
contig00058-orf00115	immunoglobulin heavy chain variable region [Homo sapiens]	gi|39938010|gb|AAR32424.1|	32.31	1.6

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contig00058-orf00117	hypothetical protein Aple02001724 [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|32035216|ref|ZP 00135244.1|	39.39	0.000004
contig00058-orf00119	glutaredoxin 2 [Neisseria meningitidis MC58]	gi|15677580|ref|NP 274737.1|	79.81	4E-98
contig00058-orf00123	GTP pyrophosphokinase [Neisseria meningitidis MC58]	gi|15677581|ref|NP 274738.1|	97.56	0
contig00058-orf00124	alcohol dehydrogenase [Neisseria meningitidis MC58]	gi|15676452|ref|NP 273591.1|	95.29	1E-165
contig00058-orf00127	COG1012: NAD-dependent aldehyde dehydrogenases [Actinobacillus pleuropneumoniae serovar 1 str. 4074]	gi|46143349|ref|ZP 00204449.1|	84.55	0
contig00058-orf00129	PREDICTED: BTB and CNC homology 1 isoform 2 [Pan troglodytes]	gi|114683802|ref|XP 001161541.1|	33.87	2.8
contig00058-orf00131	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	51.61	0.97
contig00058-orf00133	hypothetical protein NMA1952 [Neisseria meningitidis Z2491]	gi|15794835|ref|NP 284657.1|	97.56	0
contig00058-orf00135	putative DNA polymerase III, alpha subunit [Neisseria gonorrhoeae FA 1090]	gi|59800539|ref|YP 207251.1|	95.98	0
contig00058-orf00136	hypothetical protein [Plasmodium berghei strain ANKA]	gi|68070755|ref|XP 677290.1|	34	0.12
contig00058-orf00137	ribokinase [Chromobacterium violaceum ATCC 12472]	gi|34498475|ref|NP 902690.1|	50	6E-63
contig00058-orf00138	regulator [Neisseria meningitidis Z2491]	gi|15794772|ref|NP 284594.1|	72.07	6E-71
contig00058-orf00141	phage transposase [Neisseria meningitidis Z2491]	gi|15794213|ref|NP 284035.1|	93.84	0
contig00058-orf00142	hypothetical protein NMB1082 [Neisseria meningitidis MC58]	gi|15676963|ref|NP 274114.1|	91.3	1E-15
contig00058-orf00143	phage transposase [Neisseria meningitidis Z2491]	gi|15794215|ref|NP 284037.1|	88.49	3E-147
contig00058-orf00144	hypothetical protein NMA1287 [Neisseria meningitidis Z2491]	gi|15794216|ref|NP 284038.1|	85.37	2E-14
contig00058-orf00145	hypothetical protein NMA1287 [Neisseria meningitidis Z2491]	gi|15794216|ref|NP 284038.1|	69.64	7E-15
contig00058-orf00147	PREDICTED: hypothetical protein [Homo sapiens]	gi|88954673|ref|XP 372913.3|	30.61	3.7
contig00058-orf00151	stringent starvation protein A [Methylococcus capsulatus str. Bath]	gi|53803979|ref|YP 114392.1|	46.67	6.4
contig00058-orf00152	ACL049Wp [Ashbya gossypii ATCC 10895]	gi|45185639|ref|NP 983355.1|	29.87	2.8
contig00058-orf00154	putative phage associated protein [Neisseria gonorrhoeae FA 1090]	gi|59800902|ref|YP 207614.1|	65.18	2E-74
contig00058-orf00155	hypothetical protein NMA1290 [Neisseria meningitidis Z2491]	gi|15794219|ref|NP 284041.1|	76.36	8E-19
contig00058-orf00157	hypothetical protein HD1520 [Haemophilus ducreyi 35000HP]	gi|33152568|ref|NP 873921.1|	50.91	1E-22
contig00058-orf00158	hypothetical protein amb2120 [Magnetospirillum magneticum AMB-1]	gi|83311219|ref|YP 421483.1|	45.16	4.7
contig00058-orf00159	host-nuclease inhibitor protein [Neisseria meningitidis Z2491]	gi|15794220|ref|NP 284042.1|	80.23	4E-73
contig00058-orf00162	E16-related protein [Neisseria meningitidis MC58]	gi|15676876|ref|NP 274021.1|	61.31	3E-38
contig00058-orf00165	putative bacteriophage DNA transposition protein B [Neisseria meningitidis MC58]	gi|15676964|ref|NP 274115.1|	50	1E-21
contig00058-orf00168	hypothetical protein ACIAD2145 [Acinetobacter sp. ADP1]	gi|50085260|ref|YP 046770.1|	53.18	2E-37
contig00058-orf00169	hypothetical protein NMB0988 [Neisseria meningitidis MC58]	gi|15676879|ref|NP 274024.1|	70.97	0.0007
contig00058-orf00171	hypothetical protein NMA1190 [Neisseria meningitidis Z2491]	gi|15794134|ref|NP 283956.1|	92.5	2E-34
contig00058-orf00172	hypothetical protein NMA1191 [Neisseria meningitidis Z2491]	gi|15794135|ref|NP 283957.1|	85.29	1E-59
contig00058-orf00174	hypothetical protein NMA1307 [Neisseria meningitidis Z2491]	gi|15794236|ref|NP 284058.1|	96.88	3E-30
contig00058-orf00175	hypothetical protein NMB1089 [Neisseria meningitidis MC58]	gi|15676970|ref|NP 274121.1|	67.57	2E-34
contig00058-orf00176	hypothetical protein NMA1310 [Neisseria meningitidis Z2491]	gi|15794239|ref|NP 284061.1|	100	3E-44

Query	NR Database Subject	Subject ID	% ID	E value
contig00058-orf00177	hypothetical protein NMA1311 [Neisseria meningitidis Z2491]	gi|15794240|ref|NP 284062.1|	100	8E-30
contig00058-orf00179	DNA-binding protein [Neisseria meningitidis Z2491]	gi|15794241|ref|NP 284063.1|	74.25	7E-63
contig00058-orf00180	hypothetical protein NMA1852 [Neisseria meningitidis Z2491]	gi|15794740|ref|NP 284562.1|	50.19	2E-142
contig00058-orf00182	Mu-like prophage protein [Psychrobacter arcticus 273-4]	gi|71065562|ref|YP 264289.1|	23.08	6E-14
contig00058-orf00184	COG2369: Uncharacterized protein, homolog of phage Mu protein gp30 [Vibrio cholerae O395]	gi|75826458|ref|ZP 00755893.1|	46.32	4E-53
contig00058-orf00185	hypothetical protein UM05499.1 [Ustilago maydis 521]	gi|71022833|ref|XP 761646.1|	29.17	0.19
contig00058-orf00186	PREDICTED: similar to Collagen alpha 2(IV) chain precursor [Bos taurus]	gi|76631926|ref|XP 585435.2|	42.86	2.5
contig00058-orf00187	hypothetical protein Ta0272 [Thermoplasma acidophilum DSM 1728]	gi|16081414|ref|NP 393752.1|	28.57	0.56
contig00058-orf00189	hypothetical protein MCA2923 [Methylococcus capsulatus str. Bath]	gi|53802937|ref|YP 115315.1|	34.59	7E-46
contig00058-orf00191	#N/A	gi|67545316|ref|ZP 00423239.1|	29.03	0.00006
contig00058-orf00193	mu-like prophage Flumu G protein [Syntrophus aciditrophicus SB]	gi|85858391|ref|YP 460593.1|	35.81	6E-11
contig00058-orf00194	hypothetical protein ROS217 23357 [Roseovarius sp. 217]	gi|85703731|ref|ZP 01034835.1|	29.76	0.15
contig00058-orf00195	hypothetical protein SO 0679 [Shewanella oneidensis MR-1]	gi|24372270|ref|NP 716312.1|	27.98	2E-15
contig00058-orf00198	hypothetical protein BCE 4074 [Bacillus cereus ATCC 10987]	gi|42783121|ref|NP 980368.1|	34.88	4.7
contig00058-orf00200	phage tail tape meausure protein, TP901 family, putative [Wolbachia endosymbiont of Drosophila ananassae]	gi|58698944|ref|ZP 00373803.1|	39.96	3E-62
contig00058-orf00202	hypothetical protein RSc0874 [Ralstonia solanacearum GMI1000]	gi|17545593|ref|NP 518995.1|	37.21	5E-15
contig00058-orf00204	hypothetical protein Paer2 01005921 [Pseudomonas aeruginosa 2192]	gi|84322790|ref|ZP 00970871.1|	32.97	4E-57
contig00058-orf00206	hypothetical protein MCA2672 [Methylococcus capsulatus str. Bath]	gi|53803122|ref|YP 115076.1|	36.16	2E-63
contig00058-orf00208	multiple ligand-binding protein 1 [Streptococcus sp.]	gi|1403575|emb|CAA59349.1|	40.82	0.065
contig00058-orf00209	hypothetical protein Sfri 1687 [Shewanella frigidimarina NCIMB 400]	gi|114562863|ref|YP 750376.1|	33.33	2E-10
contig00058-orf00210	hypothetical protein RSc0877 [Ralstonia solanacearum GMI1000]	gi|17545596|ref|NP 518998.1|	40.28	3E-09
contig00058-orf00212	hypothetical protein RSc0879 [Ralstonia solanacearum GMI1000]	gi|17545598|ref|NP 519000.1|	28	8E-25
contig00058-orf00215	hypothetical protein DP1597 [Desulfotalea psychrophila LSv54]	gi|51245449|ref|YP 065333.1|	31.82	3.7
contig00058-orf00218	transcriptional regulator, putative [Sulfitobacter sp. EE-36]	gi|83943125|ref|ZP 00955585.1|	41.46	1.2
contig00058-orf00221	hypothetical protein RSc0854 [Ralstonia solanacearum GMI1000]	gi|17545573|ref|NP 518975.1|	38.15	4E-23
contig00058-orf00222	hypothetical protein Saci 1794 [Sulfolobus acidocaldarius DSM 639]	gi|70607523|ref|YP 256393.1|	44.44	0.19
contig00058-orf00225	translational regulator [Escherichia coli O157:H7 str. Sakai]	gi|15834251|ref|NP 313024.1|	45.71	0.003
contig00058-orf00227	DNA adenine methylase [Methylobacillus flagellatus KT]	gi|91777030|ref|YP 546786.1|	73.48	3E-50
contig00058-orf00228	hypothetical protein XfasaDRAFT 1973 [Xylella fastidiosa Dixon]	gi|71274665|ref|ZP 00650953.1|	53.7	6E-08
contig00058-orf00229	putative ABC transporter ATP-binding protein [Neisseria meningitidis MC58]	gi|15676301|ref|NP 273436.1|	99.28	0
contig00058-orf00231	putative type I restriction-modification system (HsdR) [Acinetobacter sp. ADP1]	gi|50086398|ref|YP 047908.1|	63.14	0
contig00058-orf00233	type I restriction-modification system specificity determinant [Geobacter uraniumreducens Rf4]	gi|88935113|ref|ZP 01140750.1|	66.5	6E-70
contig00058-orf00233	type I restriction-modification system specificity determinant [Geobacter uraniumreducens Rf4]	gi|88935113|ref|ZP 01140750.1|	33.22	2E-28

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contig00058-orf00235	HsdM protein [Mannheimia succiniciproducens MBEL55E]	gi|52426220|ref|YP 089357.1|	69.29	0
contig00058-orf00237	L-aspartate oxidase [Neisseria meningitidis Z2491]	gi|15794967|ref|NP 284789.1|	94.41	0
contig00058-orf00240	quinolinate synthetase [Neisseria gonorrhoeae FA 1090]	gi|59801900|ref|YP 208612.1|	98.11	0
contig00058-orf00242	hypothetical protein NMB0395 [Neisseria meningitidis MC58]	gi|15676309|ref|NP 273444.1|	98.08	2E-176
contig00058-orf00244	putative Rhs family protein [Pseudomonas aeruginosa UCBPP-PA14]	gi|116049601|ref|YP 791594.1|	51.61	0.34
contig00058-orf00245	hypothetical protein TTHERM 01123880 [Tetrahymena thermophila SB210]	gi|89284461|gb|EAR82505.1|	22.12	1.4
contig00058-orf00247	putative nicotinate-nucleotide pyrophosphorylase [Neisseria gonorrhoeae FA 1090]	gi|59801898|ref|YP 208610.1|	95.52	1E-136
contig00058-orf00253	monofunctional biosynthetic peptidoglycan transglycosylase [Neisseria meningitidis Z2491]	gi|15795001|ref|NP 284823.1|	87.12	1E-115
contig00058-orf00254	#N/A	gi|9087131|sp|P95400|AROE NEIPH	97.03	1E-128
contig00058-orf00256	glutamine synthetase [Neisseria meningitidis MC58]	gi|15676274|ref|NP 273408.1|	97.25	0
contig00058-orf00258	transposase, truncated [Neisseria meningitidis MC58]	gi|15677991|ref|NP 273449.1|	94.44	0.039
contig00058-orf00260	putative zinc-binding alcohol dehydrogenas [Neisseria gonorrhoeae FA 1090]	gi|59800641|ref|YP 207353.1|	96.61	3E-175
contig00058-orf00261	#N/A	gi|585759|sp|P38047|PUPB PSEPU	33.5	2E-50
contig00058-orf00264	outer membrane ferripyoverdine receptor [Pseudomonas syringae pv. phaseolicola 1448A]	gi|71737812|ref|YP 274101.1|	37.63	4E-44
contig00058-orf00267	hypothetical protein NMB0529 [Neisseria meningitidis MC58]	gi|15676436|ref|NP 273574.1|	91.51	2E-112
contig00058-orf00268	membrane protein [Neisseria meningitidis Z2491]	gi|15793684|ref|NP 283506.1|	95.51	2E-43
contig00058-orf00270	hypothetical protein NGO1461 [Neisseria gonorrhoeae FA 1090]	gi|59801802|ref|YP 208514.1|	58.33	0.006
contig00058-orf00272	hypothetical protein NMA0704 [Neisseria meningitidis Z2491]	gi|15793683|ref|NP 283505.1|	91.34	2E-65
contig00058-orf00273	hypothetical protein NMB0526 [Neisseria meningitidis MC58]	gi|15676433|ref|NP 273571.1|	94.19	5E-82
contig00058-orf00276	putative aluminum resistance protein [Neisseria meningitidis MC58]	gi|15676432|ref|NP 273570.1|	97.72	3E-121
contig00058-orf00278	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase [Neisseria meningitidis MC58]	gi|15677255|ref|NP 274408.1|	97.17	1E-113
contig00058-orf00281	phosphogluconate dehydratase [Neisseria gonorrhoeae FA 1090]	gi|59801134|ref|YP 207846.1|	98.04	0
contig00058-orf00284	glucose-6-phosphate 1-dehydrogenase [Neisseria gonorrhoeae FA 1090]	gi|59801135|ref|YP 207847.1|	91.68	0
contig00058-orf00288	hypothetical protein NGO0716 [Neisseria gonorrhoeae FA 1090]	gi|59801136|ref|YP 207848.1|	76.96	1E-90
contig00058-orf00289	glucokinase [Neisseria meningitidis MC58]	gi|15677251|ref|NP 274404.1|	90.57	6E-166
contig00058-orf00290	RpiR/YebK/YfhH family protein [Neisseria meningitidis MC58]	gi|15677250|ref|NP 274403.1|	97.52	3E-149
contig00058-orf00293	glucose-6-phosphate isomerase [Neisseria meningitidis MC58]	gi|15677249|ref|NP 274402.1|	94.33	0
contig00058-orf00296	hypothetical protein NMA0903 [Neisseria meningitidis Z2491]	gi|15793869|ref|NP 283691.1|	89.95	7E-99
contig00058-orf00297	hypothetical protein Daro 0097 [Dechloromonas aromatica RCB]	gi|71905739|ref|YP 283326.1|	38.89	8E-50
contig00058-orf00298	N-(5'-phosphoribosyl)anthranilate isomerase [Neisseria gonorrhoeae FA 1090]	gi|59800712|ref|YP 207424.1|	72.68	4E-71
contig00058-orf00299	hypothetical protein NMB1480 [Neisseria meningitidis MC58]	gi|15677333|ref|NP 274488.1|	85.42	2E-15
contig00058-orf00301	putative membrane protein [Polaromonas naphthalenivorans CJ2]	gi|84712374|ref|ZP 01020286.1|	31.53	0.000005
contig00058-orf00303	transcription termination factor Rho [Neisseria meningitidis MC58]	gi|15676520|ref|NP 273661.1|	95.47	0

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contig00058-orf00305	hypothetical protein NMB1619 [Neisseria meningitidis MC58]	gi|15677469|ref|NP 274625.1|	85.27	2E-62
contig00058-orf00307	hypothetical protein NGO1274 [Neisseria gonorrhoeae FA 1090]	gi|59801631|ref|YP 208343.1|	74.52	3E-144
contig00058-orf00309	peptide chain release factor 3 [Neisseria meningitidis Z2491]	gi|15793806|ref|NP 283628.1|	98.68	0
contig00058-orf00312	hypothetical protein NMA0944 [Neisseria meningitidis Z2491]	gi|15793902|ref|NP 283724.1|	45.18	2E-26
contig00058-orf00313	dithiobiotin synthetase [Neisseria meningitidis MC58]	gi|15676631|ref|NP 273775.1|	91.55	5E-97
contig00058-orf00315	putative adenosylmethionine-8-amino-7-oxononanoate aminotranferase [Neisseria gonorrhoeae FA 1090]	gi|59800755|ref|YP 207467.1|	95.76	0
contig00058-orf00317	putative murein transglycosylase / nitrite reductase transcriptional regulator [Neisseria gonorrhoeae FA 1090]	gi|59801036|ref|YP 207748.1|	56.49	0
contig00058-orf00318	IS1106 transposase [Neisseria meningitidis MC58]	gi|15676882|ref|NP 274027.1|	94.74	2E-14
contig00058-orf00319	multidrug efflux pump channel protein [Neisseria meningitidis MC58]	gi|15677561|ref|NP 274717.1|	78.33	1E-170
contig00058-orf00321	multiple transferable resistance system protein MtrD [Neisseria meningitidis MC58]	gi|15677562|ref|NP 274718.1|	89.66	0
contig00058-orf00323	#N/A	gi|1171060|sp|P43505|MTRC NEIGO	85.29	5E-160
contig00059-orf00003	hypothetical protein NMB1983 [Neisseria meningitidis MC58]	gi|15677812|ref|NP 274976.1|	76.68	3E-94
contig00059-orf00004	resolvase [Ralstonia eutropha JMP134]	gi|72384321|ref|YP 293674.1|	57.14	5E-40
contig00059-orf00007	C-5 cytosine-specific DNA methylase [Chlorobium phaeobacteroides BS1]	gi|67938989|ref|ZP 00531504.1|	62.78	3E-153
contig00059-orf00008	Histidine Kinase [Leeuwenhoekiella blandensis MED217]	gi|86141747|ref|ZP 01060271.1|	40.86	1E-138
contig00059-orf00009	hypothetical protein MED217 01415 [Leeuwenhoekiella blandensis MED217]	gi|86141748|ref|ZP 01060272.1|	28.15	5E-31
contig00059-orf00010	DNA polymerase V subunit UmuD [Salmonella typhimurium LT2]	gi|16765334|ref|NP 460949.1|	39.02	6E-09
contig00059-orf00011	DNA polymerase IV [Oceanospirillum sp. MED92]	gi|89091944|ref|ZP 01164899.1|	44.34	4E-91
contig00059-orf00013	hypothetical protein NMB0909 [Neisseria meningitidis MC58]	gi|15676804|ref|NP 273949.1|	45.45	1E-10
contig00060-orf00001	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	93.71	0
contig00060-orf00001	transcription-repair coupling factor [Neisseria meningitidis Z2491]	gi|15794391|ref|NP 284213.1|	68.06	4E-19
contig00060-orf00004	cytidine and deoxycytidylate deaminase family protein [Neisseria meningitidis MC58]	gi|15676827|ref|NP 273972.1|	69.33	3E-86
contig00060-orf00005	tRNA delta(2)-isopentenylpyrophosphate transferase [Neisseria meningitidis Z2491]	gi|15794076|ref|NP 283898.1|	70.61	1E-121
contig00060-orf00008	3-phosphoshikimate 1-carboxyvinyltransferase [Neisseria meningitidis MC58]	gi|15677291|ref|NP 274444.1|	96.51	0
contig00060-orf00012	anthranilate synthase component I [Neisseria meningitidis Z2491]	gi|15794182|ref|NP 284004.1|	97.76	0
contig00060-orf00014	hypothetical protein NMB0047 [Neisseria meningitidis MC58]	gi|15675987|ref|NP 273113.1|	82.98	1E-41
contig00060-orf00015	phosphoribosylaminoimidazole carboxylase ATPase subunit [Neisseria meningitidis MC58]	gi|15676907|ref|NP 274053.1|	91.27	0
contig00060-orf00017	hypothetical protein NGO0876 [Neisseria gonorrhoeae FA 1090]	gi|59801277|ref|YP 207989.1|	76.23	3E-49
contig00060-orf00019	hypothetical protein NMA1237 [Neisseria meningitidis Z2491]	gi|15794177|ref|NP 283999.1|	71.5	8E-67
contig00060-orf00022	pyruvate dehydrogenase subunit E1 [Neisseria gonorrhoeae FA 1090]	gi|59800998|ref|YP 207710.1|	96.17	0

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contig00060-orf00023	ABC transporter family protein [Tetrahymena thermophila SB210]	gi|89300254|gb|EAR98242.1|	38.33	6.3
contig00060-orf00024	dihydrolipoamide acetyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59800997|ref|YP 207709.1|	93.03	0
contig00060-orf00027	dihydrolipoamide dehydrogenase (E3 component of pyruvate and 2-oxoglutarate dehydrogenase complexes) [Neisseria meningitidis Z2491]	gi|15794449|ref|NP 284271.1|	95.29	0
contig00060-orf00029	tRNA (guanine-N(7))-methyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801008|ref|YP 207720.1|	81.2	7E-110
contig00060-orf00031	riboflavin synthase subunit alpha [Neisseria gonorrhoeae FA 1090]	gi|59801170|ref|YP 207882.1|	74.75	1E-81
contig00060-orf00032	hypothetical protein NMA1415 [Neisseria meningitidis Z2491]	gi|15794327|ref|NP 284149.1|	83.62	2E-132
contig00060-orf00035	periplasmic protein [Neisseria meningitidis Z2491]	gi|15794326|ref|NP 284148.1|	57.36	1E-37
contig00060-orf00036	ribulose-phosphate 3-epimerase [Neisseria meningitidis MC58]	gi|15677116|ref|NP 274268.1|	89.69	9E-101
contig00060-orf00038	hypothetical protein NGO1083 [Neisseria gonorrhoeae FA 1090]	gi|59801450|ref|YP 208162.1|	78.57	1E-26
contig00060-orf00040	ATP phosphoribosyltransferase regulatory subunit [Neisseria meningitidis MC58]	gi|15676712|ref|NP 273856.1|	91.1	0
contig00060-orf00041	adenylosuccinate synthetase [Neisseria meningitidis Z2491]	gi|15793980|ref|NP 283802.1|	95.83	0
contig00060-orf00042	hypothetical protein NGO0549 [Neisseria gonorrhoeae FA 1090]	gi|59800983|ref|YP 207695.1|	71.05	2E-42
contig00060-orf00044	hypothetical protein NMA1462 [Neisseria meningitidis Z2491]	gi|15794364|ref|NP 284186.1|	72.5	6E-62
contig00060-orf00046	putative transposase [Neisseria meningitidis MC58]	gi|77358698|ref|YP 338293.1|	94.44	3E-13
contig00060-orf00047	putative dnaJ-family protein [Neisseria gonorrhoeae FA 1090]	gi|59800985|ref|YP 207697.1|	37.28	4E-38
contig00060-orf00049	integral membrane protein [Neisseria meningitidis Z2491]	gi|15794362|ref|NP 284184.1|	75.28	4E-108
contig00060-orf00051	aspartate ammonia-lyase [Neisseria meningitidis MC58]	gi|15676916|ref|NP 274063.1|	94.41	0
contig00061-orf00001	extracellular solute-binding protein [Ralstonia eutropha JMP134]	gi|73541817|ref|YP 296337.1|	45.09	3E-133
contig00061-orf00002	lipoprotein [Neisseria meningitidis Z2491]	gi|15793295|ref|NP 283117.1|	48.26	2E-41
contig00061-orf00004	fused ribonuclease BN/uncharacterized domain-containing protein [Neisseria meningitidis Z2491]	gi|15793680|ref|NP 283502.1|	81.36	4E-135
contig00061-orf00006	trp repressor binding protein [Chromobacterium violaceum ATCC 12472]	gi|34496264|ref|NP 900479.1|	68.21	6E-64
contig00061-orf00009	hypothetical protein PP 0487 [Pseudomonas putida KT2440]	gi|26987228|ref|NP 742653.1|	47.31	4E-65
contig00061-orf00010	hypothetical protein RF 1098 [Rickettsia felis URRWXCal2]	gi|67459490|ref|YP 247114.1|	25.99	5E-15
contig00061-orf00014	hypothetical protein Pcryo 0802 [Psychrobacter cryohalolentis K5]	gi|93005632|ref|YP 580069.1|	44.75	3E-42
contig00061-orf00015	glucose/galactose transporter [Neisseria meningitidis MC58]	gi|15676441|ref|NP 273580.1|	89.43	0
contig00061-orf00016	membrane protein [Neisseria meningitidis Z2491]	gi|15793690|ref|NP 283512.1|	72.09	5E-48
contig00061-orf00018	aromatic amino acid aminotransferase [Neisseria meningitidis Z2491]	gi|15793696|ref|NP 283518.1|	96.47	0
contig00062-orf00002	#N/A	gi|84363291|ref|ZP 00987883.1|	48.94	1E-15
contig00062-orf00004	ATP-dependent protease ATP-binding protein [Neisseria meningitidis Z2491]	gi|15793996|ref|NP 283818.1|	92.51	0
contig00062-orf00005	hypothetical protein NMA1046 [Neisseria meningitidis Z2491]	gi|15793997|ref|NP 283819.1|	84.47	4E-46
contig00062-orf00006	transcriptional regulator [Neisseria meningitidis Z2491]	gi|15793998|ref|NP 283820.1|	98.51	4E-32
contig00062-orf00009	hypothetical protein CV 1536 [Chromobacterium violaceum ATCC 12472]	gi|34496991|ref|NP 901206.1|	55.36	2E-30
contig00062-orf00010	hypothetical protein NGO1252 [Neisseria gonorrhoeae FA 1090]	gi|59801611|ref|YP 208323.1|	73.36	1E-103
contig00062-orf00011	hemolysin III [Chromobacterium violaceum ATCC 12472]	gi|34498797|ref|NP 903012.1|	65.22	2E-75

Query	NR Database Subject	Subject ID	% ID	E value
contig00062-orf00014	protein-PII uridylyltransferase [Neisseria meningitidis MC58]	gi|15677076|ref|NP 274228.1|	93.54	0
contig00062-orf00015	transcriptional regulator [Neisseria meningitidis MC58]	gi|15677077|ref|NP 274229.1|	87.62	2E-38
contig00062-orf00017	50S ribosomal protein L25/general stress protein Ctc [Neisseria meningitidis Z2491]	gi|15794042|ref|NP 283864.1|	95.26	4E-97
contig00062-orf00018	ribose-phosphate pyrophosphokinase [Neisseria meningitidis MC58]	gi|15676771|ref|NP 273916.1|	97.86	5E-175
contig00062-orf00019	putative isopentenyl monophosphate kinase [Neisseria gonorrhoeae FA 1090]	gi|59800881|ref|YP 207593.1|	74.64	8E-110
contig00062-orf00022	outer membrane lipoprotein LolB [Neisseria meningitidis MC58]	gi|15676769|ref|NP 273914.1|	58.52	2E-57
contig00062-orf00023	hypothetical protein NMB0872 [Neisseria meningitidis MC58]	gi|15676768|ref|NP 273913.1|	53.36	2E-172
contig00062-orf00027	hypothetical protein ebA5123 [Aromatoleum aromaticum EbN1]	gi|56478345|ref|YP 159934.1|	43.37	1E-27
contig00062-orf00028	UTP--glucose-1-phosphate uridylyltransferase [Neisseria meningitidis MC58]	gi|15676538|ref|NP 273681.1|	88.46	1E-144
contig00062-orf00029	RNA-binding protein [Neisseria meningitidis Z2491]	gi|15793972|ref|NP 283794.1|	88.07	2E-110
contig00062-orf00033	4-hydroxybenzoate octaprenyltransferase [Neisseria meningitidis MC58]	gi|15676633|ref|NP 273777.1|	74.05	3E-54
contig00062-orf00033	4-hydroxybenzoate octaprenyltransferase [Neisseria meningitidis MC58]	gi|15676633|ref|NP 273777.1|	76.47	3E-54
contig00062-orf00034	4-hydroxybenzoate octaprenyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59800759|ref|YP 207471.1|	66.09	7E-39
contig00062-orf00035	PTS system, nitrogen regulatory IIA protein [Neisseria meningitidis MC58]	gi|15676634|ref|NP 273778.1|	85.23	1E-58
contig00062-orf00037	HPr kinase/phosphorylase [Neisseria gonorrhoeae FA 1090]	gi|59800761|ref|YP 207473.1|	93.12	1E-165
contig00062-orf00039	hypothetical protein NGO0315 [Neisseria gonorrhoeae FA 1090]	gi|59800762|ref|YP 207474.1|	83.45	2E-131
contig00062-orf00044	ribosomal biogenesis GTPase [Neisseria gonorrhoeae FA 1090]	gi|59800763|ref|YP 207475.1|	97.76	1E-169
contig00062-orf00045	insertion element IS1106 transposase [Neisseria meningitidis Z2491]	gi|15794535|ref|NP 284357.1|	62.07	0.33
contig00062-orf00046	succinyl-diaminopimelate desuccinylase [Neisseria gonorrhoeae FA 1090]	gi|59801375|ref|YP 208087.1|	96.59	0
contig00062-orf00047	putative methylated-DNA--protein-cysteine methyltransferase [Neisseria meningitidis MC58]	gi|15677380|ref|NP 274535.1|	86.45	8E-118
contig00063-orf00002	putative transcriptional accessory protein Tex [Neisseria meningitidis MC58]	gi|15676011|ref|NP 273139.1|	95.65	0
contig00063-orf00005	TLDD protein [Neisseria meningitidis Z2491]	gi|15793375|ref|NP 283197.1|	90	0
contig00063-orf00007	Metallothionein [Paroedura masobe]	gi|78057029|emb|CAJ32316.1|	35.42	0.55
contig00063-orf00008	sugar permease [Thermoplasma volcanium GSS1]	gi|13541976|ref|NP 111664.1|	32.26	2.1
contig00063-orf00009	hypothetical protein RHE CH03136 [Rhizobium etli CFN 42]	gi|86358737|ref|YP 470629.1|	36.03	4E-19
contig00063-orf00011	PREDICTED: similar to Hypothetical protein MGC75993 [Gallus gallus]	gi|50758913|ref|XP 417476.1|	55.17	0.96
contig00063-orf00013	PREDICTED: similar to F-box and leucine-rich repeat protein 11 [Rattus norvegicus]	gi|62641716|ref|XP 341984.2|	28.57	3.7
contig00063-orf00015	hypothetical protein NMA2018 [Neisseria meningitidis Z2491]	gi|15794898|ref|NP 284720.1|	61.43	1E-20
contig00063-orf00017	hypothetical protein NMA2018 [Neisseria meningitidis Z2491]	gi|15794898|ref|NP 284720.1|	50.68	5E-15
contig00063-orf00018	hypothetical protein RSc2685 [Ralstonia solanacearum GMI1000]	gi|17547404|ref|NP 520806.1|	31.48	0.57
contig00063-orf00020	conserved hypothetical protein [Polaromonas naphthalenivorans CJ2]	gi|84711185|ref|ZP 01019487.1|	40.64	2E-36
contig00063-orf00023	hypothetical protein ZC262.3 [Caenorhabditis elegans]	gi|17556817|ref|NP 498833.1|	38.64	1.1
contig00063-orf00029	hypothetical protein NAP1 13828 [Erythrobacter sp. NAP1]	gi|85709969|ref|ZP 01041034.1|	56.01	9E-148
contig00063-orf00031	hypothetical protein NMB0545 [Neisseria meningitidis MC58]	gi|15676451|ref|NP 273590.1|	97.67	0

Query	NR Database Subject	Subject ID	% ID	E value
contig00063-orf00033	hypothetical protein XautDRAFT 2617 [Xanthobacter autotrophicus Py2]	gi|89360419|ref|ZP 01198238.1|	36.92	8
contig00063-orf00036	putative sodium-dependent transporter [Neisseria gonorrhoeae FA 1090]	gi|59802397|ref|YP 209109.1|	87.62	0
contig00063-orf00039	putative amidase [Neisseria gonorrhoeae FA 1090]	gi|59801840|ref|YP 208552.1|	75.54	4E-164
contig00063-orf00040	hypothetical protein NMB0457 [Neisseria meningitidis MC58]	gi|15676368|ref|NP 273504.1|	73.51	2E-60
contig00063-orf00041	aspartate-semialdehyde dehydrogenase [Neisseria meningitidis Z2491]	gi|15793362|ref|NP 283184.1|	98.11	0
contig00063-orf00044	hypothetical protein NGO0117 [Neisseria gonorrhoeae FA 1090]	gi|59800577|ref|YP 207289.1|	94.41	0
contig00067-orf00001	carboxy-terminal protease for penicillin-binding protein 3 [Shigella flexneri 2a str. 301]	gi|56479889|ref|NP 707289.2|	98.55	4E-31
contig00069-orf00002	TrbM conjugal transfer protein precursor [Plasmid pB3]	gi|55418020|ref|YP 133920.1|	49.7	1E-34
contig00069-orf00003	ATNFXL1 (ARABIDOPSIS THALIANA NF-X-LIKE 1); protein binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	gi|15218447|ref|NP 172488.1|	43.75	8.2
contig00069-orf00004	probable conjugal transfer protein TraL [Xylella fastidiosa Ann-1]	gi|71900545|ref|ZP 00682673.1|	39.88	1E-34
contig00069-orf00005	OSJNBb0008G24.19 [Oryza sativa Japonica Group]	gi|19571123|dbj|BAB86547.1|	37.7	0.26
contig00070-orf00002	Binding-protein-dependent transport systems inner membrane component:Substrate-binding region of ABC-type glycine betaine transport system [Enterococcus faecium DO]	gi|69249960|ref|ZP 00605071.1|	59.44	1E-130
contig00070-orf00003	IS1655 transposase [Neisseria meningitidis Z2491]	gi|15793509|ref|NP 283331.1|	92.72	2E-79
contig00070-orf00004	putative mercury transport periplasmic protein [Neisseria meningitidis MC58]	gi|15677139|ref|NP 274292.1|	72.46	7E-22
contig00070-orf00006	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	65.73	3E-120
contig00070-orf00008	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	78.63	1E-48
contig00070-orf00008	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	81.82	1E-48
contig00070-orf00009	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E]	gi|52425046|ref|YP 088183.1|	66.67	4E-17
contig00070-orf00010	CRISPR-associated helicase Cas3 [Methylococcus capsulatus str. Bath]	gi|53804974|ref|YP 113170.1|	46.04	3E-142
contig00070-orf00011	CRISPR-associated protein, CT1134 [Prosthecochloris vibrioformis DSM 265]	gi|71481563|ref|ZP 00661269.1|	40.97	2E-23
contig00070-orf00013	CRISPR-associated Csd1 family protein [Methylococcus capsulatus str. Bath]	gi|53804984|ref|YP 113168.1|	46.59	6E-129
contig00070-orf00014	CRISPR-associated protein TM1801 [Prosthecochloris vibrioformis DSM 265]	gi|71481565|ref|ZP 00661271.1|	62.67	2E-100
contig00070-orf00015	RecB family exonuclease [Actinobacillus succinogenes 130Z]	gi|75428693|ref|ZP 00731822.1|	75.62	3E-84
contig00071-orf00001	comEA-related protein [Neisseria meningitidis MC58]	gi|15676221|ref|NP 273353.1|	70	4E-16
contig00071-orf00003	probable enoyl-CoA hydratase [Xanthobacter autotrophicus Py2]	gi|89358066|ref|ZP 01195888.1|	48.28	2.2
contig00072-orf00002	very long chain acyl-CoA dehydrogenase-related protein [Neisseria meningitidis MC58]	gi|15677147|ref|NP 274300.1|	93.43	0
contig00072-orf00003	hypothetical protein Psyc 2082 [Psychrobacter arcticus 273-4]	gi|71066636|ref|YP 265363.1|	60.7	4E-55
contig00073-orf00002	pilin gene inverting protein PivNM-1A [Neisseria meningitidis MC58]	gi|15677404|ref|NP 274559.1|	58.86	3E-95
contig00073-orf00004	#N/A	gi|28828351|gb|AAL93018.2|AC116 032 7	28.95	0.16
contig00073-orf00004	#N/A	gi|28828351|gb|AAL93018.2|AC116 032 7	24.11	1.8

Query	NR Database Subject	Subject ID	% ID	E value
contig00074-orf00001	elongation factor Tu [Neisseria meningitidis MC58]	gi|15676067|ref|NP 273197.1|	99.21	0
contig00075-orf00002	glycine betaine transporter [Bacillus sp. NRRL B-14911]	gi|89100777|ref|ZP 01173631.1|	32.31	9E-52
contig00075-orf00004	ENSANGP00000006436 [Anopheles gambiae str. PEST]	gi|58392831|ref|XP 319654.2|	26.13	7E-35
contig00075-orf00006	sugar kinase [Thermoanaerobacter tengcongensis MB4]	gi|20808554|ref|NP 623725.1|	39.45	2E-27
contig00075-orf00007	hypothetical protein MS1159 [Mannheimia succiniciproducens MBEL55E]	gi|52425214|ref|YP 088351.1|	69.51	7E-26
contig00075-orf00008	recombination associated protein [Photorhabdus luminescens subsp. laumondii TTO1]	gi|37527784|ref|NP 931129.1|	52.94	1.2
contig00075-orf00011	FeoB protein [Mannheimia succiniciproducens MBEL55E]	gi|52425212|ref|YP 088349.1|	72.21	0
contig00075-orf00012	hypothetical protein MS1156 [Mannheimia succiniciproducens MBEL55E]	gi|52425211|ref|YP 088348.1|	66.67	0.017
contig00075-orf00014	hypothetical protein NMA1791 [Neisseria meningitidis Z2491]	gi|15794682|ref|NP 284504.1|	88.78	0
contig00075-orf00017	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase [Neisseria meningitidis Z2491]	gi|15794277|ref|NP 284099.1|	93.89	0
contig00075-orf00018	hypothetical protein glr0328 [Gloeobacter violaceus PCC 7421]	gi|37519897|ref|NP 923274.1|	46.76	6E-48
contig00075-orf00022	permease [Neisseria meningitidis Z2491]	gi|15793419|ref|NP 283241.1|	75.26	2E-168
contig00075-orf00024	hypothetical protein NGO0938 [Neisseria gonorrhoeae FA 1090]	gi|59801333|ref|YP 208045.1|	81.36	1E-21
contig00075-orf00027	hypothetical protein MED217 12124 [Leeuwenhoekiella blandensis MED217]	gi|86142393|ref|ZP 01060903.1|	44.28	3E-82
contig00075-orf00028	hypothetical protein NMB1159 [Neisseria meningitidis MC58]	gi|15677035|ref|NP 274187.1|	75.19	5E-75
contig00075-orf00028	hypothetical protein NMB1159 [Neisseria meningitidis MC58]	gi|15677035|ref|NP 274187.1|	52.03	5E-75
contig00075-orf00029	nickel-dependent hydrogenase, b-type cytochrome subunit [Neisseria meningitidis MC58]	gi|15677034|ref|NP 274186.1|	68.42	1E-65
contig00075-orf00032	hypothetical protein NMB1963 [Neisseria meningitidis MC58]	gi|15677793|ref|NP 274957.1|	39.88	3E-26
contig00075-orf00033	hypothetical protein NMA1720 [Neisseria meningitidis Z2491]	gi|15794613|ref|NP 284435.1|	75.8	7E-66
contig00075-orf00035	DNA repair protein RadC [Neisseria meningitidis MC58]	gi|15676925|ref|NP 274072.1|	82.59	1E-97
contig00075-orf00036	spermidine/putrescine ABC transporter, ATP-binding protein [Neisseria meningitidis MC58]	gi|15676514|ref|NP 273654.1|	92.16	0
contig00075-orf00038	polyamine permease inner membrane protein [Neisseria meningitidis Z2491]	gi|15793790|ref|NP 283612.1|	95.81	3E-152
contig00075-orf00039	spermidine/putrescine ABC transporter, permease protein [Neisseria meningitidis MC58]	gi|15676516|ref|NP 273656.1|	97.29	2E-125
contig00075-orf00041	oxidoreductase [Neisseria meningitidis Z2491]	gi|15793792|ref|NP 283614.1|	83.99	0
contig00075-orf00043	hypothetical protein NMB0938 [Neisseria meningitidis MC58]	gi|15676831|ref|NP 273976.1|	44.4	4E-54
contig00075-orf00045	hypothetical protein NGO6151 [Neisseria gonorrhoeae FA 1090]	gi|59801043|ref|YP 207755.1|	58.73	6E-16
contig00075-orf00047	ribonucleotide-diphosphate reductase beta subunit [Neisseria gonorrhoeae FA 1090]	gi|59801042|ref|YP 207754.1|	95.76	0
contig00075-orf00048	#N/A	gi|42630519|ref|ZP 00156058.1|	64.78	1E-116
contig00075-orf00050	ribonucleotide-diphosphate reductase subunit alpha [Neisseria meningitidis Z2491]	gi|15794401|ref|NP 284223.1|	94.86	0
contig00075-orf00051	chaperone protein HscB [Neisseria meningitidis MC58]	gi|15677246|ref|NP 274399.1|	77.71	1E-67

Query	NR Database Subject	Subject ID	% ID	E value
contig00075-orf00053	HesB/YadR/YfhF family protein [Neisseria meningitidis MC58]	gi|15677244|ref|NP 274397.1|	90.74	3E-53
contig00075-orf00056	hypothetical protein PM1196 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15603061|ref|NP 246133.1|	61.73	3E-17
contig00075-orf00058	scaffold protein [Neisseria meningitidis Z2491]	gi|15794489|ref|NP 284311.1|	99.22	1E-67
contig00075-orf00060	hypothetical protein NMA1595 [Neisseria meningitidis Z2491]	gi|15794488|ref|NP 284310.1|	100	0.000002
contig00075-orf00063	NifS-like aminotranfserase [Neisseria meningitidis Z2491]	gi|15794487|ref|NP 284309.1|	98.27	0
contig00075-orf00064	hypothetical protein NGO0637 [Neisseria gonorrhoeae FA 1090]	gi|59801064|ref|YP 207776.1|	93.24	1E-62
contig00075-orf00066	L-lactate dehydrogenase [Neisseria meningitidis Z2491]	gi|15794485|ref|NP 284307.1|	97.66	0
contig00075-orf00067	putative RNA methyltransferase [Neisseria gonorrhoeae FA 1090]	gi|59801230|ref|YP 207942.1|	60.38	8E-76
contig00075-orf00068	hypothetical protein VchoR 02002087 [Vibrio cholerae RC385]	gi|116216117|ref|ZP 01482006.1|	32.69	0.064
contig00075-orf00069	RNA polymerase sigma factor RpoE [Chromobacterium violaceum ATCC	gi|34497513|ref|NP 901728.1|	65.08	5E-69
contig00075-orf00070	hypothetical protein NGO0820 [Neisseria gonorrhoeae FA 1090]	gi|59801231|ref|YP 207943.1|	47.46	8E-100
contig00075-orf00072	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Neisseria meningitidis Z2491]	gi|15794271|ref|NP 284093.1|	89.34	8E-159
contig00075-orf00075	hypothetical protein NMB1138 [Neisseria meningitidis MC58]	gi|15677015|ref|NP 274167.1|	80.45	1E-56
contig00075-orf00077	hypothetical protein [Plasmodium chabaudi chabaudi]	gi|70943398|ref|XP 741750.1|	48.39	2.1
contig00075-orf00078	ENSANGP00000020885 [Anopheles gambiae str. PEST]	gi|58391471|ref|XP 318620.2|	20.93	0.016
contig00075-orf00078	ENSANGP00000020885 [Anopheles gambiae str. PEST]	gi|58391471|ref|XP 318620.2|	25.64	3.4
contig00075-orf00078	ENSANGP00000020885 [Anopheles gambiae str. PEST]	gi|58391471|ref|XP 318620.2|	22.97	4.5
contig00075-orf00078	ENSANGP00000020885 [Anopheles gambiae str. PEST]	gi|58391471|ref|XP 318620.2|	22.87	10
contig00076-orf00001	hypothetical protein NGO0015 [Neisseria gonorrhoeae FA 1090]	gi|59800484|ref|YP 207196.1|	81.25	3.6
contig00076-orf00003	sulphate-binding protein [Neisseria meningitidis Z2491]	gi|15794178|ref|NP 284000.1|	70.66	1E-144
contig00076-orf00005	hypothetical protein Reut B4623 [Ralstonia eutropha JMP134]	gi|73538450|ref|YP 298817.1|	54.14	2E-87
contig00076-orf00010	biotin synthetase [Neisseria meningitidis MC58]	gi|15677022|ref|NP 274174.1|	95.17	0
contig00076-orf00011	hypothetical protein NGO0814 [Neisseria gonorrhoeae FA 1090]	gi|59801226|ref|YP 207938.1|	50	0.11
contig00076-orf00014	fructose-1,6-bisphosphatase [Neisseria meningitidis Z2491]	gi|15794192|ref|NP 284014.1|	78.88	1E-142
contig00076-orf00016	fimbriae-associated protein Fap1 [Streptococcus parasanguinis]	gi|3929312|gb|AAC79868.1|	24.04	0.11
contig00076-orf00016	fimbriae-associated protein Fap1 [Streptococcus parasanguinis]	gi|3929312|gb|AAC79868.1|	23.53	0.2
contig00076-orf00016	fimbriae-associated protein Fap1 [Streptococcus parasanguinis]	gi|3929312|gb|AAC79868.1|	29.63	8.2
contig00076-orf00019	poly(A) polymerase [Neisseria meningitidis Z2491]	gi|15794003|ref|NP 283825.1|	71.3	1E-167
contig00076-orf00020	putative tRNA pseudouridine synthase B [Neisseria gonorrhoeae FA 1090]	gi|59801069|ref|YP 207781.1|	86.75	5E-147
contig00076-orf00022	ribosome-binding factor A [Neisseria gonorrhoeae FA 1090]	gi|59801071|ref|YP 207783.1|	90.24	2E-58
contig00076-orf00023	hypothetical protein PM0652 [Pasteurella multocida subsp. multocida str. Pm70]	gi|15602517|ref|NP 245589.1|	56.3	5E-106
contig00076-orf00024	recombinase A [Neisseria meningitidis MC58]	gi|15677302|ref|NP 274457.1|	90.23	9E-157
contig00076-orf00025	COG1180: Pyruvate-formate lyase-activating enzyme [Yersinia frederiksenii ATCC 33641]	gi|77974839|ref|ZP 00830377.1|	62.7	2E-86
contig00076-orf00026	hypothetical protein NMB0513 [Neisseria meningitidis MC58]	gi|15676422|ref|NP 273559.1|	97	4E-54
contig00076-orf00028	formate acetyltransferase [Haemophilus influenzae Rd KW20]	gi|16272145|ref|NP 438348.1|	80.55	0

Query	NR Database Subject	Subject ID	% ID	E value
contig00076-orf00031	bacterioferritin B [Neisseria meningitidis MC58]	gi|15677079|ref|NP 274231.1|	94.27	3E-79
contig00076-orf00032	bacterioferritin A [Neisseria meningitidis MC58]	gi|15677080|ref|NP 274232.1|	94.81	5E-82
contig00076-orf00035	GTP-binding protein [Neisseria meningitidis Z2491]	gi|15794291|ref|NP 284113.1|	99.17	0
contig00076-orf00037	hypothetical protein Pcar 0125 [Pelobacter carbinolicus DSM 2380]	gi|77917742|ref|YP 355557.1|	48.65	9E-176
contig00076-orf00038	putative NTP-binding protein TniB [Pelobacter carbinolicus DSM 2380]	gi|77917741|ref|YP 355556.1|	60.43	3E-90
contig00076-orf00039	hypothetical protein Tcr 1645 [Thiomicrospira crunogena XCL-2]	gi|78485986|ref|YP 391911.1|	43.58	3E-81
contig00076-orf00040	hypothetical protein NGO0253 [Neisseria gonorrhoeae FA 1090]	gi|59800705|ref|YP 207417.1|	81.22	5E-83
contig00076-orf00042	Hypothetical Protein RRSL 03341 [Ralstonia solanacearum UW551]	gi|83746900|ref|ZP 00943947.1|	32.52	9E-82
contig00076-orf00043	lipoyl synthase [Neisseria meningitidis Z2491]	gi|15794299|ref|NP 284121.1|	97.81	0
contig00076-orf00044	lipoate-protein ligase B [Neisseria meningitidis MC58]	gi|77358711|ref|NP 274242.2|	91.71	5E-106
contig00076-orf00045	hypothetical protein NGO0791 [Neisseria gonorrhoeae FA 1090]	gi|59801205|ref|YP 207917.1|	74.44	8E-32
contig00076-orf00049	ATP-dependent protease La [Neisseria meningitidis MC58]	gi|15677103|ref|NP 274255.1|	89.76	0
contig00076-orf00051	DNA-binding protein HU-beta [Neisseria meningitidis MC58]	gi|15677102|ref|NP 274254.1|	96.43	2E-37
contig00076-orf00053	hypothetical protein pB171 061 [Escherichia coli]	gi|10955411|ref|NP 053123.1|	37.25	2.1
contig00076-orf00054	peptidyl-tRNA hydrolase [Neisseria meningitidis MC58]	gi|15676693|ref|NP 273837.1|	83.33	8E-86
contig00076-orf00058	hypothetical protein NMB0796 [Neisseria meningitidis MC58]	gi|15676694|ref|NP 273838.1|	74.14	1E-16
contig00076-orf00059	hypothetical protein NMA1006 [Neisseria meningitidis Z2491]	gi|15793962|ref|NP 283784.1|	83.92	2E-65
contig00076-orf00060	hypothetical protein NMB1327 [Neisseria meningitidis MC58]	gi|15677193|ref|NP 274346.1|	51.75	6E-108
contig00076-orf00060	hypothetical protein NMB1327 [Neisseria meningitidis MC58]	gi|15677193|ref|NP 274346.1|	23.56	2.4
contig00076-orf00061	transferase [Neisseria meningitidis Z2491]	gi|15794614|ref|NP 284436.1|	75.19	2E-115
contig00076-orf00063	hypothetical protein Mfla 0881 [Methylobacillus flagellatus KT]	gi|91775234|ref|YP 544990.1|	39.56	6E-32
contig00076-orf00064	hypothetical protein NGO0853 [Neisseria gonorrhoeae FA 1090]	gi|59801257|ref|YP 207969.1|	56.47	0.000002
contig00076-orf00065	hypothetical protein NGO0972 [Neisseria gonorrhoeae FA 1090]	gi|59801358|ref|YP 208070.1|	65.79	1E-80
contig00076-orf00066	DNA polymerase III, epsilon subunit [Neisseria meningitidis MC58]	gi|15677367|ref|NP 274522.1|	81.03	4E-102
contig00076-orf00067	hypothetical protein NGO0322 [Neisseria gonorrhoeae FA 1090]	gi|59800769|ref|YP 207481.1|	48.7	1E-37
contig00076-orf00068	hypothetical protein NGO0666 [Neisseria gonorrhoeae FA 1090]	gi|59801093|ref|YP 207805.1|	48.36	7E-15
contig00077-orf00003	unnamed protein product [Aspergillus oryzae]	gi|83771637|dbj|BAE61767.1|	36	3.7
contig00077-orf00005	hypothetical protein RMe0058 [Ralstonia metallidurans CH34]	gi|56550614|ref|YP 161680.1|	35.89	1E-31
contig00077-orf00006	ENSANGP00000020926 [Anopheles gambiae str. PEST]	gi|58396311|ref|XP 321814.2|	30.12	0.15
contig00078-orf00001	hypothetical protein NGO1559 [Neisseria gonorrhoeae FA 1090]	gi|59801892|ref|YP 208604.1|	74.44	5E-90
contig00078-orf00002	hypothetical protein CV 0489 [Chromobacterium violaceum ATCC 12472]	gi|34495944|ref|NP 900159.1|	47.64	1E-50
contig00078-orf00004	branched-chain amino acid aminotransferase [Neisseria meningitidis MC58]	gi|15676252|ref|NP 273386.1|	93.07	3E-171
contig00078-orf00006	hypothetical protein NMA2149 [Neisseria meningitidis Z2491]	gi|15795020|ref|NP 284842.1|	83.15	7E-25
contig00078-orf00008	hypothetical protein NGO1662 [Neisseria gonorrhoeae FA 1090]	gi|59801987|ref|YP 208699.1|	89.46	0
contig00078-orf00011	RNA polymerase beta" chain [Eimeria tenella strain Penn State]	gi|31442388|ref|NP 852645.1|	36.36	1.2
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	20.77	0.0000001
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	21.75	0.000005

Query	NR Database Subject	Subject ID	% ID	E value
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	20.24	0.00002
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	22.62	0.0001
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	20.77	0.002
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	20.46	0.34
contig00078-orf00012	hypothetical protein [Trypanosoma cruzi strain CL Brener]	gi|71402299|ref|XP 804081.1|	21.19	0.75
contig00078-orf00014	thymidylate synthase [Neisseria gonorrhoeae FA 1090]	gi|59801705|ref|YP 208417.1|	94.7	6E-148
contig00078-orf00016	glutamate dehydrogenase [Neisseria meningitidis Z2491]	gi|15794847|ref|NP 284669.1|	92.1	0
contig00078-orf00018	peptidase M16-like [Nitrosospira multiformis ATCC 25196]	gi|82703850|ref|YP 413416.1|	42.23	9E-91
contig00078-orf00019	lipoprotein [Neisseria meningitidis Z2491]	gi|15793247|ref|NP 283069.1|	75.84	2E-106
contig00078-orf00021	putative cytochrome synthesis protein [Neisseria gonorrhoeae FA 1090]	gi|59800564|ref|YP 207276.1|	83.04	0
contig00078-orf00022	putative cytochrome c-type biogenesis protein [Neisseria meningitidis MC58]	gi|15677642|ref|NP 274801.1|	81.54	0
contig00078-orf00026	cytochrome c4 [Neisseria meningitidis MC58]	gi|15677643|ref|NP 274802.1|	80.19	6E-80
contig00078-orf00027	GTPase EngB [Neisseria meningitidis Z2491]	gi|15793641|ref|NP 283463.1|	88.78	3E-97
contig00078-orf00029	biopolymer transport protein [Neisseria meningitidis MC58]	gi|15677574|ref|NP 274731.1|	78.57	6E-48
contig00078-orf00030	biopolymer transport protein [Neisseria meningitidis MC58]	gi|15677575|ref|NP 274732.1|	76.26	1E-90
contig00078-orf00031	#N/A	gi|3915153|sp|P95374|TONB NEIMC	68.18	0.000001
contig00078-orf00031	#N/A	gi|3915153|sp|P95374|TONB NEIMC	48.72	0.00002
contig00078-orf00033	hypothetical protein NMA2048 [Neisseria meningitidis Z2491]	gi|15794926|ref|NP 284748.1|	82.99	5E-67
contig00078-orf00034	hypothetical protein NMA2047 [Neisseria meningitidis Z2491]	gi|15794925|ref|NP 284747.1|	69.88	2E-28
contig00078-orf00037	hypothetical protein NGO1516 [Neisseria gonorrhoeae FA 1090]	gi|59801854|ref|YP 208566.1|	88.48	0
contig00078-orf00038	PilC protein [Neisseria gonorrhoeae]	gi|2337846|emb|CAA04546.1|	38.27	3E-100
contig00078-orf00041	carbamoyl phosphate synthase small subunit [Neisseria meningitidis Z2491]	gi|15793598|ref|NP 283420.1|	96.53	0
contig00078-orf00044	hypothetical protein LreuDRAFT 0557 [Lactobacillus reuteri JCM 1112]	gi|89091024|ref|ZP 01164053.1|	68.75	3E-24
contig00078-orf00045	hypothetical protein NGO0050 [Neisseria gonorrhoeae FA 1090]	gi|59800517|ref|YP 207229.1|	94.57	1E-66
contig00079-orf00003	Peptidoglycan-binding LysM:Peptidase M23B [Acidovorax sp. JS42]	gi|110595066|ref|ZP 01383404.1|	59.7	2E-39
contig00079-orf00004	3-oxoacid CoA-transferase subunit A [Myxococcus xanthus DK 1622]	gi|108764087|ref|YP 631972.1|	50	5.5
contig00079-orf00005	stationary phase survival protein SurE [Thiobacillus denitrificans ATCC 25259]	gi|74316853|ref|YP 314593.1|	53.69	4E-75
contig00079-orf00006	heat shock protein HtpX [Haemophilus somnus 129PT]	gi|113461073|ref|YP 719141.1|	57.95	7E-78
contig00079-orf00008	hypothetical protein PsycPRwfDRAFT 0658 [Psychrobacter sp. PRwf-1]	gi|91770936|ref|ZP 01272756.1|	34.72	7E-30
contig00079-orf00010	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein [Ralstonia eutropha H16]	gi|113868810|ref|YP 727299.1|	58.06	3E-116
contig00079-orf00014	DNA mismatch repair protein [Pseudomonas entomophila L48]	gi|104783874|ref|YP 610372.1|	46.09	6E-152
contig00079-orf00016	NAD-dependent deacetylase [Gramella forsetii KT0803]	gi|117577599|emb|CAL66068.1|	53.78	2E-55
contig00079-orf00019	monoamine oxidase B [Gallus gallus]	gi|50882521|gb|AAT85676.1|	34.88	3.1
contig00080-orf00001	acetyltransferase [Leptospira borgpetersenii serovar Hardjo-bovis L550]	gi|116328669|ref|YP 798389.1|	48.48	4.1

Query	NR Database Subject	Subject ID	% ID	E value
contig00080-orf00002	hypothetical protein PF10 0189 [Plasmodium falciparum 3D7]	gi|23507993|ref|NP 700663.1|	25.56	0.64
contig00080-orf00003	hypothetical protein SAV 6583 [Streptomyces avermitilis MA-4680]	gi|29833125|ref|NP 827759.1|	34.83	0.65
contig00080-orf00005	hypothetical protein AjsDRAFT 3666 [Acidovorax sp. JS42]	gi|110593724|ref|ZP 01382075.1|	32.99	0.0000009
contig00080-orf00009	pNL9 p8 [Neisseria lactamica]	gi|83701213|gb|ABC41155.1|	33.15	3E-36
contig00080-orf00011	pilin gene inverting protein homolog PivNG [Neisseria gonorrhoeae]	gi|1617515|gb|AAC82509.1|	52.34	4E-86
contig00080-orf00012	putative pyrazinamidase/nicotinamidase PncA [Photobacterium profundum 3TCK]	gi|90415124|ref|ZP 01223078.1|	43.08	1E-19
contig00080-orf00016	metal-dependent phosphohydrolase [Flavobacteria bacterium BBFL7]	gi|89890961|ref|ZP 01202470.1|	25.39	4E-13
contig00080-orf00017	hypothetical protein PsycPRwfDRAFT 2184 [Psychrobacter sp. PRwf-1]	gi|91769335|ref|ZP 01271169.1|	30.56	0.0002
contig00080-orf00018	Sec-independent protein translocase TatC [Thiobacillus denitrificans ATCC 25259]	gi|74317720|ref|YP 315460.1|	60.35	2E-66
contig00080-orf00019	twin-arginine translocation protein TatB [Acidovorax sp. JS42]	gi|110596367|ref|ZP 01384679.1|	39.36	0.0000006
contig00080-orf00020	Sec-independent protein translocase protein TatA [Bordetella avium 197N]	gi|115424380|emb|CAJ50933.1|	55.93	5E-09
contig00080-orf00022	diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases [Ralstonia eutropha H16]	gi|113869353|ref|YP 727842.1|	59.05	3E-33
contig00080-orf00023	phosphoribosyl-ATP pyrophosphatase [Thiobacillus denitrificans ATCC 25259]	gi|74317724|ref|YP 315464.1|	59.41	8E-28
contig00080-orf00025	hypothetical protein PaerP 01002804 [Pseudomonas aeruginosa PA7]	gi|94415436|ref|ZP 01295277.1|	60	2E-40
contig00080-orf00027	imidazole glycerol phosphate synthase subunit hisF [Methylobacillus flagellatus KT]	gi|91774610|ref|YP 544366.1|	74.9	3E-104
contig00080-orf00028	major facilitator family transporter [Sphingomonas sp. SKA58]	gi|94496794|ref|ZP 01303369.1|	32	0.84
contig00080-orf00030	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase [Ralstonia eutropha H16]	gi|113869358|ref|YP 727847.1|	70.08	3E-92
contig00080-orf00031	imidazole glycerol phosphate synthase subunit [Bordetella avium 197N]	gi|115424374|emb|CAJ50927.1|	52.21	2E-58
contig00080-orf00035	L-lactate permease [Haemophilus somnus 129PT]	gi|113460853|ref|YP 718920.1|	60.36	6E-165
contig00080-orf00037	GMP synthase [Ralstonia eutropha H16]	gi|113868007|ref|YP 726496.1|	71.69	0
contig00080-orf00038	conserved hypothetical protein [Aspergillus terreus NIH2624]	gi|115391111|ref|XP 001213060.1|	30.77	0.28
contig00080-orf00040	SsrA-binding protein [Thiobacillus denitrificans ATCC 25259]	gi|74317774|ref|YP 315514.1|	70.27	1E-58
contig00080-orf00042	DNA repair protein RadA [Ralstonia eutropha H16]	gi|113868090|ref|YP 726579.1|	66.81	6E-159
contig00080-orf00044	peptidase S41A, protease [Thiobacillus denitrificans ATCC 25259]	gi|74318410|ref|YP 316150.1|	52.01	2E-116
contig00080-orf00048	M23 family peptidase [Thiobacillus denitrificans ATCC 25259]	gi|74318411|ref|YP 316151.1|	36.6	5E-20
contig00080-orf00048	M23 family peptidase [Thiobacillus denitrificans ATCC 25259]	gi|74318411|ref|YP 316151.1|	21.57	0.035
contig00080-orf00049	hypothetical protein PaerP 01001988 [Pseudomonas aeruginosa PA7]	gi|94416145|ref|ZP 01295975.1|	47.59	8E-31
contig00080-orf00050	hypothetical protein P3TCK 24701 [Photobacterium profundum 3TCK]	gi|90412044|ref|ZP 01220051.1|	44.39	4E-44
contig00080-orf00051	Holliday junction resolvase-like protein [Nitrosomonas eutropha C91]	gi|114330469|ref|YP 746691.1|	55.07	3E-35
contig00080-orf00054	hypothetical protein MBMO EBAC080-L32B05.33 [uncultured marine bacterium 463]	gi|41582290|gb|AAS07904.1|	22.65	5E-08
contig00080-orf00056	PREDICTED: hypothetical protein [Pan troglodytes]	gi|114638312|ref|XP 001146342.1|	36.14	0.036

Query	NR Database Subject	Subject ID	% ID	E value
contig00080-orf00057	hypothetical protein UTI89 C4248 [Escherichia coli UTI89]	gi|91213220|ref|YP 543206.1|	37.61	2E-17
contig00080-orf00058	NUDIX hydrolase [Clostridium sp. OhILAs]	gi|106894349|ref|ZP 01361469.1|	41.52	6E-34
contig00080-orf00060	Dihydroneopterin aldolase family protein [Oceanobacter sp. RED65]	gi|94499958|ref|ZP 01306493.1|	35.34	6E-18
contig00080-orf00061	#N/A	gi|115312025|sp|Q39DI4|Y5888 BURS3	56.63	1E-35
contig00080-orf00063	phospholipase [Ralstonia eutropha H16]	gi|116694298|ref|YP 728509.1|	28.12	2E-17
contig00080-orf00066	hypothetical protein HS 0243 [Haemophilus somnus 129PT]	gi|113460389|ref|YP 718451.1|	76.85	9E-97
contig00080-orf00067	prephenate dehydratase / chorismate mutase [Ralstonia metallidurans CH34]	gi|94309661|ref|YP 582871.1|	51.81	8E-102
contig00080-orf00069	hypothetical protein 51 [Moniliophthora perniciosa]	gi|49147088|ref|YP 025873.1|	37.78	3.2
contig00080-orf00071	ompR [Neisseria meningitidis]	gi|1050721|emb|CAA63142.1|	94.18	5E-95
contig00080-orf00072	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]	gi|91775068|ref|YP 544824.1|	32.17	4E-54
contig00080-orf00074	long-chain fatty-acid-CoA ligase [Thiobacillus denitrificans ATCC 25259]	gi|74318042|ref|YP 315782.1|	37.95	3E-23
contig00080-orf00074	long-chain fatty-acid-CoA ligase [Thiobacillus denitrificans ATCC 25259]	gi|74318042|ref|YP 315782.1|	23.48	5E-12
contig00080-orf00075	SSU ribosomal protein S16P [Saccharophagus degradans 2-40]	gi|90020850|ref|YP 526677.1|	64.63	3E-25
contig00080-orf00076	16S rRNA processing protein RimM [Methylobacillus flagellatus KT]	gi|91776685|ref|YP 546441.1|	38.79	3E-31
contig00080-orf00077	tRNA (guanine-N(1)-)-methyltransferase [Pseudomonas entomophila L48]	gi|104783231|ref|YP 609729.1|	58.37	1E-65
contig00080-orf00078	ribosomal protein L19 [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619048|ref|ZP 01406064.1|	83.19	3E-42
contig00080-orf00079	hypothetical protein Rgryl 01000051 [Rickettsiella grylli]	gi|94493528|ref|ZP 01300731.1|	29.53	1E-14
contig00080-orf00081	tpc [Neisseria gonorrhoeae]	gi|1237078|emb|CAA92429.1|	92.21	4E-32
contig00080-orf00081	tpc [Neisseria gonorrhoeae]	gi|1237078|emb|CAA92429.1|	43.79	3E-17
contig00080-orf00082	folC [Neisseria gonorrhoeae]	gi|1237077|emb|CAA92428.1|	91.27	0
contig00080-orf00083	#N/A	gi|21311753|gb|AAM46838.1|AF493 544 1	25.88	0.83
contig00080-orf00084	hypothetical protein H16 A0778 [Ralstonia eutropha H16]	gi|113866804|ref|YP 725293.1|	34.91	3E-13
contig00080-orf00085	ABC transporter related [Rubrobacter xylanophilus DSM 9941]	gi|108803351|ref|YP 643288.1|	63.33	1E-86
contig00080-orf00089	dimethyladenosine transferase [Thiobacillus denitrificans ATCC 25259]	gi|74318358|ref|YP 316098.1|	55.12	2E-70
contig00080-orf00091	putative NADH-dependent flavin oxidoreductase [Escherichia coli UTI89]	gi|91209361|ref|YP 539347.1|	37.83	7E-64
contig00080-orf00094	putative hemolysin [Streptomyces ambofaciens ATCC 23877]	gi|117165111|emb|CAJ88665.1|	42.86	1E-53
contig00080-orf00095	lyso-ornithine lipid acyltransferase [Methylobacillus flagellatus KT]	gi|91774823|ref|YP 544579.1|	37.9	5E-37
contig00080-orf00098	sigma 70 (RpoD) [Methylobacillus flagellatus KT]	gi|91776674|ref|YP 546430.1|	61.57	0
contig00080-orf00102	DNA primase [Methylobacillus flagellatus KT]	gi|91776675|ref|YP 546431.1|	56.96	2E-136
contig00080-orf00105	phosphoglycerate transporter protein PgtP [Escherichia coli]	gi|92110273|emb|CAJ87539.1|	51.66	2E-128
contig00080-orf00109	putative outer membrane protein OmpU [Neisseria meningitidis]	gi|4206707|gb|AAD11779.1|	23.08	1E-19
contig00080-orf00110	pyruvate:ferredoxin oxidoreductase, delta subunit [uncultured methanogenic archaeon RC-I]	gi|110622602|emb|CAJ37880.1|	31.91	9.3
contig00080-orf00113	hypothetical protein Cfetf 01000306 [Campylobacter fetus subsp. fetus 82-40]	gi|113198305|ref|ZP 01409807.1|	36.36	1.3

Query	NR Database Subject	Subject ID	% ID	E value
contig00080-orf00114	hypothetical protein PaerPA 01005069 [Pseudomonas aeruginosa PACS2]	gi|107103996|ref|ZP 01367914.1|	26.93	7E-87
contig00080-orf00116	hypothetical protein Tbd 0252 [Thiobacillus denitrificans ATCC 25259]	gi|74316270|ref|YP 314010.1|	50.5	2E-36
contig00080-orf00119	#N/A	gi|9106265|gb|AAF84087.1|AE003961 11	30.08	4E-38
contig00080-orf00122	hypothetical protein Cfetf 01000895 [Campylobacter fetus subsp. fetus 82-40]	gi|113198879|ref|ZP 01410381.1|	67.66	4E-174
contig00080-orf00125	extra-cytoplasmic solute receptor [Ralstonia eutropha H16]	gi|116694239|ref|YP 728450.1|	32.31	1.5
contig00080-orf00127	PREDICTED: similar to CG8771-PA [Tribolium castaneum]	gi|91076074|ref|XP 967484.1|	31.58	9.2
contig00080-orf00128	SecF protein [Acidovorax sp. JS42]	gi|110594836|ref|ZP 01383177.1|	64.55	4E-105
contig00080-orf00130	protein-export membrane protein SecD [Acidovorax sp. JS42]	gi|110594837|ref|ZP 01383178.1|	56.84	0
contig00080-orf00131	preprotein translocase, YajC subunit [Mariprofundus ferrooxydans PV-1]	gi|114777996|ref|ZP 01452896.1|	45.21	1E-13
contig00080-orf00132	putative histone deacetylase-family protein [Burkholderia xenovorans LB400]	gi|91778592|ref|YP 553800.1|	43.46	8E-62
contig00080-orf00134	putative lipoprotein GNA2132 [Neisseria meningitidis]	gi|32455015|gb|AAP83187.1|	36.13	7E-24
contig00080-orf00136	hypothetical protein PaerP 01000363 [Pseudomonas aeruginosa PA7]	gi|94418209|ref|ZP 01298025.1|	37.57	2E-27
contig00080-orf00137	DNA polymerase alpha subunit, putative [Plasmodium falciparum 3D7]	gi|23509824|ref|NP 702491.1|	45.71	1.4
contig00080-orf00139	putative transferase [Shigella flexneri 5 str. 8401]	gi|110807128|ref|YP 690648.1|	61.99	2E-61
contig00080-orf00140	Maf-like protein [Pseudomonas entomophila L48]	gi|104780293|ref|YP 606791.1|	49.74	5E-40
contig00080-orf00141	putative thiosulphate sulphur transferase [Neisseria gonorrhoeae]	gi|7453625|gb|AAF62913.1|	24.73	0.001
contig00080-orf00142	Glutamate dehydrogenase/leucine dehydrogenase [Clostridium sp. OhILAs]	gi|106893090|ref|ZP 01360216.1|	62.04	4E-140
contig00080-orf00145	phosphoglycolate phosphatase [Thiobacillus denitrificans ATCC 25259]	gi|74318247|ref|YP 315987.1|	46.35	6E-37
contig00080-orf00146	regulatory protein RecX [Burkholderia xenovorans LB400]	gi|91785108|ref|YP 560314.1|	41.89	2E-17
contig00080-orf00149	hypothetical protein HS 1665 [Haemophilus somnus 129PT]	gi|113461801|ref|YP 719870.1|	59.52	6E-34
contig00080-orf00150	strongly similar to rhodanese sulfur transferase and phage shock protein pspE [Candidatus Kuenenia stuttgartiensis]	gi|91201375|emb|CAJ74435.1|	48.75	1E-17
contig00080-orf00152	putative DNA-binding protein [Mannheimia haemolytica]	gi|110735229|gb|ABG89185.1|	84.55	8E-28
contig00080-orf00154	MtrA [Neisseria meningitidis]	gi|40805150|gb|AAR91918.1|	54.97	4E-87
contig00080-orf00156	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Glucose-inhibited division protein A:Pyridine nucleotide-disulphide oxidoreductase dimerisation region [Psychromonas ingrahamii 37]	gi|106883918|ref|ZP 01351309.1|	62.39	4E-147
contig00080-orf00158	peroxiredoxin family protein/glutaredoxin [Vibrio alginolyticus 12G01]	gi|91227291|ref|ZP 01261716.1|	74.68	2E-105
contig00080-orf00159	mitochondrial putative malate:quinone oxidoreductase [Toxoplasma gondii]	gi|92399525|gb|ABE76504.1|	53.85	4.1
contig00080-orf00160	lyso-ornithine lipid acyltransferase [Methylobacillus flagellatus KT]	gi|91774823|ref|YP 544579.1|	35.5	3E-27
contig00080-orf00161	fpg [Neisseria meningitidis]	gi|93117321|gb|ABE99578.1|	82.56	3E-122
contig00080-orf00163	generic methyl-transferase [Nitrosomonas eutropha C91]	gi|114332142|ref|YP 748364.1|	34.13	6E-23
contig00080-orf00166	tryptophan synthase subunit beta [Thiobacillus denitrificans ATCC 25259]	gi|74317932|ref|YP 315672.1|	74.25	1E-167
contig00080-orf00169	fumarase [Candidatus Koribacter versatilis Ellin345]	gi|94969769|ref|YP 591817.1|	73	0
contig00080-orf00172	ferredoxin [Ralstonia metallidurans CH34]	gi|94313228|ref|YP 586437.1|	53.92	3E-64

Query	NR Database Subject	Subject ID	% ID	E value
contig00080-orf00173	putative fumarate reductase flavoprotein subunit [Endoriftia persephone 'Hot96 1+Hot96 2']	gi|110589320|gb|ABG77169.1|	51.2	1E-50
contig00080-orf00175	uptake hydrogenase [Clostridium saccharoperbutylacetonicum]	gi|56387326|gb|AAV86075.1|	41.81	2E-69
contig00080-orf00175	uptake hydrogenase [Clostridium saccharoperbutylacetonicum]	gi|56387326|gb|AAV86075.1|	33.93	2E-69
contig00080-orf00180	Sodium/sulphate symporter [Psychrobacter sp. PRwf-1]	gi|91770801|ref|ZP 01272623.1|	63.98	1E-162
contig00080-orf00182	potassium transporter peripheral membrane component [Pseudomonas entomophila L48]	gi|104779335|ref|YP 605833.1|	48.18	9E-23
contig00080-orf00182	potassium transporter peripheral membrane component [Pseudomonas entomophila L48]	gi|104779335|ref|YP 605833.1|	30	2.1
contig00080-orf00186	potassium transporter peripheral membrane component [Thiobacillus denitrificans ATCC 25259]	gi|74316038|ref|YP 313778.1|	50.64	6E-122
contig00080-orf00187	hypothetical protein PSEEN1061 [Pseudomonas entomophila L48]	gi|104780277|ref|YP 606775.1|	30.8	1E-19
contig00080-orf00188	outer membrane protein II [Neisseria meningitidis]	gi|55793508|gb|AAV65747.1|	40.06	2E-54
contig00080-orf00191	CTP synthetase [Haemophilus somnus 129PT]	gi|113460697|ref|YP 718763.1|	66.97	0
contig00080-orf00195	trk system potassium uptake membrane protein TrkH [Thiobacillus denitrificans ATCC 25259]	gi|74316039|ref|YP 313779.1|	51.76	7E-122
contig00080-orf00197	hypothetical protein lwe2081 [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116873497|ref|YP 850278.1|	31.67	2E-10
contig00081-orf00003	prolyl-tRNA synthetase [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619295|ref|YP 858106.1|	63.48	0
contig00081-orf00006	hypothetical protein PaerP 01003520 [Pseudomonas aeruginosa PA7]	gi|94414764|ref|ZP 01294619.1|	47.84	1E-72
contig00081-orf00010	CDP-6-deoxy-delta-3,4-glucoseen reductase [Burkholderia ambifaria AMMD]	gi|115352588|ref|YP 774427.1|	42.18	1E-70
contig00081-orf00011	2-isopropylmalate synthase [Oceanobacter sp. RED65]	gi|94501177|ref|ZP 01307700.1|	61.84	4E-179
contig00081-orf00013	PecM protein [Ralstonia eutropha H16]	gi|113866108|ref|YP 724597.1|	50.56	4E-48
contig00081-orf00017	lipocalin-like [Psychrobacter sp. PRwf-1]	gi|91771322|ref|ZP 01273130.1|	53.21	7E-45
contig00081-orf00020	hypothetical protein Ccur5 01001379 [Campylobacter curvus 525.92]	gi|109673721|ref|ZP 01375895.1|	63.33	0.0002
contig00081-orf00022	hypothetical protein PaerP 01000484 [Pseudomonas aeruginosa PA7]	gi|94417706|ref|ZP 01297523.1|	49.08	0
contig00081-orf00024	hypothetical protein PaerP 01000167 [Pseudomonas aeruginosa PA7]	gi|94418018|ref|ZP 01297834.1|	57.72	2E-33
contig00082-orf00001	hypothetical protein VAS14 04053 [Vibrio angustum S14]	gi|90578846|ref|ZP 01234656.1|	58.82	0.00007
contig00085-orf00001	hypothetical protein pMU1 p7 [Eikenella corrodens]	gi|66968617|ref|YP 245394.1|	34.76	6E-30
contig00085-orf00002	putative integral membrane protein [Eikenella corrodens]	gi|66968615|ref|YP 245392.1|	36.25	2E-09
contig00085-orf00004	putative Tsp protein (T cell and B cell stimulating antigen) [Eikenella corrodens]	gi|66968616|ref|YP 245393.1|	39.76	6E-12
contig00085-orf00004	putative Tsp protein (T cell and B cell stimulating antigen) [Eikenella corrodens]	gi|66968616|ref|YP 245393.1|	43.18	2E-09
contig00086-orf00001	transposase [Klebsiella pneumoniae]	gi|38639767|ref|NP 943536.1|	39.24	1E-51
contig00088-orf00001	Serine O-acetyltransferase [Saccharophagus degradans 2-40]	gi|90020731|ref|YP 526558.1|	54.15	4E-78
contig00088-orf00003	GrpE protein [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269390|ref|ZP 01493634.1|	47.44	7E-34
contig00088-orf00007	molecular chaperone protein DnaK [Thiobacillus denitrificans ATCC 25259]	gi|74317556|ref|YP 315296.1|	79.47	0
contig00088-orf00008	PREDICTED: similar to CG15099-PA [Apis mellifera]	gi|110757042|ref|XP 395999.3|	39.53	0.82
contig00088-orf00013	ATPase [Ralstonia eutropha H16]	gi|113866942|ref|YP 725431.1|	61.35	3E-144

Query	NR Database Subject	Subject ID	% ID	E value
contig00088-orf00016	acetolactate synthase isozyme III large subunit [Bordetella avium 197N]	gi|115423734|emb|CAJ50284.1|	66.02	0
contig00088-orf00018	acetolactate synthase, small subunit [Acidovorax sp. JS42]	gi|110594972|ref|ZP 01383311.1|	70.32	7E-57
contig00088-orf00021	Antibiotic biosynthesis monooxygenase [Salinispora tropica CNB-440]	gi|113943301|ref|ZP 01429003.1|	40.86	4E-13
contig00088-orf00023	ketol-acid reductoisomerase [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111618982|ref|ZP 01405999.1|	79.59	4E-152
contig00088-orf00025	hypothetical protein RPB 3223 [Rhodopseudomonas palustris HaA2]	gi|86750334|ref|YP 486830.1|	64.86	7E-24
contig00088-orf00027	putative transmembrane two-component sensor histidine kinase/response regulator hybrid [Rhizobium leguminosarum bv. viciae 3841]	gi|116250178|ref|YP 766016.1|	27.03	7.1
contig00088-orf00028	hypothetical membrane associated protein [Photobacterium profundum 3TCK]	gi|90411137|ref|ZP 01219150.1|	29.29	2E-28
contig00088-orf00029	hypothetical protein [Paramecium bursaria Chlorella virus 1]	gi|9631969|ref|NP 048758.1|	35.15	3E-35
contig00088-orf00033	oligopeptidase A [Thiobacillus denitrificans ATCC 25259]	gi|74318451|ref|YP 316191.1|	55.15	0
contig00089-orf00001	extracellular solute-binding protein, family 3 [Psychrobacter sp. PRwf-1]	gi|91769295|ref|ZP 01271129.1|	64.83	6E-82
contig00089-orf00003	Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine [Psychrobacter sp. PRwf-1]	gi|91769296|ref|ZP 01271130.1|	58.23	2E-79
contig00089-orf00004	polar amino acid ABC transporter, ATP-binding protein [Haemophilus somnus 129PT]	gi|113460356|ref|YP 718417.1|	78.14	3E-104
contig00089-orf00006	ABC transporter ATPase [Ralstonia eutropha H16]	gi|113868082|ref|YP 726571.1|	53.51	2E-179
contig00089-orf00006	ABC transporter ATPase [Ralstonia eutropha H16]	gi|113868082|ref|YP 726571.1|	27.87	1E-18
contig00089-orf00007	PREDICTED: similar to Homeobox protein SIX1 (Sine oculis homeobox homolog 1) [Bos taurus]	gi|61809153|ref|XP 588692.1|	43.24	4.1
contig00089-orf00009	hypothetical protein Tbd 2502 [Thiobacillus denitrificans ATCC 25259]	gi|74318520|ref|YP 316260.1|	33.82	0.043
contig00089-orf00010	putative GTP cyclohydrolase [Ralstonia eutropha H16]	gi|113868689|ref|YP 727178.1|	57.03	2E-81
contig00089-orf00014	Cystathionine gamma-synthase [Flavobacterium johnsoniae UW101]	gi|90590715|ref|ZP 01246361.1|	46.07	5E-86
contig00089-orf00015	putative heat shock protein HslJ [Vibrio angustum S14]	gi|90578980|ref|ZP 01234790.1|	29.11	0.000007
contig00089-orf00017	hypothetical protein PaerPA 01000739 [Pseudomonas aeruginosa PACS2]	gi|107099721|ref|ZP 01363639.1|	39.92	2E-53
contig00089-orf00019	hypothetical protein CburR 01000914 [Coxiella burnetii RSA 331]	gi|95927307|ref|ZP 01310067.1|	57.32	2E-89
contig00089-orf00026	heavy metal translocating P-type ATPase [Thiobacillus denitrificans ATCC 25259]	gi|74318062|ref|YP 315802.1|	48.16	8E-171
contig00089-orf00028	transposase [Neisseria meningitidis]	gi|13445209|emb|CAC34951.1|	87.23	4E-15
contig00089-orf00029	unnamed protein product [Neisseria meningitidis]	gi|6900477|emb|CAB72065.1|	96.88	1E-08
contig00092-orf00001	hypothetical protein CC1G 12542 [Coprinopsis cinerea okayama7#130]	gi|116505403|gb|EAU88298.1|	26.77	3
contig00092-orf00003	pyridine nucleotide transhydrogenase [Vibrio alginolyticus 12G01]	gi|91226113|ref|ZP 01261003.1|	78.26	0
contig00092-orf00005	probable amino acid efflux protein [Bordetella avium 197N]	gi|115422191|emb|CAJ48715.1|	38.38	9E-22
contig00092-orf00007	short-chain dehydrogenase/reductase SDR [Salinispora tropica CNB-440]	gi|113946265|ref|ZP 01431956.1|	30.68	0.033
contig00092-orf00010	NAD(P) transhydrogenase subunit alpha [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618516|ref|YP 858505.1|	71.29	1E-170
contig00092-orf00011	lactoylglutathione lyase [Bordetella avium 197N]	gi|115421796|emb|CAJ48307.1|	78.63	1E-56
contig00092-orf00013	N6-adenine-specific DNA methylase [Ralstonia eutropha H16]	gi|113869087|ref|YP 727576.1|	42.34	8E-79

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contig00092-orf00016	fumarase C [Neisseria subflava]	gi|46488610|gb|AAS99578.1|	98.48	0
contig00092-orf00018	hypothetical protein ABO 0205 [Alcanivorax borkumensis SK2]	gi|110833066|ref|YP 691925.1|	46.71	1E-59
contig00092-orf00019	ribonuclease PH [Acidovorax sp. JS42]	gi|110595245|ref|ZP 01383580.1|	65.52	2E-74
contig00092-orf00020	transcriptional repressor-molybdenum-binding protein [Ralstonia eutropha H16]	gi|113866699|ref|YP 725188.1|	46.48	5E-23
contig00092-orf00022	aspartate kinase [Ralstonia eutropha H16]	gi|113867245|ref|YP 725734.1|	69.25	6E-145
contig00092-orf00028	putative paraquat-inducible protein A [Photobacterium profundum 3TCK]	gi|90413932|ref|ZP 01221917.1|	34.05	1E-51
contig00092-orf00030	putative paraquat-inducible protein B [Photobacterium profundum 3TCK]	gi|90413933|ref|ZP 01221918.1|	37.06	6E-95
contig00092-orf00032	hypothetical protein P3TCK 07711 [Photobacterium profundum 3TCK]	gi|90413934|ref|ZP 01221919.1|	31.11	4E-09
contig00092-orf00034	Glutathione S-transferase-like [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111617050|ref|ZP 01404080.1|	36.84	1E-27
contig00092-orf00035	two-component system sensor ATPase [Thiobacillus denitrificans ATCC 25259]	gi|74316248|ref|YP 313988.1|	41.23	3E-39
contig00092-orf00036	argininosuccinate lyase [Thiobacillus denitrificans ATCC 25259]	gi|74316247|ref|YP 313987.1|	76.61	0
contig00092-orf00037	cytidylate kinase [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116268971|ref|ZP 01493216.1|	53.43	1E-46
contig00092-orf00039	LysR family transcriptional regulator [Burkholderia xenovorans LB400]	gi|91780930|ref|YP 556137.1|	39.47	4.1
contig00092-orf00041	30S ribosomal protein S1 [Ralstonia eutropha H16]	gi|113866824|ref|YP 725313.1|	73.04	0
contig00092-orf00042	integration host factor, beta subunit [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116268973|ref|ZP 01493218.1|	73.68	1E-26
contig00092-orf00046	ATPase [Ralstonia eutropha H16]	gi|113868297|ref|YP 726786.1|	46.91	5E-92
contig00092-orf00048	Nucleoside diphosphate kinase [alpha proteobacterium HTCC2255]	gi|114771468|ref|ZP 01448883.1|	73.76	5E-55
contig00092-orf00049	hypothetical protein Tbd 0591 [Thiobacillus denitrificans ATCC 25259]	gi|74316609|ref|YP 314349.1|	70.41	4E-146
contig00092-orf00050	tetratricopeptide TPR 2 [Methylobacillus flagellatus KT]	gi|91775975|ref|YP 545731.1|	33.89	3E-25
contig00092-orf00051	putative membrane protein [Bordetella avium 197N]	gi|115423421|emb|CAJ49955.1|	44.29	0.0000001
contig00092-orf00053	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Methylobacillus flagellatus KT]	gi|91775973|ref|YP 545729.1|	72.97	1E-161
contig00092-orf00056	Protein of unknown function DUF323 [Flavobacterium johnsoniae UW101]	gi|90588805|ref|ZP 01244456.1|	44.93	6E-53
contig00092-orf00060	major outer membrane protein [Flavobacterium columnare]	gi|37694421|gb|AAQ99141.1|	58.9	2E-111
contig00092-orf00062	nitric oxide reductase [Neisseria meningitidis]	gi|6900346|emb|CAB71958.1|	94.67	0
contig00092-orf00064	Bbp10 [Bordetella phage BPP-1]	gi|41179371|ref|NP 958679.1|	52.51	2E-42
contig00092-orf00067	hypothetical protein Ccur5 01000054 [Campylobacter curvus 525.92]	gi|109675025|ref|ZP 01377179.1|	38.59	9E-49
contig00092-orf00068	hypothetical protein Ccur5 01000054 [Campylobacter curvus 525.92]	gi|109675025|ref|ZP 01377179.1|	39.14	2E-47
contig00092-orf00070	PREDICTED: cell division cycle 2-like 5 isoform 5 [Pan troglodytes]	gi|114613060|ref|XP 001140018.1|	29.77	0.037
contig00092-orf00071	MOBP protein [Homo sapiens]	gi|49899229|gb|AAH75796.1|	32.76	0.37
contig00092-orf00072	putative outer membrane protein OmpU [Neisseria meningitidis]	gi|4206707|gb|AAD11779.1|	24.87	4E-16
contig00092-orf00073	Prokaryotic transcription elongation factor GreB [Acidovorax sp. JS42]	gi|110594001|ref|ZP 01382350.1|	66.23	2E-46
contig00092-orf00074	30S ribosomal protein S15 [Bordetella avium 197N]	gi|115423729|emb|CAJ50279.1|	66.29	1E-21
contig00092-orf00075	Os03g0747900 [Oryza sativa (japonica cultivar-group)]	gi|115455325|ref|NP 001051263.1|	30.26	1.9
contig00092-orf00076	disulphide bond formation protein DsbB [Chromohalobacter salexigens DSM 3043]	gi|92114771|ref|YP 574699.1|	34.09	2E-15
contig00092-orf00077	Sodium:alanine symporter [Clostridium sp. OhILAs]	gi|106893861|ref|ZP 01360985.1|	57.45	1E-123

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contig00092-orf00078	hypothetical protein SAV 1872 [Streptomyces avermitilis MA-4680]	gi|29828414|ref|NP 823048.1|	46.67	9.2
contig00094-orf00001	conserved hypothetical protein [Chlorobium ferrooxidans DSM 13031]	gi|110598784|ref|ZP 01387044.1|	73.21	3E-15
contig00094-orf00003	Filamentation induced by cAMP protein Fic [Psychromonas ingrahamii 37]	gi|106883076|ref|ZP 01350475.1|	52.83	4E-77
contig00094-orf00004	PREDICTED: similar to dystonin isoform a [Bos taurus]	gi|76649774|ref|XP 615341.2|	28.95	0.63
contig00094-orf00007	YafJ [Neisseria gonorrhoeae]	gi|2661442|emb|CAA05723.1|	84.15	5E-123
contig00094-orf00009	conserved hypothetical protein [uncultured methanogenic archaeon RC-I]	gi|110621405|emb|CAJ36683.1|	25	3.8
contig00094-orf00010	HesB/YadR/YfhF [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619432|ref|ZP 01406443.1|	80.65	4E-39
contig00094-orf00011	putative regulatory protein [Neisseria meningitidis]	gi|6900347|emb|CAB71959.1|	56.47	7E-72
contig00094-orf00012	hypothetical protein SNOG 09853 [Phaeosphaeria nodorum SN15]	gi|111061998|gb|EAT83118.1|	26.67	2.4
contig00094-orf00013	DNA topoisomerase IV subunit A [Burkholderia ambifaria AMMD]	gi|115352446|ref|YP 774285.1|	58.6	0
contig00094-orf00016	Rsp [Neisseria gonorrhoeae]	gi|3851181|gb|AAC82507.1|	48.48	7E-85
contig00094-orf00017	PilR [Xanthomonas campestris pv. campestris]	gi|37784396|gb|AAP43028.1|	46.29	2E-111
contig00094-orf00018	conserved hypothetical protein; putative membrane protein [Psychrobacter sp. PRwf-1]	gi|91770540|ref|ZP 01272365.1|	63.16	1E-08
contig00094-orf00020	dTDP-D-glucose-4,6-dehydratase [Vibrio cholerae]	gi|29725994|gb|AAO88925.1|	84.14	4E-168
contig00094-orf00021	glucose-1-phosphate thymidylyltransferase [Vibrio cholerae]	gi|29725990|gb|AAO88922.1|	81.94	1E-138
contig00095-orf00001	hypothetical protein Suden 1624 [Sulfurimonas denitrificans DSM 1251]	gi|78777821|ref|YP 394136.1|	31.25	0.012
contig00095-orf00003	hypothetical protein FP2506 01480 [Fulvimarina pelagi HTCC2506]	gi|114706414|ref|ZP 01439316.1|	44.8	1E-14
contig00095-orf00004	hypothetical protein RL3478 [Rhizobium leguminosarum bv. viciae 3841]	gi|116253220|ref|YP 769058.1|	45.95	3E-11
contig00095-orf00007	putative dipeptide binding periplasmic protein [Sinorhizobium medicae	gi|113874227|ref|ZP 01414355.1|	44	2.4
contig00095-orf00009	hypothetical protein AaveDRAFT 1483 [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619383|ref|ZP 01406395.1|	25.58	0.07
contig00095-orf00011	GTP-binding protein, HSR1-related [Psychromonas ingrahamii 37]	gi|106883252|ref|ZP 01350650.1|	29.41	4.1
contig00095-orf00013	PREDICTED: similar to centrosomal protein 2 isoform 1 [Rattus norvegicus]	gi|109469097|ref|XP 230784.4|	27.71	1.8
contig00096-orf00001	pNL9 p1 [Neisseria lactamica]	gi|83701206|gb|ABC41148.1|	63.64	3E-30
contig00096-orf00002	replication-associated protein [Beet curly top virus]	gi|9626214|ref|NP 040557.1|	42.11	5.5
contig00096-orf00003	hypothetical protein [Neisseria lactamica]	gi|81366998|gb|ABB71601.1|	61.07	4E-130
contig00096-orf00006	hypothetical protein [Neisseria lactamica]	gi|81366999|gb|ABB71602.1|	40.91	0.005
contig00096-orf00007	hypothetical protein P700755 22593 [Psychroflexus torquis ATCC 700755]	gi|91221894|ref|ZP 01257522.1|	28.81	5.4
contig00096-orf00008	hypothetical protein pMU1 p1 [Eikenella corrodens]	gi|66968611|ref|YP 245388.1|	24.62	0.057
contig00096-orf00010	pNL9 p6 [Neisseria lactamica]	gi|83701211|gb|ABC41153.1|	25.84	0.057
contig00096-orf00013	16S RNA m2G1207 methylase [Buchnera aphidicola str. Cc (Cinara cedri)]	gi|116515142|ref|YP 802771.1|	29.63	3.6
contig00097-orf00001	hypothetical protein CburR 01001813 [Coxiella burnetii RSA 331]	gi|95926370|ref|ZP 01309162.1|	61.11	0.0000002
contig00099-orf00001	LOC445869 protein [Xenopus laevis]	gi|50417540|gb|AAH77509.1|	39.58	3.2
contig00099-orf00002	secreted thioredoxin, putative [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116873338|ref|YP 850119.1|	24.76	5E-08
contig00099-orf00003	low molecular weight protein-tyrosine-phosphatase [Haemophilus somnus 129PT]	gi|113460960|ref|YP 719027.1|	56.85	4E-47

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contig00099-orf00005	putative modular polyketide synthase [Streptomyces ambofaciens ATCC 23877]	gi|117164639|emb|CAJ88185.1|	29.89	0.094
contig00099-orf00005	putative modular polyketide synthase [Streptomyces ambofaciens ATCC 23877]	gi|117164639|emb|CAJ88185.1|	27.52	0.61
contig00099-orf00007	hypothetical protein PaerP 01001213 [Pseudomonas aeruginosa PA7]	gi|94417017|ref|ZP 01296839.1|	60.53	5E-64
contig00099-orf00008	novel protein similar to human titin (TTN) [Danio rerio]	gi|27884114|emb|CAD61245.1|	35.71	5.1
contig00099-orf00009	IntD [Dichelobacter nodosus]	gi|56961720|gb|AAW31811.1|	44.71	4E-76
contig00099-orf00010	hypothetical protein [Escherichia coli]	gi|92110314|emb|CAJ87582.1|	24.52	0.053
contig00099-orf00011	prophage regulatory protein [Escherichia coli UTI89]	gi|91210122|ref|YP 540108.1|	36.36	0.000002
contig00099-orf00013	Bcep22gp24 [Burkholderia phage Bcep22]	gi|38640331|ref|NP 944252.1|	48.21	0.02
contig00099-orf00014	zinc finger protein Dj-ZicA [Dugesia japonica]	gi|117307393|dbj|BAE94141.2|	36.96	0.85
contig00099-orf00015	Putative phage small subunit terminase [Bordetella avium 197N]	gi|115422395|emb|CAJ48920.1|	63.21	4E-18
contig00099-orf00016	hypothetical protein SAV 4435 [Streptomyces avermitilis MA-4680]	gi|29830978|ref|NP 825612.1|	42.86	2.4
contig00099-orf00017	hypothetical protein [Frankia sp. ArI3]	gi|14268371|emb|CAC39344.1|	55.17	1.8
contig00099-orf00019	conserved hypothetical protein [Acidovorax sp. JS42]	gi|110592771|ref|ZP 01381126.1|	29.66	2E-27
contig00099-orf00023	Orf562 [Dichelobacter nodosus]	gi|56961721|gb|AAW31812.1|	35.14	4E-67
contig00099-orf00025	putative cell surface polysaccharide export ABC-2 transporter permease protein, close relative of Y20822wzm2 [Sinorhizobium medicae WSM419]	gi|113874796|ref|ZP 01414923.1|	40	4.1
contig00099-orf00027	hypothetical protein PBC5p01 [Sinorhizobium phage PBC5]	gi|18071226|ref|NP 542261.1|	55.84	1E-13
contig00099-orf00028	outer membrane protein [Haemophilus somnus 129PT]	gi|113460889|ref|YP 718956.1|	42.57	2E-26
contig00099-orf00029	outer membrane protein [Haemophilus somnus 129PT]	gi|113460889|ref|YP 718956.1|	44.83	3E-58
contig00099-orf00029	outer membrane protein [Haemophilus somnus 129PT]	gi|113460889|ref|YP 718956.1|	42.75	3E-58
contig00099-orf00030	mitomycin resistance protein [Chlorobium ferrooxidans DSM 13031]	gi|110597367|ref|ZP 01385654.1|	55.32	5E-27
contig00099-orf00033	conserved hypothetical protein [Campylobacter concisus 13826]	gi|109671563|ref|ZP 01373814.1|	33.54	3E-15
contig00101-orf00002	UDP-N-acetylglucosamine pyrophosphorylase/glucosamine-1-phosphate acetyltransferase [Ralstonia eutropha H16]	gi|113866293|ref|YP 724782.1|	56.17	7E-136
contig00101-orf00004	hypothetical protein CAGL0A01408g [Candida glabrata CBS138]	gi|50284801|ref|XP 444828.1|	42	0.29
contig00101-orf00007	pyrimidine 5-nucleotidase [Burkholderia cenocepacia AU 1054]	gi|107024028|ref|YP 622355.1|	37.97	6E-30
contig00101-orf00008	ABC transporter periplasmic binding protein, thiB subfamily [Herpetosiphon aurantiacus ATCC 23779]	gi|113939465|ref|ZP 01425319.1|	40.69	2E-63
contig00101-orf00009	F53H4.2 [Caenorhabditis elegans]	gi|17568091|ref|NP 510608.1|	32.26	7
contig00101-orf00010	5'-3' exonuclease [Streptomyces avermitilis MA-4680]	gi|29833256|ref|NP 827890.1|	46.15	5.3
contig00101-orf00012	Os05g0105900 [Oryza sativa (japonica cultivar-group)]	gi|115461629|ref|NP 001054414.1|	28.77	0.045
contig00101-orf00014	Phage putative head morphogenesis protein, SPP1 gp7 [Clostridium phytofermentans ISDg]	gi|106887498|ref|ZP 01354799.1|	30.98	0.0000008
contig00101-orf00016	YD repeat [Herpetosiphon aurantiacus ATCC 23779]	gi|113941087|ref|ZP 01426898.1|	32.65	3E-14
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	30.69	1E-43
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	22.98	1E-08
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	26.37	6E-08

Query	NR Database Subject	Subject ID	% ID	E value
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	24.36	0.00002
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	21.76	0.88
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	29	2.6
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	25.86	2.6
contig00102-orf00003	hemagglutinin [Moraxella catarrhalis]	gi|22000944|gb|AAL78284.1|	29.63	5.7
contig00104-orf00001	putative transposase [Streptococcus pneumoniae]	gi|5019554|emb|CAB44497.1|	45.78	4E-14
contig00106-orf00001	Putative transposase [Escherichia coli]	gi|59889757|emb|CAH19112.1|	53.16	2E-46
contig00106-orf00002	fimbrial protein [Verminephrobacter eiseniae EF01-2]	gi|111613153|ref|ZP 01400236.1|	32.39	1E-11
contig00106-orf00005	#N/A	gi|97201345|sp|Q8FH88|SYY ECOL6	62.65	1E-157
contig00106-orf00006	hypothetical malaria antigen [Plasmodium falciparum 3D7]	gi|23619203|ref|NP 705165.1|	33.33	1.4
contig00106-orf00007	translation-associated GTPase [Thiobacillus denitrificans ATCC 25259]	gi|74316408|ref|YP 314148.1|	74.93	6E-156
contig00106-orf00008	glutamate racemase [Thiobacillus denitrificans ATCC 25259]	gi|74317540|ref|YP 315280.1|	62.55	6E-81
contig00106-orf00011	Methyltransferase FkbM [Chlorobium ferrooxidans DSM 13031]	gi|110597269|ref|ZP 01385557.1|	33.72	0.0000001
contig00106-orf00012	methyltransferase [Granulibacter bethesdensis CGDNIH1]	gi|114328199|ref|YP 745356.1|	34.15	0.0000003
contig00106-orf00014	protein translocase subunit yidC [Thiobacillus denitrificans ATCC 25259]	gi|74318843|ref|YP 316583.1|	44.93	2E-119
contig00106-orf00016	hypothetical protein VAS14 22402 [Vibrio angustum S14]	gi|90581130|ref|ZP 01236929.1|	66.15	1E-21
contig00106-orf00017	50S ribosomal protein L34 [Bordetella avium 197N]	gi|115424469|emb|CAJ51023.1|	87.5	0.00009
contig00106-orf00018	ribonuclease P protein component [Shewanella denitrificans OS217]	gi|91795122|ref|YP 564773.1|	39.45	3E-12
contig00106-orf00021	PREDICTED: similar to TCF3 (E2A) fusion partner (in childhood Leukemia) isoform 1 [Macaca mulatta]	gi|109125964|ref|XP 001116845.1|	28.8	0.13
contig00106-orf00022	chromosomal replication initiator protein DnaA [Shewanella sp. ANA-3]	gi|117610800|gb|ABK46254.1|	43.96	4E-100
contig00106-orf00023	DNA polymerase III beta chain [Nitrosospira sp. NIJS18]	gi|81251085|gb|ABB69885.1|	59.35	5E-110
contig00106-orf00025	hypothetical protein Mfla 0583 [Methylobacillus flagellatus KT]	gi|91774938|ref|YP 544694.1|	46.95	1E-34
contig00106-orf00028	microcin-processing peptidase 1 [Methylobacillus flagellatus KT]	gi|91774939|ref|YP 544695.1|	56.84	3E-135
contig00106-orf00030	Glycosyl transferase, group 1 [Psychrobacter sp. PRwf-1]	gi|91770027|ref|ZP 01271857.1|	40.57	5E-76
contig00106-orf00032	tRNA-dihydrouridine synthase A [Burkholderia xenovorans LB400]	gi|91783334|ref|YP 558540.1|	60.76	1E-102
contig00106-orf00034	hypothetical protein PaerP 01002386 [Pseudomonas aeruginosa PA7]	gi|94415816|ref|ZP 01295651.1|	33.99	6E-18
contig00107-orf00001	transposase [Neisseria meningitidis]	gi|3860540|emb|CAA04676.1|	91.77	8E-81
contig00107-orf00002	CRISPR-associated Cas1 family protein [Myxococcus xanthus DK 1622]	gi|108763792|ref|YP 635128.1|	62.6	8E-39
contig00107-orf00004	protein of unknown function DUF196 [Desulfovibrio vulgaris subsp. vulgaris DP4]	gi|114847456|ref|ZP 01457763.1|	62.92	9E-27
contig00107-orf00007	hypothetical protein Shewmr7 0446 [Shewanella sp. MR-7]	gi|114045956|ref|YP 736506.1|	69.44	9E-08
contig00107-orf00008	sirohaem synthase [Neisseria meningitidis]	gi|1752671|emb|CAA71251.1|	57.3	2E-127
contig00107-orf00009	hypothetical protein BBFL7 01871 [Flavobacteria bacterium BBFL7]	gi|89890049|ref|ZP 01201560.1|	46.67	7.1
contig00107-orf00010	sulfate adenylyltransferase subunit 2 [Ralstonia metallidurans CH34]	gi|94311745|ref|YP 584955.1|	77.63	1E-111
contig00107-orf00012	carbonate dehydratase [Sulfurimonas denitrificans DSM 1251]	gi|78777434|ref|YP 393749.1|	46.59	1E-60

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contig00107-orf00013	chaperone protein HchA [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618372|ref|YP 857620.1|	58.16	4E-89
contig00107-orf00014	hypothetical protein MGC146462 [Xenopus (Silurana) tropicalis]	gi|116487394|gb|AAI25737.1|	40.54	3.2
contig00107-orf00015	AraC family transcriptional regulator [Pseudomonas entomophila L48]	gi|104781853|ref|YP 608351.1|	41.88	4E-39
contig00107-orf00018	phosphoadenosine phosphosulfate reductase [Ralstonia eutropha H16]	gi|113868952|ref|YP 727441.1|	55.14	8E-72
contig00107-orf00019	DinB [Neisseria meningitidis]	gi|93117311|gb|ABE99573.1|	94.64	3E-179
contig00107-orf00021	putative protein involved in catabolism of external DNA [Burkholderia xenovorans LB400]	gi|91782667|ref|YP 557873.1|	50.18	1E-73
contig00107-orf00023	#N/A	gi|42691|emb|CAA28253.1|	35.9	4E-48
contig00108-orf00001	lipoprotein releasing system, ATP-binding protein [Thiobacillus denitrificans ATCC 25259]	gi|74317778|ref|YP 315518.1|	54.91	4E-59
contig00108-orf00002	ABC transporter permease [Ralstonia eutropha H16]	gi|113867193|ref|YP 725682.1|	54.09	2E-113
contig00108-orf00003	ErfK/YbiS/YcfS/YnhG [Mycobacterium sp. KMS]	gi|92913792|ref|ZP 01282420.1|	31.25	0.82
contig00108-orf00004	recombination protein RecR [Thiobacillus denitrificans ATCC 25259]	gi|74316535|ref|YP 314275.1|	57.44	5E-59
contig00108-orf00005	hypothetical protein CburR 01001945 [Coxiella burnetii RSA 331]	gi|95926232|ref|ZP 01309040.1|	24.52	2E-30
contig00108-orf00006	arsenate reductase [Ralstonia eutropha H16]	gi|113868047|ref|YP 726536.1|	60.19	5E-31
contig00108-orf00007	aminomethyltransferase [Ralstonia eutropha H16]	gi|113867578|ref|YP 726067.1|	34.8	3E-23
contig00108-orf00009	ATP-dependent DNA helicase Rep [Thiobacillus denitrificans ATCC 25259]	gi|74316184|ref|YP 313924.1|	54.46	0
contig00108-orf00010	Phage integrase [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619799|ref|ZP 01406803.1|	53.49	0.0002
contig00108-orf00012	predicted protein [Coprinopsis cinerea okayama7#130]	gi|116505980|gb|EAU88875.1|	44	4.1
contig00108-orf00013	PREDICTED: similar to pleiomorphic adenoma gene-like 1 [Macaca mulatta]	gi|109073754|ref|XP 001098027.1|	56.67	5.4
contig00108-orf00014	hypothetical protein PaerP 01002548 [Pseudomonas aeruginosa PA7]	gi|94415771|ref|ZP 01295607.1|	67.75	2E-146
contig00108-orf00016	hypothetical protein PaerP 01002549 [Pseudomonas aeruginosa PA7]	gi|94415772|ref|ZP 01295608.1|	51.53	2E-55
contig00108-orf00017	hypothetical protein Cjejd 01001121 [Campylobacter jejuni subsp. doylei	gi|109691255|ref|ZP 01378324.1|	38.46	3.1
contig00108-orf00019	putative aminotransferase [Photorhabdus temperata]	gi|23092544|gb|AAN08355.1|	75.94	1E-178
contig00108-orf00020	polyprotein [Human coxsackievirus A1]	gi|33304551|gb|AAQ02675.1|	56.52	0.64
contig00108-orf00021	ubiquinone/menaquinone biosynthesis methyltransferase [Ralstonia eutropha H16]	gi|113866474|ref|YP 724963.1|	67.63	1E-92
contig00108-orf00024	hypothetical protein RED65 15993 [Oceanobacter sp. RED65]	gi|94500587|ref|ZP 01307118.1|	58.04	3E-30
contig00108-orf00025	PREDICTED: similar to predicted protein [Tribolium castaneum]	gi|91086961|ref|XP 973074.1|	36.96	4.1
contig00108-orf00027	hypothetical protein Ccur5 01001943 [Campylobacter curvus 525.92]	gi|109673144|ref|ZP 01375360.1|	31.9	2E-39
contig00108-orf00028	anaerobic C4-dicarboxylate transporter [Photobacterium profundum 3TCK]	gi|90411459|ref|ZP 01219470.1|	71.69	3E-140
contig00108-orf00029	hypothetical protein H16 A2957 [Ralstonia eutropha H16]	gi|113868912|ref|YP 727401.1|	45.76	9E-08
contig00108-orf00030	caffeoyl-CoA O-methyltransferase [Solibacter usitatus Ellin6076]	gi|116625511|ref|YP 827667.1|	48.57	5E-48
contig00108-orf00032	tetratricopeptide region [Methylobacillus flagellatus KT]	gi|91776689|ref|YP 546445.1|	25.93	0.000007
contig00108-orf00033	phosphoribosylaminoimidazole carboxylase, catalytic subunit [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619504|ref|YP 854595.1|	81.31	2E-37
contig00108-orf00035	putative ATP-binding protein [Neisseria meningitidis]	gi|5051458|emb|CAB44978.1|	95.13	0

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contig00108-orf00036	inosine-5'-monophosphate dehydrogenase [Thiobacillus denitrificans ATCC 25259]	gi|74317770|ref|YP 315510.1|	75.88	0
contig00108-orf00039	Phosphopyruvate hydratase [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269661|ref|ZP 01493904.1|	72.07	1E-169
contig00108-orf00040	hypothetical protein GB2207 10953 [marine gamma proteobacterium HTCC2207]	gi|90416191|ref|ZP 01224123.1|	44.57	1E-13
contig00108-orf00044	hypothetical protein PCNPT3 12458 [Psychromonas sp. CNPT3]	gi|90406853|ref|ZP 01215045.1|	36.59	7
contig00108-orf00045	non-structural polyprotein [Semliki forest virus]	gi|21655312|gb|AAM64226.1|	33.33	0.86
contig00108-orf00047	DEAD/DEAH box helicase [Thiobacillus denitrificans ATCC 25259]	gi|74318833|ref|YP 316573.1|	60.16	1E-114
contig00108-orf00049	conserved hypothetical protein [Stigmatella aurantiaca DW4/3-1]	gi|115372746|ref|ZP 01460052.1|	50.33	1E-81
contig00108-orf00051	membrane protein, putative [uncultured marine bacterium 560]	gi|40063034|gb|AAR37890.1|	20.88	0.28
contig00108-orf00053	#N/A	gi|94413815|ref|ZP 01293691.1|	36.87	6E-50
contig00108-orf00054	elongation factor P [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618817|ref|YP 857718.1|	69.35	1E-70
contig00108-orf00058	DNA gyrase subunit A [Thiobacillus denitrificans ATCC 25259]	gi|74316966|ref|YP 314706.1|	63.16	0
contig00108-orf00058	DNA gyrase subunit A [Thiobacillus denitrificans ATCC 25259]	gi|74316966|ref|YP 314706.1|	37.86	0.0000008
contig00108-orf00059	O-acetylhomoserine/O-acetylserine sulfhydrylase [Oceanobacter sp. RED65]	gi|94500572|ref|ZP 01307103.1|	72.13	2E-155
contig00108-orf00061	#N/A	gi|20271140|gb|AAM18525.1|AF495 855 1	62.65	0
contig00108-orf00065	recombination associated protein [Saccharophagus degradans 2-40]	gi|90020123|ref|YP 525950.1|	36.58	3E-49
contig00108-orf00067	hypothetical protein PF14 0586 [Plasmodium falciparum 3D7]	gi|23509808|ref|NP 702475.1|	36.54	0.000003
contig00108-orf00067	hypothetical protein PF14 0586 [Plasmodium falciparum 3D7]	gi|23509808|ref|NP 702475.1|	44.12	1.1
contig00108-orf00069	deoxycytidine triphosphate deaminase [Ralstonia eutropha H16]	gi|113868886|ref|YP 727375.1|	84.04	1E-92
contig00108-orf00075	#N/A	gi|1683354|gb|AAB32262.1|S75490	50.55	1E-78
contig00108-orf00079	glutamate--cysteine ligase GshA [Thiobacillus denitrificans ATCC 25259]	gi|74318426|ref|YP 316166.1|	62.77	4E-119
contig00108-orf00081	3-isopropylmalate dehydratase, large subunit [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619761|ref|ZP 01406766.1|	73.08	0
contig00108-orf00083	Entericidin EcnAB [Psychrobacter sp. PRwf-1]	gi|91770883|ref|ZP 01272704.1|	53.66	0.00001
contig00108-orf00084	hypothetical protein PaerP 01005693 [Pseudomonas aeruginosa PA7]	gi|94412520|ref|ZP 01292437.1|	75.83	7E-94
contig00108-orf00086	hypothetical protein Tbd 2429 [Thiobacillus denitrificans ATCC 25259]	gi|74318447|ref|YP 316187.1|	35.76	1E-20
contig00108-orf00090	3-isopropylmalate dehydrogenase [Oceanobacter sp. RED65]	gi|94498951|ref|ZP 01305489.1|	69.25	2E-134
contig00108-orf00093	hypothetical protein H16 A0040 [Ralstonia eutropha H16]	gi|113866071|ref|YP 724560.1|	42.37	2E-23
contig00108-orf00095	putative virion core protein [Burkholderia ambifaria AMMD]	gi|115359020|ref|YP 776158.1|	55.71	6E-85
contig00108-orf00100	hypothetical protein AaveDRAFT 3238 [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111617526|ref|ZP 01404555.1|	32.33	6E-53
contig00108-orf00102	S-adenosylmethionine decarboxylase proenzyme [Synechococcus sp. BL107]	gi|116072583|ref|ZP 01469849.1|	47.62	3E-14
contig00108-orf00104	FAD dependent oxidoreductase [Candidatus Koribacter versatilis Ellin345]	gi|94967143|ref|YP 589191.1|	35.63	2E-63
contig00108-orf00107	DNA polymerase III chi subunit, HolC [Acidovorax sp. JS42]	gi|110593893|ref|ZP 01382242.1|	30.82	1E-10
contig00108-orf00109	Mip [Tatlockia micdadei]	gi|7249222|gb|AAB19821.2|	47.37	3E-49

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contig00108-orf00111	sec-23 interacting protein P125 [Aedes aegypti]	gi|108873924|gb|EAT38149.1|	38.64	9.3
contig00108-orf00114	phosphoribosylglycinamide formyltransferase [Acidovorax sp. JS42]	gi|110595873|ref|ZP 01384197.1|	61.86	9E-60
contig00108-orf00115	hypothetical protein mh2546 [Mannheimia haemolytica]	gi|110735247|gb|ABG89194.1|	34.29	7E-16
contig00108-orf00117	nuclease [Nitrosomonas eutropha C91]	gi|114331479|ref|YP 747701.1|	43.75	1E-14
contig00108-orf00118	ribose 5-phosphate isomerase [Alcanivorax borkumensis SK2]	gi|110835467|ref|YP 694326.1|	52.13	9E-58
contig00108-orf00121	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Burkholderia cenocepacia AU 1054]	gi|107028879|ref|YP 625974.1|	72.78	1E-53
contig00108-orf00122	Dihydroxy-acid dehydratase [Psychrobacter sp. PRwf-1]	gi|91770419|ref|ZP 01272245.1|	77.49	0
contig00108-orf00124	Iron-sulfur cluster-binding protein [Ralstonia eutropha H16]	gi|116694051|ref|YP 728262.1|	62.76	2E-170
contig00108-orf00126	hypothetical protein H16 B0092 [Ralstonia eutropha H16]	gi|116694052|ref|YP 728263.1|	38.64	9E-35
contig00108-orf00128	Protein of unknown function DUF224, cysteine-rich region [Psychromonas ingrahamii 37]	gi|106881407|ref|ZP 01348812.1|	54.03	4E-74
contig00108-orf00129	Drug resistance transporter EmrB/QacA subfamily [Psychrobacter sp. PRwf-1]	gi|91769290|ref|ZP 01271124.1|	51.99	9E-107
contig00109-orf00002	putative integrase [Shigella flexneri 5 str. 8401]	gi|110804320|ref|YP 687840.1|	42.9	2E-71
contig00113-orf00001	hypothetical protein PsycPRwfDRAFT 0357 [Psychrobacter sp. PRwf-1]	gi|91771097|ref|ZP 01272913.1|	36.25	6E-33
contig00113-orf00002	Protein of unknown function DUF560 [Psychrobacter sp. PRwf-1]	gi|91771098|ref|ZP 01272914.1|	36.36	4E-86
contig00113-orf00004	Organic Anion Transporter family member (oat-1) [Caenorhabditis elegans]	gi|25145172|ref|NP 501442.2|	36.17	4.1
contig00113-orf00006	putative transmembrane component of ABC transporter [Rhizobium leguminosarum bv. viciae 3841]	gi|116250821|ref|YP 766659.1|	57.79	2E-78
contig00113-orf00008	putative ATP-binding component of ABC transporter [Rhizobium leguminosarum bv. viciae 3841]	gi|116250820|ref|YP 766658.1|	48.72	1E-54
contig00113-orf00011	class 2 porin protein [Neisseria meningitidis]	gi|3033451|gb|AAC14689.1|	31.15	5E-28
contig00113-orf00012	extracellular solute-binding protein, family 5 [Psychrobacter sp. PRwf-1]	gi|91769518|ref|ZP 01271351.1|	48.03	5E-135
contig00113-orf00015	putative Xaa-Pro aminopeptidase [Burkholderia xenovorans LB400]	gi|91785339|ref|YP 560545.1|	55.17	0
contig00113-orf00017	SRRM2 protein [Homo sapiens]	gi|47124032|gb|AAH70050.1|	26.61	0.026
contig00113-orf00019	Binding-protein-dependent transport systems inner membrane component [Psychrobacter sp. PRwf-1]	gi|91769521|ref|ZP 01271354.1|	73.53	3E-132
contig00113-orf00022	OppC [Xenorhabdus nematophila]	gi|38146747|gb|AAR11775.1|	70.53	3E-116
contig00113-orf00024	putative ABC transporter, ATP-binding protein [Photobacterium profundum 3TCK]	gi|90413921|ref|ZP 01221906.1|	58.3	2E-175
contig00113-orf00026	orf7 [Saccharomyces cerevisiae]	gi|886951|emb|CAA88282.1|	36.54	3.2
contig00113-orf00027	hypothetical protein Ccur5 01001887 [Campylobacter curvus 525.92]	gi|109673218|ref|ZP 01375419.1|	26.09	0.0004
contig00113-orf00028	PvLEA1 protein [Polypedilum vanderplanki]	gi|90959527|dbj|BAE92616.1|	37.14	0.0005
contig00113-orf00028	PvLEA1 protein [Polypedilum vanderplanki]	gi|90959527|dbj|BAE92616.1|	22.86	7
contig00113-orf00028	PvLEA1 protein [Polypedilum vanderplanki]	gi|90959527|dbj|BAE92616.1|	26.47	9.1
contig00113-orf00029	Succinyl-CoA ligase, alpha subunit [Psychrobacter sp. PRwf-1]	gi|91770002|ref|ZP 01271832.1|	83.74	2E-110
contig00113-orf00032	Succinyl-CoA synthetase, beta subunit [Psychrobacter sp. PRwf-1]	gi|91770003|ref|ZP 01271833.1|	82.73	1E-163

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contig00113-orf00034	transcription factor SOX-9 [Bufo bufo]	gi|110835872|emb|CAH10150.1|	23.6	1.9
contig00113-orf00036	Dihydrolipoamide dehydrogenase [Acidovorax sp. JS42]	gi|110594177|ref|ZP 01382524.1|	65.4	2E-170
contig00113-orf00042	unnamed protein product [Macaca fascicularis]	gi|67969966|dbj|BAE01330.1|	34.48	1.4
contig00113-orf00044	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116270381|ref|ZP 01494619.1|	68.11	3E-119
contig00113-orf00049	2-oxoglutarate dehydrogenase E1 component [Bordetella avium 197N]	gi|115422287|emb|CAJ48811.1|	55.46	0
contig00113-orf00050	citrate synthase [Methylobacillus flagellatus KT]	gi|91774417|ref|YP 544173.1|	68.92	2E-176
contig00113-orf00051	TPR repeat-containing protein [Hyphomonas neptunium ATCC 15444]	gi|114797711|ref|YP 760686.1|	34.21	0.000001
contig00113-orf00052	succinate dehydrogenase and fumarate reductase iron-sulfur protein [Acidovorax sp. JS42]	gi|110593325|ref|ZP 01381678.1|	76.82	1E-105
contig00113-orf00053	succinate dehydrogenase flavoprotein subunit [Burkholderia pseudomallei K96243]	gi|53722739|ref|YP 111724.1|	67.81	0
contig00113-orf00054	succinate dehydrogenase, cytochrome b subunit [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269213|ref|ZP 01493458.1|	45.05	2E-28
contig00113-orf00055	succinate dehydrogenase, cytochrome b subunit [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269212|ref|ZP 01493457.1|	45.45	1E-11
contig00113-orf00057	SodC [Haemophilus influenzae]	gi|33335434|gb|AAQ12654.1|	84.18	3E-78
contig00113-orf00058	protein of unknown function DUF1232 [Shewanella baltica OS195]	gi|113947605|ref|ZP 01433270.1|	37.36	1E-14
contig00113-orf00060	PREDICTED: similar to kismet CG3696-PA, isoform A [Apis mellifera]	gi|110761792|ref|XP 001122253.1|	24.59	0.71
contig00113-orf00062	cysteine synthase [Frankia sp. CcI3]	gi|86741123|ref|YP 481523.1|	66.34	3E-99
contig00113-orf00064	cytochrome b [Globodera pallida]	gi|61387259|gb|AAX45301.1|	29.36	0.0004
contig00113-orf00066	diaminopimelate epimerase [Thiobacillus denitrificans ATCC 25259]	gi|74318544|ref|YP 316284.1|	54.84	4E-71
contig00113-orf00067	TetR family transcriptional regulator [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619886|ref|YP 858655.1|	39.09	3E-29
contig00113-orf00068	hypothetical protein Bpse17 02004709 [Burkholderia pseudomallei 1710a]	gi|90290600|ref|ZP 01210251.1|	49.54	1E-80
contig00113-orf00070	prophage CP-933H unknown protein [Escherichia coli UTI89]	gi|91211960|ref|YP 541946.1|	27.14	0.000002
contig00113-orf00073	MATE efflux family protein [Psychromonas ingrahamii 37]	gi|106882599|ref|ZP 01350001.1|	35.24	2E-75
contig00113-orf00075	#N/A	gi|110590448|pdb|2GW8|A	89.29	8E-52
contig00113-orf00079	phosphoribosylformylglycinamidine synthase [Shigella flexneri 5 str. 8401]	gi|110806487|ref|YP 690007.1|	56.37	0
contig00113-orf00081	unknown [Aeromonas hydrophila]	gi|44151578|gb|AAS46713.1|	33.73	7E-29
contig00113-orf00083	dihydroorotase [Ralstonia eutropha H16]	gi|113866508|ref|YP 724997.1|	63.27	1E-120
contig00113-orf00085	hypothetical protein RHA1 ro11252 [Rhodococcus jostii RHA1]	gi|111027079|ref|YP 709057.1|	24.64	0.058
contig00113-orf00086	redox protein, regulator of disulfide-bond formation [Ralstonia eutropha H16]	gi|113868718|ref|YP 727207.1|	55	2E-10
contig00113-orf00087	cation/multidrug efflux system outer membrane porin [Ralstonia eutropha H16]	gi|113867762|ref|YP 726251.1|	41.3	4.1
contig00113-orf00088	AT5g64600/MUB3 12 [Arabidopsis thaliana]	gi|18700109|gb|AAL77666.1|	31.07	0.13
contig00113-orf00089	TatD-related deoxyribonuclease [Thiobacillus denitrificans ATCC 25259]	gi|74317558|ref|YP 315298.1|	54.62	2E-74
contig00113-orf00090	type IV fimbriae assembly protein [Alcanivorax borkumensis SK2]	gi|110833937|ref|YP 692796.1|	40.74	2E-17

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contig00113-orf00092	DNA polymerase III subunit delta' [Ralstonia eutropha H16]	gi|113867581|ref|YP 726070.1|	37.31	6E-53
contig00113-orf00093	hypothetical protein [uncultured bacterium]	gi|63021945|gb|AAY26549.1|	50	3.1
contig00113-orf00095	PREDICTED: hypothetical protein [Rattus norvegicus]	gi|109500375|ref|XP 001071381.1|	37.1	0.006
contig00113-orf00095	PREDICTED: hypothetical protein [Rattus norvegicus]	gi|109500375|ref|XP 001071381.1|	34.43	0.31
contig00113-orf00095	PREDICTED: hypothetical protein [Rattus norvegicus]	gi|109500375|ref|XP 001071381.1|	32.39	0.41
contig00113-orf00095	PREDICTED: hypothetical protein [Rattus norvegicus]	gi|109500375|ref|XP 001071381.1|	38.1	0.69
contig00113-orf00095	PREDICTED: hypothetical protein [Rattus norvegicus]	gi|109500375|ref|XP 001071381.1|	31.82	1.5
contig00113-orf00098	PDZ domain-containing protein [Myxococcus xanthus DK 1622]	gi|108763062|ref|YP 634842.1|	46.67	9.3
contig00113-orf00100	putative deoxyribonucleotide triphosphate pyrophosphatase [Thiobacillus denitrificans ATCC 25259]	gi|74316496|ref|YP 314236.1|	61.34	2E-65
contig00113-orf00103	coproporphyrinogen III oxidase [Thiobacillus denitrificans ATCC 25259]	gi|74316497|ref|YP 314237.1|	58.42	4E-121
contig00113-orf00104	Opa protein [Neisseria lactamica]	gi|8347007|emb|CAB93954.1|	33.75	3E-28
contig00113-orf00105	endoribonuclease L-PSP [Pseudomonas entomophila L48]	gi|104784344|ref|YP 610842.1|	64.57	3E-41
contig00113-orf00107	diadenosine tetraphosphatase [Thiobacillus denitrificans ATCC 25259]	gi|74316186|ref|YP 313926.1|	45.25	1E-61
contig00113-orf00108	transaldolase [Thiobacillus denitrificans ATCC 25259]	gi|74316683|ref|YP 314423.1|	50.84	3E-81
contig00113-orf00112	capsule expression protein KpsF/GutQ [Thiobacillus denitrificans ATCC 25259]	gi|74316556|ref|YP 314296.1|	57.96	6E-90
contig00113-orf00115	putative tRNA and rRNA cytosine-C5-methylase [Thiobacillus denitrificans ATCC 25259]	gi|74318616|ref|YP 316356.1|	53.94	3E-113
contig00113-orf00124	putative transcriptional regulator [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116268555|ref|ZP 01492801.1|	53.47	5E-38
contig00113-orf00128	hypothetical protein LGAS 0990 [Lactobacillus gasseri ATCC 33323]	gi|116629634|ref|YP 814806.1|	29.86	6E-16
contig00113-orf00130	Hemerythrin HHE cation binding region [Acidovorax sp. JS42]	gi|110594512|ref|ZP 01382856.1|	37.04	6E-19
contig00113-orf00133	#N/A	gi|15811622|gb|AAL09030.1|AF416 565 1	58.4	2E-38
contig00113-orf00134	hypothetical protein ATEG 01265 [Aspergillus terreus NIH2624]	gi|115384166|ref|XP 001208630.1|	31.53	0.003
contig00113-orf00138	protein translocase subunit secA [Methylobacillus flagellatus KT]	gi|91776586|ref|YP 546342.1|	64.56	0
contig00113-orf00141	#N/A	gi|109894963|sp|Q5F7G0|SYQ NEIG1	95.55	0
contig00113-orf00143	predicted protein [Aspergillus terreus NIH2624]	gi|115384006|ref|XP 001208550.1|	65	4.2
contig00113-orf00144	glycerol-3-phosphate regulon repressor [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117620109|ref|YP 856187.1|	47.35	5E-58
contig00113-orf00146	hypothetical protein UTI89 C1960 [Escherichia coli UTI89]	gi|91210981|ref|YP 540967.1|	38.46	4E-23
contig00113-orf00148	3-phosphoserine aminotransferase [Neisseria gonorrhoeae]	gi|36939176|gb|AAQ86953.1|	87.77	0
contig00113-orf00149	#N/A	gi|91208368|sp|Q3SKW9|Y699 THIDA	51.8	7E-37
contig00113-orf00153	NusA antitermination factor [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116268552|ref|ZP 01492798.1|	57.89	2E-154
contig00113-orf00155	translation initiation factor IF-2 [Thiobacillus denitrificans ATCC 25259]	gi|74316715|ref|YP 314455.1|	75.84	0
contig00113-orf00155	translation initiation factor IF-2 [Thiobacillus denitrificans ATCC 25259]	gi|74316715|ref|YP 314455.1|	43.18	0.000007

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contig00113-orf00157	putative SCO1/SenC family protein, [Thiobacillus denitrificans ATCC 25259]	gi|74316355|ref|YP 314095.1|	45	1E-39
contig00113-orf00159	ATP phosphoribosyltransferase catalytic subunit [Thiobacillus denitrificans ATCC 25259]	gi|74317908|ref|YP 315648.1|	74.3	2E-88
contig00113-orf00160	hypothetical protein [Staphylococcus aureus]	gi|28465878|dbj|BAB46990.2|	43.37	2E-44
contig00113-orf00162	histidinol dehydrogenase [Methylobacillus flagellatus KT]	gi|91774604|ref|YP 544360.1|	69	3E-167
contig00113-orf00163	sulphate transport system permease protein 1 [Verminephrobacter eiseniae EF01-2]	gi|111614008|ref|ZP 01401086.1|	63.96	1E-90
contig00113-orf00166	Sulphate transport system permease protein 2:Sulfate ABC transporter, permease protein CysW [Psychrobacter sp. PRwf-1]	gi|91769280|ref|ZP 01271114.1|	77.5	1E-90
contig00113-orf00169	Secreted protein [Salinispora tropica CNB-440]	gi|113944472|ref|ZP 01430171.1|	37.5	1.4
contig00113-orf00170	Sulphate transport system permease protein 2:Sulfate ABC transporter, permease protein CysT [Psychrobacter sp. PRwf-1]	gi|91769279|ref|ZP 01271113.1|	76.28	2E-106
contig00113-orf00171	conserved hypothetical protein [Acidovorax sp. JS42]	gi|110592439|ref|ZP 01380795.1|	46.53	1E-23
contig00113-orf00172	hypothetical protein AjsDRAFT 2974 [Acidovorax sp. JS42]	gi|110593029|ref|ZP 01381383.1|	34.67	0.003
contig00113-orf00174	oxygen-insensitive NAD(P)H nitroreductase [Vibrio alginolyticus 12G01]	gi|91223156|ref|ZP 01258422.1|	52.07	7E-60
contig00113-orf00176	membrane protein [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269693|ref|ZP 01493936.1|	50	0.00003
contig00113-orf00179	hypothetical protein Bxe A0678 [Burkholderia xenovorans LB400]	gi|91785102|ref|YP 560308.1|	21.29	3E-14
contig00113-orf00182	exodeoxyribonuclease V, gamma subunit [Geobacter sp. FRC-32]	gi|110601583|ref|ZP 01389763.1|	33.91	2E-150
contig00113-orf00184	TonB-dependent outer membrane receptor [Haemophilus somnus 129PT]	gi|113460327|ref|YP 718388.1|	37.11	7E-78
contig00113-orf00185	TonB-dependent outer membrane receptor [Haemophilus somnus 129PT]	gi|113460327|ref|YP 718388.1|	38.42	6E-70
contig00113-orf00186	hypothetical protein VAS14 02266 [Vibrio angustum S14]	gi|90579749|ref|ZP 01235558.1|	66	6E-13
contig00115-orf00001	#N/A	gi|438191|emb|CAA81045.1|	77.14	9E-94
contig00115-orf00002	TonB-dependent copper receptor [Acidovorax sp. JS42]	gi|110593750|ref|ZP 01382100.1|	37.5	2E-125
contig00115-orf00004	PREDICTED: hypothetical protein isoform 1 [Strongylocentrotus purpuratus]	gi|115908485|ref|XP 780235.2|	56	9.1
contig00115-orf00006	phosphoserine phosphatase [Mariprofundus ferrooxydans PV-1]	gi|114777172|ref|ZP 01452183.1|	54.31	2E-52
contig00115-orf00008	putative phosphoesterase [Bordetella avium 197N]	gi|115422632|emb|CAJ49157.1|	52.03	1E-66
contig00115-orf00011	PREDICTED: similar to CG5946-PB, isoform B [Rattus norvegicus]	gi|109476948|ref|XP 001065840.1|	40.54	0.37
contig00115-orf00013	hypothetical protein AHA 2423 [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618132|ref|YP 856938.1|	46.58	3E-12
contig00115-orf00015	ferripyoverdine receptor [Campylobacter curvus 525.92]	gi|112802561|gb|EAT99905.1|	34.67	8E-113
contig00115-orf00017	unknown protein [Arabidopsis thaliana]	gi|22655198|gb|AAM98189.1|	33.8	0.0003
contig00115-orf00019	hypothetical protein Ccur5 01001446 [Campylobacter curvus 525.92]	gi|109673639|ref|ZP 01375815.1|	40.75	1E-120
contig00115-orf00022	hypothetical protein [Toxoplasma gondii RH]	gi|95007087|emb|CAJ20306.1|	32.56	4.2
contig00115-orf00024	PdhR protein [Salmonella typhimurium]	gi|7688351|emb|CAB89840.1|	36.63	1E-30
contig00115-orf00027	lactate permease [Alcaligenes faecalis]	gi|33469574|gb|AAQ19815.1|	66.79	0
contig00115-orf00033	#N/A	gi|109158066|pdb|2GTQ|A	95.15	0

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contig00116-orf00001	similar to site-specific DNA-methyltransferase (cytosine-specific) [Candidatus Kuenenia stuttgartiensis]	gi|91201234|emb|CAJ74294.1|	65.03	2E-103
contig00116-orf00002	unknown protein [Candidatus Kuenenia stuttgartiensis]	gi|91201233|emb|CAJ74293.1|	54.05	0.015
contig00116-orf00003	unknown protein [Candidatus Kuenenia stuttgartiensis]	gi|91201233|emb|CAJ74293.1|	61.82	1E-94
contig00116-orf00005	alanyl-tRNA synthetase [Ralstonia eutropha H16]	gi|113868727|ref|YP 727216.1|	63.14	0
contig00116-orf00006	putrescine ABC transporter, periplasmic putrescine-binding protein [Pseudomonas entomophila L48]	gi|104784200|ref|YP 610698.1|	49.56	4E-94
contig00116-orf00008	phospholipase D precursor [Neisseria gonorrhoeae]	gi|34597315|gb|AAQ77232.1|	73.23	0
contig00116-orf00010	adenosine deaminase [Pseudomonas entomophila L48]	gi|104779927|ref|YP 606425.1|	63.31	5E-111
contig00116-orf00012	#N/A	gi|13540391|gb|AAK29449.1|AF352 246 1	29.93	0.015
contig00116-orf00013	tryptophanyl-tRNA synthetase [marine gamma proteobacterium HTCC2207]	gi|90416453|ref|ZP 01224384.1|	65.67	6E-123
contig00116-orf00016	ClpB protein [Thiobacillus denitrificans ATCC 25259]	gi|74316833|ref|YP 314573.1|	71.38	0
contig00116-orf00018	hypothetical protein y1457 [Yersinia pestis KIM]	gi|22125354|ref|NP 668777.1|	50	7E-80
contig00116-orf00021	Metallophosphoesterase [Clostridium sp. OhILAs]	gi|106894146|ref|ZP 01361268.1|	38.98	6E-46
contig00116-orf00024	divalent cation transporter [Saccharophagus degradans 2-40]	gi|90022792|ref|YP 528619.1|	21.79	5E-09
contig00116-orf00027	prolipoprotein diacylglyceryl transferase [Ralstonia eutropha H16]	gi|113868940|ref|YP 727429.1|	59.86	7E-83
contig00116-orf00029	hypothetical protein V12G01 02995 [Vibrio alginolyticus 12G01]	gi|91224216|ref|ZP 01259479.1|	54.28	2E-125
contig00116-orf00032	hypothetical protein PaerP 01000591 [Pseudomonas aeruginosa PA7]	gi|94417808|ref|ZP 01297625.1|	62.15	8E-83
contig00116-orf00033	exopolyphosphatase [Bordetella avium 197N]	gi|115422024|emb|CAJ48546.1|	47.58	3E-112
contig00116-orf00035	hypothetical protein Tbd 2113 [Thiobacillus denitrificans ATCC 25259]	gi|74318131|ref|YP 315871.1|	51.16	1E-46
contig00116-orf00036	major facilitator family transporter [Mariprofundus ferrooxydans PV-1]	gi|114777019|ref|ZP 01452039.1|	42.95	4E-92
contig00116-orf00037	single-strand binding protein [alpha proteobacterium HTCC2255]	gi|114771958|ref|ZP 01449347.1|	59.35	2E-37
contig00116-orf00038	hypothetical protein V12G01 14559 [Vibrio alginolyticus 12G01]	gi|91225638|ref|ZP 01260712.1|	48.87	4E-79
contig00116-orf00039	hypothetical protein V12G01 14554 [Vibrio alginolyticus 12G01]	gi|91225637|ref|ZP 01260711.1|	49.84	3E-78
contig00116-orf00041	hypothetical protein V12G01 14549 [Vibrio alginolyticus 12G01]	gi|91225636|ref|ZP 01260710.1|	51.86	0
contig00116-orf00043	filamentous hemagglutinin / adhesin [Ralstonia eutropha H16]	gi|116694202|ref|YP 728413.1|	32.58	1E-34
contig00116-orf00045	hemagglutinin-like secreted protein [Yersinia pestis KIM]	gi|22125591|ref|NP 669014.1|	27.31	2E-139
contig00116-orf00045	hemagglutinin-like secreted protein [Yersinia pestis KIM]	gi|22125591|ref|NP 669014.1|	25.73	1E-11
contig00116-orf00045	hemagglutinin-like secreted protein [Yersinia pestis KIM]	gi|22125591|ref|NP 669014.1|	23.94	0.0000006
contig00116-orf00045	hemagglutinin-like secreted protein [Yersinia pestis KIM]	gi|22125591|ref|NP 669014.1|	22.32	0.6
contig00116-orf00046	FhaC protein [Neisseria meningitidis]	gi|6900485|emb|CAB72073.1|	50.85	6E-141
contig00116-orf00049	conserved hypothetical protein [Acidovorax sp. JS42]	gi|110592518|ref|ZP 01380874.1|	62.5	0.0006
contig00116-orf00052	putative detoxifying sulphurtransferase [Bordetella avium 197N]	gi|115423738|emb|CAJ50288.1|	48.52	7E-23
contig00116-orf00054	unnamed protein product [Neisseria meningitidis]	gi|6900477|emb|CAB72065.1|	93.1	9E-43
contig00117-orf00003	RNAse R [Thiobacillus denitrificans ATCC 25259]	gi|74316626|ref|YP 314366.1|	56.64	0

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contig00117-orf00005	molybdenum cofactor guanylyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74316060|ref|YP 313800.1|	38.15	2E-20
contig00117-orf00006	transmembrane nitrate/nitrite sensor kinase [Ralstonia eutropha H16]	gi|38637926|ref|NP 942900.1|	33.92	4E-90
contig00117-orf00007	response regulator [Ralstonia eutropha H16]	gi|116696270|ref|YP 841846.1|	56.34	1E-57
contig00117-orf00009	Thiol:disulfide interchange protein [Ralstonia eutropha H16]	gi|113869402|ref|YP 727891.1|	40.43	4E-91
contig00117-orf00012	uracil-DNA glycosylase [Haemophilus somnus 129PT]	gi|113460626|ref|YP 718692.1|	67.12	4E-88
contig00117-orf00013	hypothetical protein CdifQ 02003478 [Clostridium difficile QCD-32g58]	gi|90573179|ref|ZP 01229697.1|	52.15	3E-46
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	53.68	6E-32
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	64.71	6E-32
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	50	4E-25
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	68.75	4E-25
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	47.52	7E-21
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	58.82	7E-21
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	39.72	2E-13
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	53.33	2E-13
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	31.93	2E-11
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	62.5	2E-11
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	36.98	3E-11
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	50	3E-11
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	36.9	1E-10
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	32.16	7E-10
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	36.36	4E-09

Query	NR Database Subject	Subject ID	% ID	E value
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	30.64	5E-09
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	58.82	5E-09
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	33.52	8E-09
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	28.72	0.0000001
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	34.25	0.000001
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	35.92	0.000004
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	29.55	0.0002
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	24.61	0.006
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	39.47	0.024
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	64.71	0.024
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	24.68	0.12
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	41.3	1.8
contig00117-orf00014	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	64.29	1.8
contig00117-orf00015	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	50	0.00002
contig00117-orf00015	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	43.75	0.012
contig00117-orf00017	HI0185-like protein [Haemophilus influenzae]	gi|89892358|gb|ABD78953.1|	96.03	2E-139
contig00117-orf00018	HI0184-like protein [Haemophilus influenzae]	gi|89892360|gb|ABD78955.1|	95.64	3E-155
contig00117-orf00020	Peptidylprolyl isomerase [Desulfovibrio vulgaris subsp. vulgaris DP4]	gi|114845720|ref|ZP 01456090.1|	66.27	5E-50
contig00117-orf00022	Sodium/sulphate symporter [Psychrobacter sp. PRwf-1]	gi|91770602|ref|ZP 01272426.1|	58.44	2E-121
contig00117-orf00022	Sodium/sulphate symporter [Psychrobacter sp. PRwf-1]	gi|91770602|ref|ZP 01272426.1|	29.46	0.51
contig00117-orf00023	3-dehydroquinate dehydratase [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116871882|ref|YP 848663.1|	43.95	1E-49
contig00117-orf00025	hypothetical protein Tbd 0582 [Thiobacillus denitrificans ATCC 25259]	gi|74316600|ref|YP 314340.1|	35.01	3E-52

Query	NR Database Subject	Subject ID	% ID	E value
contig00117-orf00027	permease YjgP/YjgQ [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269083|ref|ZP 01493328.1|	36.26	4E-58
contig00117-orf00028	hypothetical protein PaerP 01002444 [Pseudomonas aeruginosa PA7]	gi|94415874|ref|ZP 01295709.1|	60.17	2E-103
contig00117-orf00030	hypothetical protein MkmsDRAFT 2739 [Mycobacterium sp. KMS]	gi|92914936|ref|ZP 01283561.1|	33.62	4E-09
contig00117-orf00031	hypothetical protein CdifQ 02002459 [Clostridium difficile QCD-32g58]	gi|90574147|ref|ZP 01230651.1|	34.78	3E-10
contig00117-orf00033	PREDICTED: similar to CG7331-PA [Tribolium castaneum]	gi|91094047|ref|XP 968716.1|	35.42	3.2
contig00117-orf00035	iron-regulated outer membrane protein [Mannheimia haemolytica]	gi|13591379|gb|AAK29743.1|	46.21	0
contig00117-orf00037	Alpha amylase, catalytic region [Psychromonas ingrahamii 37]	gi|106882268|ref|ZP 01349671.1|	50.08	5E-161
contig00118-orf00001	PREDICTED: similar to CG10542-PA [Tribolium castaneum]	gi|91090141|ref|XP 971710.1|	34.78	1.1
contig00119-orf00002	hypothetical protein Gmet A3576 [Geobacter metallireducens GS-15]	gi|78214265|ref|YP 380336.1|	29.03	0.034
contig00119-orf00004	hypothetical protein APECO1 1114 [Escherichia coli APEC O1]	gi|117624220|ref|YP 853133.1|	47.62	2E-17
contig00119-orf00005	hypothetical protein [Staphylococcus warneri]	gi|60360889|dbj|BAD90564.1|	52.38	0.00003
contig00119-orf00007	histone deacetylation-related protein [Cryptococcus neoformans var. neoformans JEC21]	gi|58265880|ref|XP 570096.1|	29.17	0.087
contig00119-orf00010	PilT protein-like [Salinispora tropica CNB-440]	gi|113946962|ref|ZP 01432639.1|	42.7	1E-14
contig00119-orf00011	antitoxin of toxin-antitoxin stability system [Synechococcus sp. RS9916]	gi|116073595|ref|ZP 01470857.1|	60.98	0.0000002
contig00119-orf00013	hypothetical protein SNOG 08200 [Phaeosphaeria nodorum SN15]	gi|111063356|gb|EAT84476.1|	42.11	9.1
contig00119-orf00016	hypothetical protein CburR 01001813 [Coxiella burnetii RSA 331]	gi|95926370|ref|ZP 01309162.1|	54.55	4E-24
contig00120-orf00001	FHA-like protein [Moraxella bovis Epp63]	gi|57157522|dbj|BAD83735.1|	44.68	5E-10
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	24.9	2E-39
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	24.25	3E-33
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	28.21	3E-28
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	27.61	1E-24
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	33.7	8E-22
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	27.7	9E-20
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	26.85	6E-19
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	23.39	8E-19
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	25.32	9E-18
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	31.56	4E-17
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	28.91	2E-16
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	40.67	3E-16
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	27.75	3E-14
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	24.93	4E-12
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	24.66	2E-11
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	29.64	2E-11
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	21.65	2E-08
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	38.75	5E-08
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	30.04	6E-08

Query	NR Database Subject	Subject ID	% ID	E value
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	22.99	0.0000001
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	34.09	0.0000002
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	36.27	0.000002
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	28.73	0.00002
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	37.8	0.002
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	35	0.008
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	42.11	0.023
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	26.44	0.023
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	32.53	0.039
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	48.84	0.087
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	30.26	0.15
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	27.54	0.19
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	33.98	0.33
contig00122-orf00004	VCBS [Geobacter sp. FRC-32]	gi|110601426|ref|ZP 01389613.1|	31.76	4.8
contig00122-orf00005	unnamed protein product [Pelotomaculum thermopropionicum SI]	gi|98661725|dbj|GAA01312.1|	34.21	0.000003
contig00122-orf00008	unnamed protein product [Pelotomaculum thermopropionicum SI]	gi|98661726|dbj|GAA01313.1|	28.06	2E-39
contig00122-orf00009	NADH dehydrogenase subunit 2 [Monoblepharella sp. JEL15]	gi|29126604|ref|NP 803507.1|	40.54	1.8
contig00122-orf00010	#N/A	gi|6644330|gb|AAF21013.1|AF2082 62 1	36.96	2.4
contig00122-orf00011	Pirin-related protein [Ralstonia eutropha H16]	gi|113867305|ref|YP 725794.1|	57.79	4E-92
contig00122-orf00012	predicted transcription regulator [uncultured methanogenic archaeon RC-I]	gi|110621023|emb|CAJ36301.1|	54.24	5E-14
contig00122-orf00013	hypothetical protein F39G3.2 [Caenorhabditis elegans]	gi|71993463|ref|NP 504273.2|	34.15	3.3
contig00123-orf00001	methionyl-tRNA synthetase [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116269107|ref|ZP 01493352.1|	62.96	0
contig00123-orf00003	PREDICTED: similar to Topoisomerase (DNA) II beta binding protein [Strongylocentrotus purpuratus]	gi|115935447|ref|XP 001188843.1|	39.47	9.3
contig00123-orf00004	oligopeptide transporter [Ralstonia eutropha H16]	gi|113869213|ref|YP 727702.1|	57.7	5E-175
contig00124-orf00001	F0F1 ATP synthase subunit epsilon [Thiobacillus denitrificans ATCC 25259]	gi|74318814|ref|YP 316554.1|	52.5	0.00006
contig00124-orf00002	F0F1 ATP synthase subunit beta [Ralstonia eutropha H16]	gi|113869573|ref|YP 728062.1|	83.05	0
contig00124-orf00004	Sodium-transporting two-sector ATPase [Verminephrobacter eiseniae EF01-2]	gi|111614626|ref|ZP 01401700.1|	52.34	8E-59
contig00124-orf00006	F0F1 ATP synthase subunit alpha [Thiobacillus denitrificans ATCC 25259]	gi|74318817|ref|YP 316557.1|	78.17	0
contig00124-orf00007	ATP synthase F1, delta subunit [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111616369|ref|ZP 01403401.1|	41.01	2E-28
contig00124-orf00008	F0F1 ATP synthase subunit B [Burkholderia xenovorans LB400]	gi|91785737|ref|YP 560943.1|	60.9	2E-39
contig00124-orf00009	ATP synthase F0, C subunit [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111616371|ref|ZP 01403403.1|	80.39	2E-16
contig00124-orf00010	ATP synthase F0, A subunit [Acidovorax sp. JS42]	gi|110596034|ref|ZP 01384355.1|	62.41	4E-96
contig00124-orf00013	chromosome segregation DNA-binding protein [Thiobacillus denitrificans ATCC 25259]	gi|74318823|ref|YP 316563.1|	51.39	2E-68
contig00124-orf00014	hypothetical protein PCNPT3 11823 [Psychromonas sp. CNPT3]	gi|90407911|ref|ZP 01216086.1|	30.67	2.8

Query	NR Database Subject	Subject ID	% ID	E value
contig00124-orf00015	Phosphate transporter [Psychrobacter sp. PRwf-1]	gi|91770272|ref|ZP 01272100.1|	61.54	5E-164
contig00124-orf00016	#N/A	gi|115311263|sp|Q5F6H5|ANMK NEIG1	70.6	4E-147
contig00124-orf00017	cytochrome c oxidase cbb3-type, subunit III [Thiobacillus denitrificans ATCC 25259]	gi|74316658|ref|YP 314398.1|	50	7E-77
contig00124-orf00018	cytochrome c oxidase, subunit CcoQ [alpha proteobacterium HTCC2255]	gi|114772376|ref|ZP 01449751.1|	45.1	0.00004
contig00124-orf00019	Cbb3-type cytochrome oxidase subunit 2 [Rubrivivax gelatinosus]	gi|58198976|gb|AAW66133.1|	72.87	1E-79
contig00124-orf00021	cytochrome c oxidase, cbb3-type, subunit I [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619187|ref|ZP 01406201.1|	77.97	0
contig00124-orf00023	hypothetical protein ABO 1522 [Alcanivorax borkumensis SK2]	gi|110834383|ref|YP 693242.1|	42.12	9E-123
contig00124-orf00024	#N/A	gi|90109268|pdb|2F46|A	52.26	8E-32
contig00124-orf00025	putative carbon-nitrogen hydrolase protein [Burkholderia xenovorans LB400]	gi|91781874|ref|YP 557080.1|	45.21	1E-67
contig00124-orf00027	1-deoxy-D-xylulose-5-phosphate synthase [Thiobacillus denitrificans ATCC 25259]	gi|74316897|ref|YP 314637.1|	61.45	0
contig00124-orf00029	prephenate dehydrogenase [Thiobacillus denitrificans ATCC 25259]	gi|74316971|ref|YP 314711.1|	40.67	1E-50
contig00124-orf00030	Aldehyde dehydrogenase [delta proteobacterium MLMS-1]	gi|94264609|ref|ZP 01288393.1|	45.95	1.4
contig00124-orf00031	WaaQ [Klebsiella pneumoniae]	gi|60459539|gb|AAX20103.1|	44.19	3E-76
contig00124-orf00032	PREDICTED: similar to Proprotein convertase subtilisin/kexin type 5 precursor (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6) (Subtilisin-like proprotein convertase 6) (SPC6) [Rattus norvegicus]	gi|109463670|ref|XP 001078022.1|	29.58	1.8
contig00124-orf00033	#N/A	gi|97274826|sp|Q5FA76|RUVC NEIG1	87.01	2E-62
contig00124-orf00034	#N/A	gi|18496624|gb|AAL74160.1|AF428 103 1	75.78	8E-131
contig00124-orf00036	IS30 family transposase [Lactobacillus brevis ATCC 367]	gi|116334292|ref|YP 795819.1|	55.77	2E-11
contig00125-orf00001	hypothetical protein T01B7.8 [Caenorhabditis elegans]	gi|17535877|ref|NP 495859.1|	32.05	0.84
contig00125-orf00002	hypothetical protein pMU1 p1 [Eikenella corrodens]	gi|66968611|ref|YP 245388.1|	36.84	2E-12
contig00125-orf00003	ATP-dependent nuclease subunit B [Granulibacter bethesdensis CGDNIH1]	gi|114328673|ref|YP 745830.1|	62.5	6.9
contig00126-orf00001	Ribonucleoside triphosphate reductase, alpha chain [Enterobacteria phage Felix 01]	gi|38707873|ref|NP 944991.1|	32.61	4.1
contig00127-orf00002	hypothetical protein PsycPRwfDRAFT 2304 [Psychrobacter sp. PRwf-1]	gi|91769455|ref|ZP 01271289.1|	26.98	7.1
contig00128-orf00001	IS30 family transposase [Lactobacillus brevis ATCC 367]	gi|116334292|ref|YP 795819.1|	55.77	4E-11
contig00131-orf00001	excinuclease ABC, C subunit [Nitrosomonas eutropha C91]	gi|114331403|ref|YP 747625.1|	55.72	0
contig00131-orf00002	NADP-dependent l-serine/l-allo-threonine dehydrogenase ydfg [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117617619|ref|YP 855033.1|	63.97	4E-87
contig00131-orf00004	putative c'cytochrome [Verminephrobacter eiseniae EF01-2]	gi|111615538|ref|ZP 01402597.1|	42.11	7E-14
contig00131-orf00008	4-oxalocrotonate tautomerase [Oceanobacter sp. RED65]	gi|94499483|ref|ZP 01306020.1|	64.29	3E-17

Query	NR Database Subject	Subject ID	% ID	E value
contig00131-orf00009	hypothetical protein PaerP 01005683 [Pseudomonas aeruginosa PA7]	gi|94412510|ref|ZP 01292427.1|	50.32	6E-80
contig00131-orf00011	putative nucleoside hydrolase protein [Sinorhizobium medicae WSM419]	gi|113871454|ref|ZP 01411583.1|	50.63	5E-84
contig00131-orf00013	putative two-domain glycosyltransferase [Campylobacter jejuni]	gi|15430479|gb|AAK95997.1|	44.99	5E-117
contig00131-orf00015	Endonuclease/exonuclease/phosphatase [Psychrobacter sp. PRwf-1]	gi|91770161|ref|ZP 01271990.1|	56.38	3E-71
contig00131-orf00016	electron transport complex protein RnfB [Psychromonas sp. CNPT3]	gi|90408373|ref|ZP 01216536.1|	58.73	2E-32
contig00131-orf00019	aldehyde dehydrogenase family protein [Saccharophagus degradans 2-40]	gi|90021634|ref|YP 527461.1|	42.7	7E-96
contig00131-orf00021	uracil permease [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618770|ref|YP 857558.1|	69.9	6E-114
contig00131-orf00024	RND efflux system, outer membrane lipoprotein, NodT [Desulfovibrio vulgaris subsp. vulgaris DP4]	gi|114846193|ref|ZP 01456550.1|	33.33	2E-12
contig00131-orf00026	RND efflux system, outer membrane lipoprotein, NodT [Caulobacter sp. K31]	gi|113932365|ref|ZP 01418267.1|	34.02	2E-26
contig00131-orf00027	putative ABC transporter permease component [Rhizobium leguminosarum bv. viciae 3841]	gi|116249500|ref|YP 765338.1|	45.5	2E-82
contig00131-orf00029	hypothetical protein Ccur5 01000988 [Campylobacter curvus 525.92]	gi|109674076|ref|ZP 01376241.1|	29.51	0.025
contig00132-orf00002	hypothetical protein PF11 0528 [Plasmodium falciparum 3D7]	gi|23508329|ref|NP 700998.1|	22.22	0.033
contig00132-orf00004	PREDICTED: similar to lengsin [Strongylocentrotus purpuratus]	gi|115752458|ref|XP 781550.2|	23.33	0.22
contig00134-orf00001	cytochrome c5 [Neisseria subflava]	gi|34481906|emb|CAE46491.1|	89.12	6E-107
contig00134-orf00002	aromatic-amino-acid aminotransferase [Neisseria subflava]	gi|34481905|emb|CAE46490.1|	96.73	0
contig00134-orf00003	dihydropteroate synthase [Neisseria subflava]	gi|34481904|emb|CAE46489.1|	94.01	1E-140
contig00134-orf00005	phosphomannomutase [Ralstonia eutropha H16]	gi|113868413|ref|YP 726902.1|	64.94	5E-159
contig00134-orf00007	DedA-family membrane-associated protein [Neisseria subflava]	gi|34481902|emb|CAE46487.1|	95.68	4E-78
contig00134-orf00010	cytoplasmic asparaginase I [Escherichia coli UTI89]	gi|91210984|ref|YP 540970.1|	33.64	1E-38
contig00134-orf00011	hydrolase, TatD family protein [Oceanobacter sp. RED65]	gi|94500341|ref|ZP 01306874.1|	34.65	3E-33
contig00134-orf00015	thiamine-monophosphate kinase [Thiobacillus denitrificans ATCC 25259]	gi|74318211|ref|YP 315951.1|	46.35	5E-67
contig00134-orf00016	phosphatidylglycerophosphatase A [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618678|ref|YP 857815.1|	51.85	9E-27
contig00134-orf00017	ApaG protein [Sinorhizobium medicae WSM419]	gi|113871534|ref|ZP 01411663.1|	40.91	6E-17
contig00134-orf00019	transposase [Neisseria meningitidis]	gi|3860540|emb|CAA04676.1|	91.82	3E-82
contig00135-orf00003	putative nucleic acid binding protein [Bordetella avium 197N]	gi|115421926|emb|CAJ48446.1|	68.19	2E-173
contig00135-orf00005	hypothetical protein PaerP 01005133 [Pseudomonas aeruginosa PA7]	gi|94413061|ref|ZP 01292954.1|	26.67	0.0002
contig00135-orf00007	hypothetical protein Bpse1 03000207 [Burkholderia pseudomallei 1655]	gi|99913918|ref|ZP 01320515.1|	67.53	3E-159
contig00135-orf00011	malate permease related permease [Lactobacillus gasseri ATCC 33323]	gi|116629142|ref|YP 814314.1|	23.25	1E-16
contig00135-orf00015	NadA [Neisseria meningitidis]	gi|83616345|gb|ABC25677.1|	23.26	0.00004
contig00136-orf00001	putrescine ABC transporter, periplasmic putrescine-binding protein [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117617823|ref|YP 858561.1|	43.03	4E-77
contig00136-orf00003	SSU ribosomal protein S20P [Thiobacillus denitrificans ATCC 25259]	gi|74317872|ref|YP 315612.1|	74.71	4E-28
contig00136-orf00006	Phospholipase A1 [Psychrobacter sp. PRwf-1]	gi|91771187|ref|ZP 01273001.1|	43.83	4E-86

Query	NR Database Subject	Subject ID	% ID	E value
contig00136-orf00008	Protein of unknown function DUF502 [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111616158|ref|ZP 01403190.1|	49.5	2E-43
contig00136-orf00009	aspartyl-tRNA synthetase [Acidovorax sp. JS42]	gi|110593837|ref|ZP 01382187.1|	71.24	0
contig00136-orf00011	hypothetical protein PSEEN4993 [Pseudomonas entomophila L48]	gi|104783917|ref|YP 610415.1|	33.04	3E-43
contig00136-orf00013	UDP-2,3-diacylglucosamine hydrolase [Haemophilus somnus 129PT]	gi|113460643|ref|YP 718709.1|	58.19	2E-68
contig00136-orf00015	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Burkholderia cenocepacia AU 1054]	gi|107023555|ref|YP 621882.1|	36.45	1E-67
contig00136-orf00017	histidinol-phosphate aminotransferase [Ralstonia eutropha H16]	gi|113869362|ref|YP 727851.1|	44.29	3E-80
contig00136-orf00019	imidazoleglycerol-phosphate dehydratase [Alcanivorax borkumensis SK2]	gi|110835142|ref|YP 694001.1|	75.51	2E-81
contig00136-orf00022	#N/A	gi|33305788|gb|AAQ02788.1|AF378124 1	29.45	0.0004
contig00136-orf00024	hypothetical protein DEHA0C09658g [Debaryomyces hansenii CBS767]	gi|50419075|ref|XP 458060.1|	23.6	5E-11
contig00136-orf00024	hypothetical protein DEHA0C09658g [Debaryomyces hansenii CBS767]	gi|50419075|ref|XP 458060.1|	20.76	0.0007
contig00136-orf00024	hypothetical protein DEHA0C09658g [Debaryomyces hansenii CBS767]	gi|50419075|ref|XP 458060.1|	24.43	0.001
contig00136-orf00024	hypothetical protein DEHA0C09658g [Debaryomyces hansenii CBS767]	gi|50419075|ref|XP 458060.1|	17.82	0.12
contig00136-orf00026	#N/A	gi|30017097|gb|AAP12796.1|AF439218 1	38.45	2E-106
contig00136-orf00027	hypothetical protein Tbd 0026 [Thiobacillus denitrificans ATCC 25259]	gi|74316044|ref|YP 313784.1|	36.27	0.000003
contig00136-orf00029	hypothetical protein Tbd 0027 [Thiobacillus denitrificans ATCC 25259]	gi|74316045|ref|YP 313785.1|	50.39	9E-29
contig00138-orf00001	#N/A	gi|91207099|sp|Q3JVA8|LPXKBURP1	38.61	3E-17
contig00138-orf00003	syntaxin, putative [Aedes aegypti]	gi|108867713|gb|EAT32384.1|	25.23	0.087
contig00138-orf00005	hypothetical protein PsycPRwfDRAFT 0699 [Psychrobacter sp. PRwf-1]	gi|91770588|ref|ZP 01272412.1|	35.66	9E-10
contig00138-orf00008	Protein of unknown function DUF343 [Acidovorax sp. JS42]	gi|110593042|ref|ZP 01381396.1|	64.41	9E-16
contig00138-orf00009	3-deoxy-D-manno-octulosonate cytidylyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74317523|ref|YP 315263.1|	57.37	2E-67
contig00138-orf00012	AraC family transcriptional regulator [Maricaulis maris MCS10]	gi|114571369|ref|YP 758049.1|	26.67	0.26
contig00138-orf00014	adenylate kinase [Pseudomonas entomophila L48]	gi|104780470|ref|YP 606968.1|	72.56	2E-84
contig00138-orf00015	orotidine 5'-phosphate decarboxylase [Vibrio alginolyticus 12G01]	gi|91226891|ref|ZP 01261488.1|	60.99	1E-66
contig00138-orf00016	conserved hypothetical protein; possible oxidoreductase [Flavobacterium johnsoniae UW101]	gi|90589273|ref|ZP 01244923.1|	47.15	2E-42
contig00138-orf00017	D-beta-D-heptose 7-phophosphate kinase [Ralstonia eutropha H16]	gi|113866829|ref|YP 725318.1|	58.09	6E-95
contig00138-orf00019	ADP-D-beta-D-heptose 6-epimerase [Ralstonia eutropha H16]	gi|113866830|ref|YP 725319.1|	64.46	3E-125
contig00138-orf00020	PREDICTED: similar to kynurenine aminotransferase III isoform 1 [Apis mellifera]	gi|110773543|ref|XP 001123061.1|	65.74	2E-155
contig00138-orf00021	putative 2-nitropropane dioxygenase [Ralstonia eutropha H16]	gi|38637919|ref|NP 942893.1|	61.32	5E-115
contig00138-orf00022	aldose 1-epimerase [Rhodococcus jostii RHA1]	gi|111021963|ref|YP 704935.1|	27.78	3E-15

Query	NR Database Subject	Subject ID	% ID	E value
contig00138-orf00025	ribosomal large subunit pseudouridine synthase B [Thiobacillus denitrificans ATCC 25259]	gi|74317276|ref|YP 315016.1|	51.93	8E-75
contig00138-orf00027	pyridoxamine 5'-phosphate oxidase [Acidovorax sp. JS42]	gi|110595390|ref|ZP 01383723.1|	58.74	1E-60
contig00138-orf00029	deoxyuridine 5'-triphosphate nucleotidohydrolase [Bordetella avium 197N]	gi|115422486|emb|CAJ49011.1|	75.34	2E-61
contig00138-orf00031	xanthine/uracil permease family protein [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619116|ref|YP 856698.1|	71.03	3E-174
contig00139-orf00001	Integrase, catalytic region [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116268564|ref|ZP 01492810.1|	56	0.045
contig00139-orf00003	major facilitator superfamily transporter AzgA family protein [Ralstonia eutropha H16]	gi|116696514|ref|YP 842090.1|	58	2E-133
contig00139-orf00006	#N/A	gi|21427156|gb|AAM53100.1|AF45 2477 1	38.06	3E-39
contig00141-orf00002	putative DNA-binding/iron metalloprotein/AP endonuclease [Ralstonia eutropha H16]	gi|113868688|ref|YP 727177.1|	62.54	3E-102
contig00141-orf00004	putative phospho-2-dehydro-3-deoxyheptonate aldolase [Neisseria meningitidis]	gi|5051419|emb|CAB44959.1|	89.46	4E-161
contig00141-orf00006	hypothetical protein V12G01 12660 [Vibrio alginolyticus 12G01]	gi|91225078|ref|ZP 01260300.1|	60	5.5
contig00141-orf00008	3-deoxy-D-manno-octulosonic-acid transferase transmembrane protein [Thiobacillus denitrificans ATCC 25259]	gi|74318716|ref|YP 316456.1|	45.38	2E-79
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	35.15	3E-20
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	48.68	3E-20
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	53.06	3E-20
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	52.54	3E-20
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	58.14	4E-12
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	37.66	4E-12
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	33.33	0.55
contig00141-orf00010	hemagluttinin domain-containing protein [Burkholderia cenocepacia HI2424]	gi|116693316|ref|YP 838849.1|	29.41	6.1
contig00141-orf00012	OmpA family protein [Burkholderia pseudomallei K96243]	gi|53721933|ref|YP 110918.1|	36.84	7E-17
contig00141-orf00014	type IV pilus assembly protein, PilB [Thiobacillus denitrificans ATCC 25259]	gi|74318388|ref|YP 316128.1|	55.93	2E-168
contig00141-orf00015	type IV pilus assembly protein PilC [Thiobacillus denitrificans ATCC 25259]	gi|74318387|ref|YP 316127.1|	54.95	2E-116
contig00141-orf00016	type IV prepilin peptidase [Neisseria gonorrhoeae]	gi|545658|gb|AAB30050.1|	74.49	1E-87
contig00141-orf00017	#N/A	gi|109824128|sp|Q5F691|COAE NEIG1	53.3	5E-50
contig00141-orf00019	riboflavin biosynthesis protein RibF [Psychromonas ingrahamii 37]	gi|106881583|ref|ZP 01348987.1|	46.83	2E-51
contig00141-orf00020	riboflavin biosynthesis protein RibF [Acidovorax avenae subsp. citrulli AAC00-	gi|111617783|ref|ZP 01404810.1|	60.71	1.1
contig00141-orf00021	hypothetical protein [Cucurbit aphid-borne yellows virus]	gi|42564246|gb|AAS20610.1|	26.76	1.4
contig00141-orf00022	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [Pseudomonas entomophila L48]	gi|104783643|ref|YP 610141.1|	64.94	9E-110
contig00141-orf00023	lipoprotein signal peptidase [Bordetella avium 197N]	gi|115422494|emb|CAJ49019.1|	56.55	6E-35

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contig00141-orf00024	PREDICTED: similar to PWWP domain containing 2 [Rattus norvegicus]	gi|109459556|ref|XP 341956.3|	29	0.63
contig00141-orf00028	putative outer membrane protein OmpU [Neisseria meningitidis]	gi|4206707|gb|AAD11779.1|	60.99	3E-157
contig00141-orf00029	PREDICTED: similar to pawn CG11101-PA [Tribolium castaneum]	gi|91086865|ref|XP 969198.1|	56.52	1.9
contig00141-orf00032	Na+/H+ antiporter NhaD or related arsenite permease [Ralstonia eutropha H16]	gi|113868549|ref|YP 727038.1|	60.04	2E-133
contig00141-orf00035	HI0164-like protein [Haemophilus influenzae]	gi|89892361|gb|ABD78956.1|	69.64	2E-162
contig00141-orf00037	Na(+)-translocating NADH-quinone reductase subunit B [Vibrio alginolyticus 12G01]	gi|91223432|ref|ZP 01258697.1|	76.16	1E-176
contig00141-orf00040	Na(+)-translocating NADH-quinone reductase subunit C [Psychromonas sp. CNPT3]	gi|90408360|ref|ZP 01216523.1|	57.49	3E-73
contig00141-orf00041	NADH-ubiquinone oxidoreductase [Photobacterium profundum 3TCK]	gi|90410924|ref|ZP 01218938.1|	68.97	2E-78
contig00141-orf00043	Na(+)-translocating NADH-quinone reductase subunit E [Haemophilus somnus 129PT]	gi|113461825|ref|YP 719894.1|	85.79	2E-87
contig00141-orf00045	Na(+)-translocating NADH-quinone reductase subunit F [Vibrio angustum S14]	gi|90579855|ref|ZP 01235663.1|	81.23	0
contig00141-orf00047	phosphopantothenate-cysteine ligase / phosphopantothenoylcysteine decarboxylase [Methylobacillus flagellatus KT]	gi|91774670|ref|YP 544426.1|	51.65	7E-107
contig00142-orf00001	transposase [Neisseria meningitidis]	gi|3860540|emb|CAA04676.1|	90.52	3E-55
contig00142-orf00004	DNA topoisomerase I [Psychromonas ingrahamii 37]	gi|106883081|ref|ZP 01350480.1|	38.3	1E-22
contig00142-orf00006	ribosomal protein L11 methyltransferase [Thiobacillus denitrificans ATCC	gi|74316198|ref|YP 313938.1|	57.77	7E-95
contig00142-orf00009	acetyl-CoA carboxylase, biotin carboxylase [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116270022|ref|ZP 01494264.1|	71.3	0
contig00142-orf00010	conserved hypothetical protein [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111616346|ref|ZP 01403378.1|	79.37	8E-23
contig00142-orf00011	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit [Yersinia pestis KIM]	gi|22124128|ref|NP 667551.1|	76.79	2E-18
contig00143-orf00001	Integrase, catalytic region [Psychromonas ingrahamii 37]	gi|106881471|ref|ZP 01348876.1|	43.08	7E-24
contig00143-orf00002	putative transposase [Neisseria meningitidis]	gi|5051414|emb|CAB44955.1|	98.15	5E-24
contig00145-orf00001	PREDICTED: similar to LD42868p [Tribolium castaneum]	gi|91077060|ref|XP 968584.1|	27.78	1.5
contig00145-orf00003	putative cullin [Arabidopsis thaliana]	gi|20268719|gb|AAM14063.1|	43.33	1.1
contig00145-orf00004	POM1, putative [Plasmodium falciparum 3D7]	gi|23509333|ref|NP 702000.1|	31.25	0.64
contig00145-orf00007	hypothetical protein VAS14 04043 [Vibrio angustum S14]	gi|90578844|ref|ZP 01234654.1|	44.05	3E-10
contig00148-orf00002	PREDICTED: similar to mucin 1, transmembrane [Rattus norvegicus]	gi|109465082|ref|XP 342282.3|	29.79	0.1
contig00148-orf00003	hypothetical protein [Neisseria meningitidis]	gi|6900499|emb|CAB72087.1|	97.14	2E-116
contig00148-orf00005	16S rRNA uridine-516 pseudouridylate synthase [Ralstonia eutropha H16]	gi|113868872|ref|YP 727361.1|	45.81	1E-46
contig00148-orf00007	adenine specific DNA-methyltransferase [Rhodococcus jostii RHA1]	gi|111018616|ref|YP 701588.1|	50.14	2E-92
contig00148-orf00009	aspartyl/glutamyl-tRNA amidotransferase subunit B [Thiobacillus denitrificans ATCC 25259]	gi|74316275|ref|YP 314015.1|	68	0
contig00148-orf00010	hypothetical protein HS 1361 [Haemophilus somnus 129PT]	gi|113461504|ref|YP 719573.1|	35.03	6E-41

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contig00148-orf00012	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A [Thiobacillus denitrificans ATCC 25259]	gi|74316276|ref|YP 314016.1|	65.73	2E-150
contig00148-orf00014	aspartyl/glutamyl-tRNA amidotransferase subunit C [Ralstonia eutropha H16]	gi|113866143|ref|YP 724632.1|	50.51	7E-22
contig00148-orf00016	cell shape determining protein, MreB/Mrl family [Polynucleobacter sp. QLW-P1DMWA-1]	gi|116270165|ref|ZP 01494406.1|	61.05	3E-113
contig00148-orf00017	rod shape-determining protein MreC [Acidovorax sp. JS42]	gi|110592668|ref|ZP 01381024.1|	33.73	3E-33
contig00148-orf00018	rod shape-determining protein MreD [Ralstonia eutropha H16]	gi|113866146|ref|YP 724635.1|	40.85	3E-21
contig00148-orf00019	peptidoglycan glycosyltransferase [Burkholderia ambifaria AMMD]	gi|115353219|ref|YP 775058.1|	45.73	4E-147
contig00148-orf00022	Rod shape-determining protein RodA [Shewanella baltica OS195]	gi|113949377|ref|ZP 01435026.1|	53.58	2E-75
contig00148-orf00023	Multiple antibiotic resistance (MarC)-related proteins [Psychrobacter sp. PRwf-1]	gi|91769699|ref|ZP 01271531.1|	53.74	7E-45
contig00148-orf00026	sulfite reductase subunit II [Klebsiella pneumoniae]	gi|110180265|gb|ABG54374.1|	53.76	2E-146
contig00148-orf00028	phosphoglucomutase, PGM {pyocin resistance} [Neisseria gonorrhoeae, mutant 1291d, Peptide Mutant, 456 aa]	gi|765317|gb|AAB32514.1|	89.13	0
contig00148-orf00030	zinc protease [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117620098|ref|YP 854955.1|	51.25	2E-75
contig00148-orf00031	baculoviral IAP repeat-containing 3 [Rattus norvegicus]	gi|54020878|ref|NP 076477.2|	30.36	0.075
contig00148-orf00034	homoserine dehydrogenase [Ralstonia eutropha H16]	gi|113868242|ref|YP 726731.1|	61.93	6E-134
contig00148-orf00037	#N/A	gi|6647285|gb|AAF21127.1|L78665	50	2E-09
contig00148-orf00041	thiol peroxidase [Pseudomonas entomophila L48]	gi|104781760|ref|YP 608258.1|	72.73	1E-59
contig00148-orf00042	PREDICTED: similar to G protein-coupled receptor 83 [Rattus norvegicus]	gi|109510866|ref|XP 231463.4|	35.29	4.1
contig00148-orf00044	coproporphyrinogen III oxidase [Shigella flexneri 5 str. 8401]	gi|110806377|ref|YP 689897.1|	71.97	1E-123
contig00148-orf00046	#N/A	gi|97050644|sp|Q2KV15|GLYA BORA1	73.56	4E-174
contig00148-orf00047	hypothetical protein DEHA0A09977g [Debaryomyces hansenii CBS767]	gi|50408069|ref|XP 456754.1|	48.39	7.2
contig00148-orf00048	peptide synthase [Pseudomonas entomophila L48]	gi|104782280|ref|YP 608778.1|	29.82	4.2
contig00148-orf00050	sugar efflux transporter [Pseudomonas entomophila L48]	gi|104781420|ref|YP 607918.1|	56.18	5E-108
contig00148-orf00052	AAA ATPase, central region [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619061|ref|ZP 01406077.1|	70.28	5E-154
contig00148-orf00057	hypothetical protein PFB0615c [Plasmodium falciparum 3D7]	gi|23593306|ref|NP 473051.2|	33.87	0.45
contig00148-orf00060	conserved hypothetical protein; putative signal peptide [Psychrobacter sp. PRwf-1]	gi|91770598|ref|ZP 01272422.1|	39.53	1E-13
contig00148-orf00062	Threonine synthase [Psychrobacter sp. PRwf-1]	gi|91770677|ref|ZP 01272500.1|	67.99	9E-179
contig00148-orf00064	Protein of unknown function UPF0044 [Acidovorax sp. JS42]	gi|110593119|ref|ZP 01381473.1|	58.43	2E-20
contig00148-orf00065	hypothetical protein PaerPA 01004920 [Pseudomonas aeruginosa PACS2]	gi|107103849|ref|ZP 01367767.1|	57.61	4E-56
contig00148-orf00067	ATP-dependent metalloprotease FtsH [Nitrosomonas eutropha C91]	gi|114331000|ref|YP 747222.1|	65.49	0
contig00148-orf00068	thioredoxin reductase [Pseudomonas entomophila L48]	gi|104780146|ref|YP 606644.1|	72.82	7E-120
contig00148-orf00072	delta-aminolevulinic acid dehydratase [Alcanivorax borkumensis SK2]	gi|110835320|ref|YP 694179.1|	75.38	1E-136
contig00148-orf00075	hypothetical protein FjohDRAFT 0302 [Flavobacterium johnsoniae UW101]	gi|90591955|ref|ZP 01247594.1|	33.86	2E-17

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contig00148-orf00076	hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]	gi|58262416|ref|XP 568618.1|	37.25	5.4
contig00148-orf00077	major facilitator superfamily (MFS)oxalate/formate antiporter [Burkholderia xenovorans LB400]	gi|91777858|ref|YP 553066.1|	62.72	3E-146
contig00148-orf00079	hypothetical protein AaveDRAFT 1185 [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111619002|ref|ZP 01406019.1|	23.43	0.001
contig00149-orf00001	ferredoxin 4Fe-4S [Pseudomonas entomophila L48]	gi|104779570|ref|YP 606068.1|	84.81	6E-37
contig00149-orf00002	hypothetical protein Tbd 0379 [Thiobacillus denitrificans ATCC 25259]	gi|74316397|ref|YP 314137.1|	48.28	2E-37
contig00149-orf00006	sucrose-phosphate synthase - like protein [Arabidopsis thaliana]	gi|62319202|dbj|BAD94390.1|	32.69	1.2
contig00149-orf00009	hypothetical protein CburD 01000149 [Coxiella burnetii Dugway 7E9-12]	gi|94492569|ref|ZP 01299776.1|	58.14	0
contig00149-orf00010	conserved hypothetical protein [Bordetella avium 197N]	gi|115424434|emb|CAJ50987.1|	27.59	8E-08
contig00149-orf00011	DNA processing protein DprA, putative [Acidovorax sp. JS42]	gi|110595166|ref|ZP 01383502.1|	50	0.00006
contig00149-orf00013	Smf protein [Ralstonia eutropha H16]	gi|113869637|ref|YP 728126.1|	49.47	6E-57
contig00149-orf00016	two component Fis family transcriptional regulator [Thiobacillus denitrificans ATCC 25259]	gi|74316037|ref|YP 313777.1|	46.79	4E-91
contig00149-orf00017	periplasmic sensor signal transduction histidine kinase [Nitrosomonas eutropha C91]	gi|114330409|ref|YP 746631.1|	37.77	8E-97
contig00149-orf00018	hypothetical protein H16 A3696 [Ralstonia eutropha H16]	gi|113869631|ref|YP 728120.1|	33.14	1E-18
contig00149-orf00019	Fmu, rRNA SAM-dependent methyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74316034|ref|YP 313774.1|	50.94	3E-102
contig00149-orf00021	alpha-glucosidase [Stigmatella aurantiaca DW4/3-1]	gi|115372190|ref|ZP 01459501.1|	34.09	9.1
contig00149-orf00022	hypothetical protein HNE 3212 [Hyphomonas neptunium ATCC 15444]	gi|114799190|ref|YP 761887.1|	34.33	0.007
contig00149-orf00023	hypothetical protein Tbd 1195 [Thiobacillus denitrificans ATCC 25259]	gi|74317213|ref|YP 314953.1|	60.61	5E-51
contig00149-orf00025	methionyl-tRNA formyltransferase [Acidovorax sp. JS42]	gi|110595162|ref|ZP 01383498.1|	55.31	5E-77
contig00149-orf00028	peptide deformylase [Thiobacillus denitrificans ATCC 25259]	gi|74316032|ref|YP 313772.1|	68.9	6E-56
contig00149-orf00029	Peptidoglycan-binding LysM [Acidovorax sp. JS42]	gi|110595165|ref|ZP 01383501.1|	32.37	1E-44
contig00149-orf00033	conserved hypothetical protein [Photobacterium profundum 3TCK]	gi|90414578|ref|ZP 01222552.1|	35.35	2E-10
contig00149-orf00035	coproporphyrinogen III oxidase [Escherichia coli UTI89]	gi|91213008|ref|YP 542994.1|	38.55	6E-69
contig00149-orf00036	putative outer-membrane heme receptor [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618308|ref|YP 855516.1|	35.19	2E-44
contig00149-orf00037	hypothetical protein PaerP 01002142 [Pseudomonas aeruginosa PA7]	gi|94416062|ref|ZP 01295893.1|	80.16	1E-112
contig00149-orf00038	anthranilate/para-aminobenzoate synthase component I [Ralstonia eutropha H16]	gi|113869041|ref|YP 727530.1|	45.62	5E-130
contig00149-orf00040	Ubiquitin system component Cue:conserved hypothetical protein [Flavobacterium johnsoniae UW101]	gi|90590125|ref|ZP 01245773.1|	35.62	1E-71
contig00149-orf00041	acyl carrier protein AcpP [Pseudomonas entomophila L48]	gi|104780785|ref|YP 607283.1|	84.62	3E-29
contig00149-orf00042	3-oxoacyl-[acyl-carrier-protein] synthase II [Bordetella avium 197N]	gi|115422208|emb|CAJ48732.1|	68.7	2E-156
contig00149-orf00046	dlgh4 protein [Xenopus (Silurana) tropicalis]	gi|114108021|gb|AAI23008.1|	28.12	1

Query	NR Database Subject	Subject ID	% ID	E value
contig00149-orf00047	AdaPtin, Small chain (clathrin associated complex) family member (aps-3) [Caenorhabditis elegans]	gi|25151042|ref|NP 740780.1|	30.51	0.16
contig00149-orf00050	pyruvate kinase [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111618274|ref|ZP 01405298.1|	55.46	4E-134
contig00149-orf00051	hypoxanthine-guanine phosphoribosyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74316795|ref|YP 314535.1|	54.86	7E-41
contig00149-orf00052	putative sugar transport PTS system IIA component [Burkholderia xenovorans LB400]	gi|91781660|ref|YP 556866.1|	34.88	5E-14
contig00149-orf00054	HPrNtr [Thiobacillus denitrificans ATCC 25259]	gi|74318431|ref|YP 316171.1|	59.77	2E-22
contig00149-orf00056	phosphoenolpyruvate--protein phosphotransferase [Thiobacillus denitrificans ATCC 25259]	gi|74318432|ref|YP 316172.1|	51.74	6E-159
contig00149-orf00061	ATP-dependent RNA helicase HrpA [Shigella flexneri 5 str. 8401]	gi|110805742|ref|YP 689262.1|	56.33	0
contig00150-orf00001	conserved hypothetical protein [Candidatus Kuenenia stuttgartiensis]	gi|91203443|emb|CAJ71096.1|	21.2	0.097
contig00150-orf00004	Helix-turn-helix, AraC type [Flavobacterium johnsoniae UW101]	gi|90588393|ref|ZP 01244045.1|	37.5	2.4
contig00151-orf00003	small-conductance mechanosensitive channel protein [Burkholderia xenovorans LB400]	gi|91784969|ref|YP 560175.1|	38.89	9E-62
contig00151-orf00004	dATP pyrophosphohydrolase [Thiobacillus denitrificans ATCC 25259]	gi|74316462|ref|YP 314202.1|	51.08	4E-34
contig00151-orf00007	Inorganic diphosphatase [Psychrobacter sp. PRwf-1]	gi|91770829|ref|ZP 01272650.1|	81.5	3E-71
contig00151-orf00009	DNA polymerase III, epsilon subunit [Methylobacillus flagellatus KT]	gi|91775906|ref|YP 545662.1|	32.86	1E-46
contig00151-orf00010	Cof-like hydrolase [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116872431|ref|YP 849212.1|	36.4	1E-36
contig00151-orf00012	thiamine biosynthesis protein [Helicobacter pylori HPAG1]	gi|108563254|ref|YP 627570.1|	49.79	7E-64
contig00151-orf00015	PfkB family carbohydrate kinase [Gramella forsetii KT0803]	gi|117576534|emb|CAL65003.1|	46.92	2E-74
contig00151-orf00016	alanine racemase [Pseudomonas entomophila L48]	gi|104784314|ref|YP 610812.1|	52.44	3E-94
contig00151-orf00018	hypothetical protein CPF 1747 [Clostridium perfringens ATCC 13124]	gi|110801054|ref|YP 696183.1|	54.55	3E-20
contig00151-orf00020	hypothetical protein CPF 1748 [Clostridium perfringens ATCC 13124]	gi|110800574|ref|YP 696184.1|	68.6	9E-178
contig00151-orf00023	OsmC/Ohr family protein [Thiobacillus denitrificans ATCC 25259]	gi|74316469|ref|YP 314209.1|	56.52	1E-37
contig00151-orf00026	GntR family transcriptional regulator [Ralstonia eutropha H16]	gi|113867029|ref|YP 725518.1|	40.49	2E-32
contig00151-orf00028	tRNA (uracil-5-)-methyltransferase [Vibrio alginolyticus 12G01]	gi|91228523|ref|ZP 01262444.1|	56.94	3E-111
contig00151-orf00030	hypothetical protein PSEEN2259 [Pseudomonas entomophila L48]	gi|104781379|ref|YP 607877.1|	48.58	5E-58
contig00151-orf00032	chorismate synthase [Ralstonia eutropha H16]	gi|113867336|ref|YP 725825.1|	73.9	1E-149
contig00151-orf00036	#N/A	gi|116667888|pdb|2HXJ|A	90.91	1E-51
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	35.64	5E-40
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	30.3	3E-31
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	25.51	2E-24

Query	NR Database Subject	Subject ID	% ID	E value
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	29.04	2E-22
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	27.38	3E-22
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	38.42	1E-20
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	24.85	2E-17
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	41.41	3E-15
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	26.37	2E-13
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	25.53	5E-12
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	40.71	8E-09
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	33.11	0.0006
contig00151-orf00041	type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	gi|40063620|gb|AAR38409.1|	28.95	0.003
contig00151-orf00042	NosL [Rhodopseudomonas palustris HaA2]	gi|86750257|ref|YP 486753.1|	40.41	8E-29
contig00151-orf00043	nitrous oxide metabolic protein [Rhodopseudomonas palustris HaA2]	gi|86750256|ref|YP 486752.1|	54.71	6E-66
contig00151-orf00044	ABC transporter related [Rhodopseudomonas palustris HaA2]	gi|86750255|ref|YP 486751.1|	46.96	7E-55
contig00151-orf00046	nosD [Bradyrhizobium japonicum]	gi|3850615|emb|CAA05519.1|	46.19	2E-107
contig00151-orf00050	nitrous-oxide reductase [Rhodopseudomonas palustris HaA2]	gi|86750253|ref|YP 486749.1|	66.55	0
contig00151-orf00053	nosR [Bradyrhizobium japonicum]	gi|3850614|emb|CAA05521.1|	48.21	0
contig00151-orf00054	acetyl-coenzyme A carboxylase carboxyl transferase subunit beta [Bordetella avium 197N]	gi|115422189|emb|CAJ48713.1|	64.16	4E-104
contig00151-orf00057	tryptophan synthase, alpha chain [Thiobacillus denitrificans ATCC 25259]	gi|74317931|ref|YP 315671.1|	59.32	1E-75
contig00151-orf00059	hypothetical protein PSEEN1676 [Pseudomonas entomophila L48]	gi|104780834|ref|YP 607332.1|	55.18	1E-57
contig00151-orf00060	apolipoprotein N-acyltransferase [Thiobacillus denitrificans ATCC 25259]	gi|74318602|ref|YP 316342.1|	39.6	4E-81
contig00151-orf00061	RNA polymerase factor sigma-32 [Nitrosomonas eutropha C91]	gi|114331030|ref|YP 747252.1|	59.57	2E-88
contig00151-orf00063	GatB/YqeY [Verminephrobacter eiseniae EF01-2]	gi|111613481|ref|ZP 01400562.1|	51.09	2E-30
contig00151-orf00064	30S ribosomal protein S21 [Thiobacillus denitrificans ATCC 25259]	gi|74318403|ref|YP 316143.1|	80	2E-16
contig00151-orf00065	glutaredoxin-like protein [Ralstonia metallidurans CH34]	gi|94312135|ref|YP 585345.1|	66.02	3E-34
contig00151-orf00066	Uracil phosphoribosyl transferase [Psychrobacter sp. PRwf-1]	gi|91770998|ref|ZP 01272817.1|	78.47	9E-91
contig00151-orf00068	conserved hypothetical protein [Acidovorax sp. JS42]	gi|110596345|ref|ZP 01384658.1|	50.72	7E-11

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contig00152-orf00001	hypothetical protein VeisDRAFT 5067 [Verminephrobacter eiseniae EF01-2]	gi|111611450|ref|ZP 01398539.1|	95.83	0.0000006
contig00152-orf00003	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [Ralstonia eutropha H16]	gi|113868508|ref|YP 726997.1|	59.14	1E-57
contig00152-orf00005	hypothetical protein PsycPRwfDRAFT 1579 [Psychrobacter sp. PRwf-1]	gi|91770013|ref|ZP 01271843.1|	37.69	3E-13
contig00152-orf00006	hypothetical protein Tbd 0638 [Thiobacillus denitrificans ATCC 25259]	gi|74316656|ref|YP 314396.1|	31.33	1E-14
contig00152-orf00008	ferredoxin [Rubrivivax gelatinosus]	gi|58198979|gb|AAW66136.1|	46.02	3E-104
contig00152-orf00014	transketolase [Thiobacillus denitrificans ATCC 25259]	gi|74316177|ref|YP 313917.1|	67.17	0
contig00152-orf00018	hypothetical protein Cjejd 01000742 [Campylobacter jejuni subsp. doylei	gi|109691394|ref|ZP 01378462.1|	35.77	6E-35
contig00152-orf00021	hypothetical protein VAS14 07659 [Vibrio angustum S14]	gi|90580588|ref|ZP 01236393.1|	59.53	5E-81
contig00152-orf00022	putative transposase [Streptococcus pneumoniae]	gi|5019554|emb|CAB44497.1|	46.91	4E-15
contig00154-orf00002	NhhA outer membrane protein [Neisseria meningitidis]	gi|14578015|gb|AAK68867.1|	66	2E-30
contig00155-orf00001	fimbrial protein [Verminephrobacter eiseniae EF01-2]	gi|111612977|ref|ZP 01400060.1|	45.88	1E-19
contig00155-orf00004	4-hydroxybenzoyl-CoA thioesterase [Clostridium phytofermentans ISDg]	gi|106887238|ref|ZP 01354551.1|	44.44	7.1
contig00156-orf00001	hypothetical protein SpneT 02001761 [Streptococcus pneumoniae TIGR4]	gi|111657011|ref|ZP 01407814.1|	49.47	7E-20
contig00157-orf00001	Integrase, catalytic region [Psychromonas ingrahamii 37]	gi|106880770|ref|ZP 01348175.1|	40.83	3E-55
contig00158-orf00001	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Chromohalobacter salexigens DSM 3043]	gi|92114934|ref|YP 574862.1|	66.95	6E-44
contig00161-orf00001	putative tRNA/rRNA methyltransferase [Bordetella avium 197N]	gi|115423202|emb|CAJ49733.1|	57.2	1E-75
contig00161-orf00003	branched chain amino acid ABC transporter [Rhodopseudomonas palustris	gi|86748948|ref|YP 485444.1|	30.56	0.002
contig00161-orf00004	conserved hypothetical protein [Sinorhizobium medicae WSM419]	gi|113877765|ref|ZP 01417039.1|	33.49	3E-30
contig00161-orf00005	dihydrodipicolinate synthase [Ralstonia eutropha H16]	gi|113867224|ref|YP 725713.1|	56.21	7E-92
contig00161-orf00006	NlpBDapX lipoprotein [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111617855|ref|ZP 01404882.1|	36.16	4E-52
contig00161-orf00008	conserved hypothetical protein [Campylobacter concisus 13826]	gi|109671715|ref|ZP 01373963.1|	34.59	2E-37
contig00161-orf00010	ribosomal large subunit pseudouridine synthase E [Methylobacillus flagellatus KT]	gi|91776490|ref|YP 546246.1|	62.5	2E-56
contig00162-orf00001	L-lactate dehydrogenase [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116871592|ref|YP 848373.1|	47.92	2E-76
contig00162-orf00004	lipoprotein GNA1870 [Neisseria meningitidis]	gi|45269113|gb|AAS56915.1|	40.68	6E-41
contig00162-orf00006	hypothetical protein PSEEN1707 [Pseudomonas entomophila L48]	gi|104780864|ref|YP 607362.1|	29.43	3E-14
contig00162-orf00007	RNA methyltransferase, TrmH family, group 1 [uncultured marine bacterium	gi|40063429|gb|AAR38240.1|	38.76	4E-38
contig00162-orf00008	inositol monophosphatase [Thiobacillus denitrificans ATCC 25259]	gi|74317178|ref|YP 314918.1|	56.11	2E-80
contig00162-orf00009	RE18408p [Drosophila melanogaster]	gi|33589428|gb|AAQ22481.1|	52	6.9
contig00162-orf00010	Type I secretion outer membrane protein, TolC [Rhodopseudomonas palustris HaA2]	gi|86748756|ref|YP 485252.1|	20.32	4E-11
contig00162-orf00011	ABC transporter related [Burkholderia ambifaria AMMD]	gi|115353200|ref|YP 775039.1|	39.97	5E-131
contig00162-orf00012	putative type I secretion protein [Sphingomonas sp. SKA58]	gi|94495049|ref|ZP 01301630.1|	42.03	3E-80
contig00162-orf00014	sulfate adenylyltransferase subunit 1 [Ralstonia eutropha H16]	gi|113868950|ref|YP 727439.1|	60.98	5E-133
contig00162-orf00020	RhtX/FptX family siderophore transporter [Myxococcus xanthus DK 1622]	gi|108762870|ref|YP 633507.1|	26.82	6E-11

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contig00162-orf00021	Os08g0447600 [Oryza sativa (japonica cultivar-group)]	gi|115476674|ref|NP 001061933.1|	41.57	0.097
contig00162-orf00022	putative photobactin outer membrane receptor precursor PhuA [Photorhabdus luminescens]	gi|22073891|gb|AAK95841.1|	47.82	7E-154
contig00162-orf00024	TetR family transcriptional regulator [Novosphingobium aromaticivorans DSM 12444]	gi|87199491|ref|YP 496748.1|	32.43	6E-08
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	30.8	3E-40
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	32.92	1E-38
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	35.15	5E-34
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	33.26	4E-33
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	36.86	4E-33
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	30.67	5E-33
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	32.69	2E-29
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	33.33	4E-29
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	28.88	2E-22
contig00162-orf00029	putative rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	gi|116250562|ref|YP 766400.1|	34.73	2E-15
contig00162-orf00032	Gamma-glutamyl phosphate reductase [Oceanobacter sp. RED65]	gi|94501228|ref|ZP 01307750.1|	65.29	2E-151
contig00162-orf00037	ADP-heptose:LPS heptosyltransferase II [Neisseria gonorrhoeae]	gi|599920|emb|CAA85504.1|	76.95	6E-155
contig00162-orf00038	cold-shock protein, DNA-binding [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117621225|ref|YP 857729.1|	30.45	9E-18
contig00162-orf00039	actin deviating protein [Tretomphalus sp. B123]	gi|60418461|gb|AAX19677.1|	40	4.1
contig00162-orf00040	5-methylaminomethyl-2-thiouridine methyltransferase [Pseudomonas entomophila L48]	gi|104780652|ref|YP 607150.1|	36.6	3E-55
contig00162-orf00041	NAD kinase [Thiobacillus denitrificans ATCC 25259]	gi|74318049|ref|YP 315789.1|	46.44	1E-71
contig00162-orf00042	hypothetical protein H16 A0447 [Ralstonia eutropha H16]	gi|113866476|ref|YP 724965.1|	23.63	8E-11
contig00162-orf00043	hypothetical protein mh0070 [Mannheimia haemolytica]	gi|110735377|gb|ABG89259.1|	36.08	5E-27
contig00162-orf00044	PREDICTED: similar to keratin associated protein [Pan troglodytes]	gi|114684729|ref|XP 001153535.1|	25.53	0.096
contig00162-orf00046	Hydroxyacylglutathione hydrolase [Psychrobacter sp. PRwf-1]	gi|91770474|ref|ZP 01272300.1|	48.24	1E-57
contig00162-orf00048	PilV [Neisseria gonorrhoeae]	gi|18175490|gb|AAL60052.1|	45.71	4E-18
contig00162-orf00049	MacA [Neisseria gonorrhoeae]	gi|56385100|gb|AAV85981.1|	79.64	1E-158
contig00162-orf00052	MacB [Neisseria gonorrhoeae]	gi|56385102|gb|AAV85982.1|	88.84	0
contig00162-orf00054	glutathione S-transferase-like [Burkholderia cenocepacia AU 1054]	gi|107026861|ref|YP 624372.1|	51.39	3E-55
contig00163-orf00001	unnamed protein product [Neisseria meningitidis]	gi|6900477|emb|CAB72065.1|	92.73	3E-24
contig00165-orf00001	putative transposase [Neisseria meningitidis]	gi|5051414|emb|CAB44955.1|	97.67	2E-17
contig00167-orf00001	deoxynucleoside kinase [Alcanivorax borkumensis SK2]	gi|110833199|ref|YP 692058.1|	40.69	6E-40
contig00167-orf00004	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase [Thiobacillus denitrificans ATCC 25259]	gi|74318069|ref|YP 315809.1|	53.91	9E-27
contig00167-orf00005	SirB family protein [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117618074|ref|YP 854870.1|	34.45	2E-11

Query	NR Database Subject	Subject ID	% ID	E value
contig00167-orf00007	methylase protein [Listeria welshimeri serovar 6b str. SLCC5334]	gi|116873097|ref|YP 849878.1|	42.7	3E-36
contig00167-orf00009	HfQ protein; putative RNA-binding regulatory protein [Bordetella avium 197N]	gi|115423414|emb|CAJ49948.1|	91.18	5E-27
contig00167-orf00013	GTP-binding protein EngA [Thiobacillus denitrificans ATCC 25259]	gi|74316616|ref|YP 314356.1|	67.49	3E-161
contig00167-orf00015	conserved hypothetical transmembrane protein [Acidovorax sp. JS42]	gi|110595076|ref|ZP 01383414.1|	33.5	5E-18
contig00167-orf00016	histidyl-tRNA synthetase [Ralstonia eutropha H16]	gi|113868337|ref|YP 726826.1|	56.22	2E-128
contig00167-orf00019	Pseudouridine synthase [Acidovorax avenae subsp. citrulli AAC00-1]	gi|111620554|ref|ZP 01407530.1|	46.21	7E-63
contig00167-orf00021	cardiolipin synthetase [Psychrobacter cryohalolentis K5]	gi|93006556|ref|YP 580993.1|	44.72	2E-104
contig00167-orf00024	uroporphyrinogen decarboxylase [Pseudomonas entomophila L48]	gi|104779618|ref|YP 606116.1|	69.41	1E-140
contig00167-orf00026	putative protoheme IX synthesis protein [Bordetella avium 197N]	gi|115423373|emb|CAJ49907.1|	26.78	4E-27
contig00167-orf00027	bifunctional uroporphyrinogen-III synthetase/uroporphyrin-III C-methyltransferase [Ralstonia eutropha H16]	gi|113868874|ref|YP 727363.1|	33	3E-30
contig00167-orf00028	uroporphyrinogen-III synthase [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	gi|117619183|ref|YP 855001.1|	30.13	7E-12
contig00167-orf00029	hypothetical protein PsycPRwfDRAFT 1807 [Psychrobacter sp. PRwf-1]	gi|91769548|ref|ZP 01271381.1|	52.87	1E-12
contig00167-orf00032	Heat shock protein DnaJ-like:Chaperone DnaJ-like [Psychrobacter sp. PRwf-1]	gi|91769547|ref|ZP 01271380.1|	48.5	1E-76
contig00167-orf00033	hypothetical protein [Neisseria gonorrhoeae]	gi|5051440|emb|CAB44948.1|	72.73	2E-11
contig00167-orf00033	hypothetical protein [Neisseria gonorrhoeae]	gi|5051440|emb|CAB44948.1|	37.84	2E-11
contig00167-orf00035	magnesium and cobalt transport protein CorA [Geobacter sp. FRC-32]	gi|110599731|ref|ZP 01387965.1|	41.5	6E-68
contig00167-orf00036	magnesium and cobalt transport protein CorA [Herpetosiphon aurantiacus ATCC 23779]	gi|113938708|ref|ZP 01424573.1|	58.46	1E-18
contig00167-orf00038	Thioesterase superfamily [Psychrobacter sp. PRwf-1]	gi|91770587|ref|ZP 01272411.1|	65.56	9E-53
contig00167-orf00041	hypothetical protein RPB 1952 [Rhodopseudomonas palustris HaA2]	gi|86749075|ref|YP 485571.1|	54.55	4E-53
contig00168-orf00001	Integrase, catalytic region [Psychromonas ingrahamii 37]	gi|106881471|ref|ZP 01348876.1|	42.38	1E-27
contig00169-orf00001	Integrase, catalytic region [Psychromonas ingrahamii 37]	gi|106881471|ref|ZP 01348876.1|	44.72	3E-23

Appendix D

Functional annotation of identified *N. sicca* 4320 ORFs.

The subject IDs of the annotated *N. sicca* 4320 were used to search the UniProt database and available functional annotation recorded. Query: *N. sicca* 4320 ORF. Cellular Component: Cellular location of activity. Molecular Function: Function of activity. Biological Process: Process in which activity takes place.

Query	Cellular Component	Molecular Function	Biological Process
contig00001-orf00001	#N/A	ATP binding	glutathione biosynthetic process
contig00001-orf00003	membrane	diacylglycerol kinase activity	phospholipid biosynthetic process
contig00001-orf00008	#N/A	long-chain-fatty-acid-CoA ligase activity	metabolic process
contig00001-orf00010	#N/A	ATP binding	#N/A
contig00001-orf00012	#N/A	guanosine-3',5'-bis(diphosphate) 3'-diphosp...	guanosine tetraphosphate metabolic process
contig00001-orf00013	RNA polymerase complex	DNA binding	transcription, DNA-dependent
contig00001-orf00015	cytoplasm	ATP binding	purine nucleotide metabolic process
contig00001-orf00016	cytoplasm	adenine phosphoribosyltransferase activity	adenine salvage
contig00001-orf00019	periplasmic space	hydrolase activity, hydrolyzing O-glycosyl ...	#N/A
contig00001-orf00020	#N/A	DNA binding	DNA integration
contig00002-orf00003	#N/A	DNA topoisomerase activity	DNA replication initiation
contig00003-orf00001	#N/A	DNA binding	DNA integration
contig00004-orf00003	integral to membrane	transporter activity	transport
contig00004-orf00006	#N/A	ATP binding	NAD biosynthetic process
contig00004-orf00008	integral to membrane	ATP binding	ATP biosynthetic process
contig00005-orf00001	chromosome	ATP binding	DNA recombination
contig00005-orf00002	cytoplasm	acetate kinase activity	organic acid metabolic process
contig00005-orf00008	#N/A	#N/A	transmembrane transport
contig00006-orf00007	#N/A	metalloendopeptidase activity	cell wall macromolecule catabolic process
contig00006-orf00009	#N/A	ATP binding	gluconeogenesis
contig00007-orf00001	cytoplasm	DNA binding	cell cycle
contig00008-orf00005	#N/A	binding	fatty acid biosynthetic process
contig00008-orf00008	integral to membrane	ion channel activity	ion transport
contig00008-orf00022	membrane	sodium:amino acid symporter activity	sodium ion transport
contig00008-orf00032	#N/A	lyase activity	pseudouridine synthesis
contig00008-orf00039	cytoplasm	ribonuclease activity	RNA processing
contig00008-orf00043	integral to membrane	#N/A	transmembrane transport
contig00008-orf00046	#N/A	#N/A	transmembrane transport
contig00008-orf00048	ribosome	rRNA binding	translation
contig00008-orf00049	ribosome	rRNA binding	translation
contig00008-orf00053	small ribosomal subunit	rRNA binding	translation
contig00008-orf00054	large ribosomal subunit	rRNA binding	translation
contig00008-orf00055	small ribosomal subunit	rRNA binding	translation
contig00008-orf00056	ribosome	rRNA binding	translation
contig00008-orf00057	ribosome	structural constituent of ribosome	translation

Query	Cellular Component	Molecular Function	Biological Process
contig00008-orf00058	ribosome	structural constituent of ribosome	translation
contig00008-orf00059	ribosome	rRNA binding	translation
contig00008-orf00060	ribosome	rRNA binding	translation
contig00008-orf00062	ribosome	rRNA binding	translation
contig00008-orf00064	large ribosomal subunit	rRNA binding	translation
contig00008-orf00065	integral to membrane	P-P-bond-hydrolysis-driven protein transmem...	protein transport
contig00008-orf00066	ribosome	rRNA binding	translation
contig00008-orf00067	#N/A	DNA binding	transcription, DNA-dependent
contig00008-orf00070	#N/A	binding	metabolic process
contig00008-orf00071	integral to membrane	protein-S-isoprenylcysteine O-methyltransfe...	C-terminal protein amino acid methylation
contig00008-orf00075	#N/A	magnesium ion binding	thiamin biosynthetic process
contig00008-orf00076	#N/A	oxidoreductase activity	oxidation reduction
contig00008-orf00079	cytoplasm	ATP binding	cysteinyl-tRNA aminoacylation
contig00008-orf00080	#N/A	#N/A	sulfur metabolic process
contig00008-orf00081	cytoplasm	catalytic activity	thiamin biosynthetic process
contig00008-orf00083	intracellular	3'-5' exonuclease activity	DNA replication
contig00008-orf00086	integral to membrane	sodium:hydrogen antiporter activity	regulation of pH
contig00008-orf00091	#N/A	protein-L-isoaspartate (D-aspartate) O-meth...	protein modification process
contig00008-orf00096	cytoplasm	aspartic-type endopeptidase activity	gluconeogenesis
contig00008-orf00097	integral to membrane	P-P-bond-hydrolysis-driven protein transmem...	protein secretion
contig00008-orf00098	#N/A	DNA binding	DNA integration
contig00008-orf00100	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00008-orf00102	membrane	#N/A	#N/A
contig00008-orf00104	signal recognition particle	7S RNA binding	SRP-dependent cotranslational protein targe...
contig00008-orf00106	membrane	#N/A	respiratory chain complex IV assembly
contig00009-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00009-orf00005	#N/A	ATP binding	#N/A
contig00009-orf00006	#N/A	helicase activity	#N/A
contig00010-orf00001	#N/A	DNA binding	DNA integration
contig00010-orf00007	#N/A	DNA binding	regulation of transcription, DNA-dependent
contig00010-orf00009	mitochondrion	3'-5'-exoribonuclease activity	mRNA catabolic process
contig00010-orf00012	#N/A	hydrolase activity	#N/A
contig00010-orf00013	#N/A	hydrolase activity	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00010-orf00018	#N/A	phosphorylase activity	carbohydrate metabolic process
contig00010-orf00020	#N/A	cation binding	glycogen catabolic process
contig00010-orf00022	membrane	protein transporter activity	protein secretion
contig00010-orf00024	#N/A	transporter activity	transport
contig00010-orf00025	#N/A	anthranilate phosphoribosyltransferase acti...	tryptophan biosynthetic process
contig00010-orf00027	#N/A	anthranilate synthase activity	biosynthetic process
contig00010-orf00032	#N/A	phosphoribosyl-ATP diphosphatase activity	histidine biosynthetic process
contig00010-orf00035	#N/A	DNA (cytosine-5-)-methyltransferase activity	DNA methylation
contig00010-orf00038	cytoplasm	imidazoleglycerol-phosphate dehydratase act...	histidine biosynthetic process
contig00010-orf00039	#N/A	single-stranded DNA binding	DNA replication
contig00010-orf00040	cell outer membrane	receptor activity	transport
contig00010-orf00042	#N/A	exonuclease activity	#N/A
contig00010-orf00050	#N/A	ATP binding	DNA modification
contig00010-orf00055	#N/A	sequence-specific DNA binding	#N/A
contig00010-orf00061	#N/A	ATP binding	#N/A
contig00010-orf00065	#N/A	4 iron, 4 sulfur cluster binding	double-strand break repair via homologous r...
contig00010-orf00067	#N/A	magnesium ion binding	DNA recombination
contig00010-orf00088	chromosome	ATP binding	DNA topological change
contig00010-orf00101	#N/A	ATP binding	#N/A
contig00010-orf00102	membrane	#N/A	unidirectional conjugation
contig00010-orf00103	#N/A	DNA binding	DNA integration
contig00010-orf00104	cell outer membrane	#N/A	#N/A
contig00010-orf00111	#N/A	ATP binding	#N/A
contig00010-orf00113	#N/A	metal ion binding	oxidation reduction
contig00010-orf00114	#N/A	ATP binding	DNA replication
contig00010-orf00120	type II protein secretion system complex	protein transporter activity	protein secretion by the type II secretion ...
contig00010-orf00123	cytoplasm	ATP binding	pantothenate biosynthetic process
contig00010-orf00129	#N/A	DNA binding	transposition, DNA-mediated
contig00010-orf00130	#N/A	DNA binding	transposition, DNA-mediated
contig00010-orf00136	#N/A	carbohydrate binding	carbohydrate metabolic process
contig00010-orf00138	#N/A	sequence-specific DNA binding	#N/A
contig00010-orf00139	#N/A	DNA binding	transposition, DNA-mediated
contig00011-orf00001	#N/A	transferase activity	#N/A
contig00011-orf00002	#N/A	transferase activity, transferring glycosyl...	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00011-orf00008	outer membrane-bounded periplasmic space	protein disulfide oxidoreductase activity	cell redox homeostasis
contig00011-orf00010	cytoplasm	GTP binding	#N/A
contig00011-orf00011	cytoplasm	ATP binding	cysteinyl-tRNA aminoacylation
contig00011-orf00012	#N/A	transferase activity	#N/A
contig00011-orf00014	ribosome	structural constituent of ribosome	translation
contig00011-orf00019	#N/A	oxidoreductase activity	cell redox homeostasis
contig00011-orf00020	#N/A	hydrolase activity	#N/A
contig00011-orf00022	cell outer membrane	iron ion binding	siderophore transport
contig00011-orf00024	cell outer membrane	iron ion binding	siderophore transport
contig00011-orf00026	cytoplasm	ATP binding	coenzyme A biosynthetic process
contig00011-orf00030	membrane	transferrin receptor activity	#N/A
contig00011-orf00031	#N/A	magnesium ion binding	nucleoside metabolic process
contig00011-orf00038	cytoplasm	FAD binding	tRNA wobble uridine modification
contig00011-orf00041	cytoplasm	ATP binding	cellular amino acid biosynthetic process
contig00011-orf00045	small ribosomal subunit	structural constituent of ribosome	translation
contig00011-orf00048	#N/A	5-formyltetrahydrofolate cyclo-ligase activity	folic acid and derivative biosynthetic process
contig00011-orf00049	#N/A	N-acetyltransferase activity	metabolic process
contig00011-orf00057	cell outer membrane	#N/A	Gram-negative-bacterium-type cell outer mem...
contig00011-orf00058	#N/A	peptidyl-prolyl cis-trans isomerase activity	protein folding
contig00011-orf00063	integral to membrane	signal transducer activity	signal transduction
contig00011-orf00068	membrane	catalytic activity	#N/A
contig00011-orf00069	#N/A	carboxylesterase activity	#N/A
contig00011-orf00070	#N/A	peptidase activity	proteolysis
contig00011-orf00072	cytoplasm	ATP binding	DNA replication
contig00011-orf00075	cytoplasm	ATP binding	leucyl-tRNA aminoacylation
contig00011-orf00078	#N/A	Type II site-specific deoxyribonuclease act...	#N/A
contig00011-orf00082	#N/A	DNA binding	DNA methylation
contig00011-orf00083	#N/A	DNA binding	DNA methylation
contig00011-orf00084	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00011-orf00087	#N/A	acetaldehyde dehydrogenase (acetylating) ac...	alcohol metabolic process
contig00011-orf00088	#N/A	DNA binding	transposition, DNA-mediated
contig00011-orf00094	integral to membrane	glutamate:sodium symporter activity	L-glutamate transport

Query	Cellular Component	Molecular Function	Biological Process
contig00011-orf00095	membrane	bile acid:sodium symporter activity	sodium ion transport
contig00011-orf00102	small ribosomal subunit	structural constituent of ribosome	translation
contig00012-orf00001	#N/A	FAD binding	oxidation reduction
contig00012-orf00002	integral to plasma membrane	#N/A	#N/A
contig00012-orf00003	#N/A	transferase activity	isoprenoid biosynthetic process
contig00012-orf00005	ribosome	rRNA binding	translation
contig00012-orf00007	ribosome	structural constituent of ribosome	translation
contig00012-orf00010	#N/A	cytochrome-c peroxidase activity	oxidation reduction
contig00012-orf00013	#N/A	transferase activity	#N/A
contig00012-orf00015	cytoplasm	#N/A	barrier septum formation
contig00012-orf00017	ribosome	structural constituent of ribosome	translation
contig00012-orf00018	ribosome	structural constituent of ribosome	translation
contig00012-orf00022	integral to membrane	binding	metabolic process
contig00013-orf00001	#N/A	DNA binding	DNA integration
contig00013-orf00002	#N/A	DNA binding	DNA integration
contig00013-orf00004	#N/A	peptidyl-prolyl cis-trans isomerase activity	protein folding
contig00013-orf00009	integral to membrane	ATP binding	cell cycle
contig00013-orf00012	integral to plasma membrane	neurotransmitter:sodium symporter activity	neurotransmitter transport
contig00013-orf00013	membrane	#N/A	#N/A
contig00014-orf00005	cytoplasm	catalytic activity	Mo-molybdopterin cofactor biosynthetic process
contig00015-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00016-orf00003	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00016-orf00004	cell outer membrane	#N/A	#N/A
contig00016-orf00006	cytoplasm	ATP binding	selenocysteine biosynthetic process
contig00016-orf00009	ribosome	rRNA binding	translation
contig00016-orf00010	ribosome	rRNA binding	translation
contig00016-orf00013	#N/A	hydrolase activity	#N/A
contig00016-orf00015	#N/A	carbohydrate binding	carbohydrate metabolic process
contig00016-orf00017	DNA polymerase III complex	ATP binding	DNA replication
contig00016-orf00021	#N/A	#N/A	DNA recombination
contig00016-orf00026	#N/A	amino acid binding	guanosine tetraphosphate metabolic process
contig00016-orf00030	#N/A	#N/A	thiamin biosynthetic process
contig00016-orf00035	cytoplasm	pyridoxine 5'-phosphate synthase activity	pyridoxine biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00017-orf00002	#N/A	binding	folic acid and derivative biosynthetic process
contig00017-orf00006	#N/A	hydrolase activity	metabolic process
contig00017-orf00007	#N/A	N-acetyltransferase activity	metabolic process
contig00017-orf00019	integral to membrane	acyltransferase activity	lipopolysaccharide core region biosynthetic...
contig00017-orf00021	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00017-orf00024	intracellular	DNA binding	DNA repair
contig00018-orf00010	outer membrane	#N/A	pathogenesis
contig00020-orf00001	#N/A	ATP binding	purine nucleotide biosynthetic process
contig00020-orf00005	integral to membrane	calcium ion binding	cell communication
contig00020-orf00007	#N/A	binding	extracellular polysaccharide biosynthetic p...
contig00021-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00021-orf00003	#N/A	binding	#N/A
contig00021-orf00004	membrane	bile acid:sodium symporter activity	sodium ion transport
contig00021-orf00010	membrane	#N/A	#N/A
contig00021-orf00022	#N/A	ATP binding	#N/A
contig00021-orf00027	cytoplasm	GTP binding	barrier septum formation
contig00021-orf00028	#N/A	#N/A	cell cycle
contig00021-orf00030	#N/A	#N/A	cell division
contig00021-orf00032	cell wall	ATP binding	cell wall organization
contig00021-orf00037	#N/A	methyltransferase activity	#N/A
contig00021-orf00042	integral to membrane	#N/A	cell cycle
contig00021-orf00045	membrane	ATP binding	peptidyl-histidine phosphorylation
contig00021-orf00047	#N/A	carbon-nitrogen ligase activity, with gluta...	#N/A
contig00021-orf00049	#N/A	carbon-nitrogen ligase activity, with gluta...	#N/A
contig00021-orf00052	cytoplasm	ATP binding	cell cycle
contig00021-orf00054	#N/A	binding	#N/A
contig00021-orf00055	#N/A	heme binding	oxygen transport
contig00022-orf00001	ribosome	structural constituent of ribosome	translation
contig00022-orf00002	ribosome	structural constituent of ribosome	translation
contig00022-orf00007	membrane	protein transporter activity	protein secretion
contig00022-orf00009	cytoplasm	acetate kinase activity	organic acid metabolic process
contig00022-orf00013	#N/A	aconitate hydratase activity	metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00022-orf00014	#N/A	aconitate hydratase activity	metabolic process
contig00022-orf00016	plasma membrane	#N/A	#N/A
contig00022-orf00019	integral to membrane	#N/A	#N/A
contig00022-orf00021	cytoplasm	lyase activity	cellular carbohydrate metabolic process
contig00022-orf00025	#N/A	catalytic activity	metabolic process
contig00023-orf00001	#N/A	acetyltransferase activity	metabolic process
contig00023-orf00003	membrane	#N/A	amino acid transport
contig00023-orf00004	#N/A	carbonate dehydratase activity	carbon utilization
contig00023-orf00005	#N/A	carbonate dehydratase activity	carbon utilization
contig00023-orf00007	integral to membrane	transporter activity	transmembrane transport
contig00023-orf00013	#N/A	dTDP-4-dehydrorhamnose 3,5-epimerase activity	lipopolysaccharide biosynthetic process
contig00023-orf00020	#N/A	nucleotidyltransferase activity	biosynthetic process
contig00023-orf00022	#N/A	FMN binding	benzene and derivative metabolic process
contig00023-orf00023	intracellular	transcription factor activity	negative regulation of transcription
contig00023-orf00025	#N/A	oxidoreductase activity	cell redox homeostasis
contig00023-orf00026	#N/A	glyceraldehyde-3-phosphate dehydrogenase (p...	glucose metabolic process
contig00023-orf00030	#N/A	aldehyde-lyase activity	aromatic amino acid family biosynthetic pro...
contig00023-orf00034	#N/A	4 iron, 4 sulfur cluster binding	tricarboxylic acid cycle
contig00023-orf00036	#N/A	ATP binding	protein folding
contig00023-orf00040	#N/A	serine-type D-Ala-D-Ala carboxypeptidase ac...	proteolysis
contig00023-orf00041	membrane	metalloendopeptidase activity	proteolysis
contig00024-orf00005	cytoplasm	ATP binding	isoleucyl-tRNA aminoacylation
contig00024-orf00007	#N/A	#N/A	iron ion transport
contig00024-orf00010	#N/A	iron ion transmembrane transporter activity	high-affinity iron ion transport
contig00024-orf00012	integral to membrane	transporter activity	transport
contig00024-orf00014	#N/A	ATP binding	#N/A
contig00024-orf00016	#N/A	ATP binding	carbohydrate metabolic process
contig00024-orf00021	#N/A	binding	primary metabolic process
contig00024-orf00023	#N/A	DNA-directed RNA polymerase activity	regulation of transcription, DNA-dependent
contig00024-orf00024	#N/A	DNA-directed RNA polymerase activity	regulation of transcription, DNA-dependent
contig00024-orf00026	#N/A	ATP binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00024-orf00031	#N/A	3-deoxy-manno-octulosonate-8-phosphatase ac...	lipopolysaccharide biosynthetic process
contig00024-orf00032	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00024-orf00034	membrane	2 iron, 2 sulfur cluster binding	electron transport chain
contig00024-orf00035	integral to membrane	electron carrier activity	respiratory electron transport chain
contig00024-orf00036	#N/A	electron carrier activity	oxidation reduction
contig00024-orf00037	#N/A	binding	metabolic process
contig00024-orf00040	integral to membrane	transporter activity	transport
contig00024-orf00042	integral to membrane	transporter activity	transport
contig00024-orf00043	membrane	acyltransferase activity	#N/A
contig00024-orf00045	#N/A	ATP binding	#N/A
contig00024-orf00049	cytoplasm	isomerase activity	queuosine biosynthetic process
contig00025-orf00003	#N/A	ATP binding	DNA repair
contig00026-orf00003	#N/A	metal ion binding	cell adhesion
contig00026-orf00014	integral to membrane	ATP binding	proteolysis
contig00026-orf00016	#N/A	electron-transferring-flavoprotein dehydrog...	oxidation reduction
contig00026-orf00019	#N/A	electron carrier activity	oxidation reduction
contig00026-orf00020	integral to membrane	substrate-specific transmembrane transporte...	carbohydrate transport
contig00026-orf00021	#N/A	D-lactate dehydrogenase activity	lactate metabolic process
contig00026-orf00026	#N/A	acyl-CoA dehydrogenase activity	oxidation reduction
contig00026-orf00029	#N/A	electron carrier activity	electron transport chain
contig00026-orf00031	#N/A	acyltransferase activity	metabolic process
contig00026-orf00032	#N/A	acyl carrier activity	#N/A
contig00027-orf00003	#N/A	DNA topoisomerase activity	DNA replication initiation
contig00027-orf00005	outer membrane-bounded periplasmic space	protein transporter activity	protein transport
contig00027-orf00014	#N/A	phosphoglycolate phosphatase activity	metabolic process
contig00027-orf00015	#N/A	malate dehydrogenase (oxaloacetate-decarbox...	oxidation reduction
contig00027-orf00016	#N/A	ATP binding	dTDP biosynthetic process
contig00027-orf00019	outer membrane-bounded periplasmic space	protein binding	cell wall organization
contig00027-orf00020	membrane	transporter activity	transport
contig00027-orf00024	#N/A	coenzyme binding	oxidation reduction
contig00027-orf00031	chromosome	ATP binding	DNA topological change
contig00027-orf00033	#N/A	hydrolase activity, acting on acid anhydrid...	#N/A
contig00027-orf00035	membrane	transporter activity	transport

Query	Cellular Component	Molecular Function	Biological Process
contig00027-orf00038	membrane	sodium:amino acid symporter activity	sodium ion transport
contig00027-orf00039	#N/A	DNA binding	DNA integration
contig00028-orf00001	#N/A	DNA binding	DNA integration
contig00028-orf00002	cytoplasm	unfolded protein binding	protein folding
contig00028-orf00003	#N/A	electron carrier activity	cell redox homeostasis
contig00028-orf00006	cytoplasm	ribonuclease activity	RNA processing
contig00028-orf00008	intracellular	DNA binding	regulation of transcription, DNA-dependent
contig00028-orf00011	membrane	ATP binding	peptidyl-histidine phosphorylation
contig00028-orf00013	#N/A	3-oxoacyl-[acyl-carrier-protein] reductase ...	fatty acid biosynthetic process
contig00028-orf00017	#N/A	transferase activity	#N/A
contig00028-orf00018	#N/A	transferase activity	#N/A
contig00028-orf00020	#N/A	[acyl-carrier-protein] S-malonyltransferase...	fatty acid biosynthetic process
contig00028-orf00023	#N/A	DNA binding	regulation of transcription, DNA-dependent
contig00028-orf00027	cytoplasm	3-oxoacyl-[acyl-carrier-protein] synthase a...	fatty acid biosynthetic process
contig00028-orf00029	#N/A	methyltransferase activity	rRNA processing
contig00028-orf00030	#N/A	inositol-1(or 4)-monophosphatase activity	#N/A
contig00028-orf00033	#N/A	glutathione transferase activity	#N/A
contig00028-orf00040	anchored to membrane	#N/A	#N/A
contig00028-orf00044	#N/A	DNA binding	transposition, DNA-mediated
contig00028-orf00045	plasma membrane	#N/A	#N/A
contig00028-orf00047	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00028-orf00050	#N/A	FAD binding	oxidation reduction
contig00028-orf00052	integral to membrane	metalloendopeptidase activity	proteolysis
contig00028-orf00055	DNA polymerase III complex	DNA binding	DNA replication
contig00028-orf00056	#N/A	#N/A	Gram-negative-bacterium-type cell outer mem...
contig00028-orf00057	#N/A	2-isopropylmalate synthase activity	leucine biosynthetic process
contig00028-orf00058	cytoplasm	aminopeptidase activity	proteolysis
contig00028-orf00066	#N/A	proline dehydrogenase activity	glutamate biosynthetic process
contig00028-orf00067	integral to membrane	proline:sodium symporter activity	proline transport
contig00028-orf00070	integral to membrane	#N/A	ubiquinone biosynthetic process
contig00028-orf00079	#N/A	ATP binding	chlorophyll biosynthetic process
contig00028-orf00087	outer membrane-bounded periplasmic space	protein disulfide oxidoreductase activity	cell redox homeostasis

Query	Cellular Component	Molecular Function	Biological Process
contig00028-orf00089	integral to membrane	undecaprenyl-diphosphatase activity	cell wall organization
contig00028-orf00091	#N/A	methyltransferase activity	metabolic process
contig00028-orf00092	cytoplasm	#N/A	#N/A
contig00028-orf00094	large ribosomal subunit	structural constituent of ribosome	translation
contig00028-orf00095	#N/A	transferase activity	nucleoside metabolic process
contig00028-orf00101	cytoplasm	arginine-tRNA ligase activity	arginyl-tRNA aminoacylation
contig00028-orf00102	cytoplasm	ATP binding	glycyl-tRNA aminoacylation
contig00028-orf00105	#N/A	nucleic acid binding	#N/A
contig00029-orf00020	integral to membrane	NADH dehydrogenase (quinone) activity	oxidation reduction
contig00029-orf00021	#N/A	dihydrofolate reductase activity	glycine biosynthetic process
contig00029-orf00032	cytoplasm	UDP-N-acetylglucosamine 1-carboxyvinyltrans...	cell cycle
contig00029-orf00035	#N/A	N-acetyltransferase activity	metabolic process
contig00030-orf00002	cytoplasm	ATP binding	DNA repair
contig00030-orf00011	#N/A	electron carrier activity	#N/A
contig00031-orf00005	cytoplasm	arginine-tRNA ligase activity	arginyl-tRNA aminoacylation
contig00031-orf00007	integral to membrane	#N/A	#N/A
contig00031-orf00010	membrane	CDP-diacylglycerol-serine O-phosphatidyltra...	CDP-diacylglycerol metabolic process
contig00031-orf00014	cytoplasm	exodeoxyribonuclease VII activity	DNA catabolic process
contig00031-orf00016	integral to membrane	transporter activity	sodium ion transport
contig00032-orf00002	integral to membrane	transporter activity	transmembrane transport
contig00032-orf00005	#N/A	ATP binding	#N/A
contig00032-orf00006	periplasmic space	hydrolase activity, hydrolyzing O-glycosyl ...	metabolic process
contig00032-orf00008	integral to membrane	electron carrier activity	oxidation reduction
contig00032-orf00009	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00032-orf00011	#N/A	RNA binding	viral genome replication
contig00032-orf00012	integral to membrane	#N/A	transmembrane transport
contig00032-orf00013	integral to membrane	#N/A	transmembrane transport
contig00032-orf00016	#N/A	methyltransferase activity	metabolic process
contig00033-orf00003	#N/A	binding	#N/A
contig00033-orf00007	#N/A	DNA binding	transposition, DNA-mediated
contig00036-orf00006	#N/A	binding	oxidation reduction
contig00036-orf00008	#N/A	oxidoreductase activity	metabolic process
contig00036-orf00010	#N/A	geranylgeranyl-diphosphate geranylgeranyltr...	carotenoid biosynthetic process
contig00036-orf00011	#N/A	ATP binding	iron-sulfur cluster assembly
contig00036-orf00014	#N/A	2 iron, 2 sulfur cluster binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00036-orf00015	#N/A	arginine decarboxylase activity	arginine catabolic process
contig00036-orf00018	#N/A	methylenetetrahydrofolate reductase (NADPH)...	methionine biosynthetic process
contig00036-orf00020	#N/A	5-methyltetrahydropteroyltriglutamate-homoc...	methionine biosynthetic process
contig00036-orf00022	#N/A	purine-nucleoside phosphorylase activity	nucleoside metabolic process
contig00037-orf00002	membrane	#N/A	#N/A
contig00037-orf00008	membrane	sodium:amino acid symporter activity	sodium ion transport
contig00037-orf00009	#N/A	aldehyde dehydrogenase (NAD) activity	oxidation reduction
contig00037-orf00012	#N/A	lyase activity	metabolic process
contig00037-orf00013	#N/A	oxidoreductase activity	#N/A
contig00037-orf00014	#N/A	proline racemase activity	#N/A
contig00037-orf00016	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00038-orf00001	#N/A	transferase activity, transferring glycosyl...	nucleoside metabolic process
contig00039-orf00001	outer membrane	#N/A	pathogenesis
contig00039-orf00007	#N/A	metalloendopeptidase activity	proteolysis
contig00039-orf00012	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00039-orf00013	membrane	lipid binding	transport
contig00039-orf00019	cell outer membrane	protein transporter activity	establishment of competence for transformation
contig00039-orf00021	cytoplasm	3-dehydroquinate synthase activity	aromatic amino acid family biosynthetic pro...
contig00039-orf00023	cytoplasm	N-acetyl-gamma-glutamyl-phosphate reductase...	arginine biosynthetic process
contig00039-orf00026	#N/A	4 iron, 4 sulfur cluster binding	rRNA processing
contig00039-orf00030	#N/A	GTP binding	small GTPase mediated signal transduction
contig00040-orf00001	#N/A	ATP binding	DNA recombination
contig00040-orf00005	#N/A	ATP binding	RNA repair
contig00040-orf00006	membrane	#N/A	#N/A
contig00040-orf00012	integral to membrane	ATP binding	transmembrane transport
contig00040-orf00014	membrane	receptor activity	transport
contig00040-orf00015	#N/A	ferredoxin-NADP+ reductase activity	oxidation reduction
contig00041-orf00001	#N/A	binding	#N/A
contig00041-orf00010	#N/A	binding	#N/A
contig00042-orf00004	#N/A	DNA topoisomerase activity	DNA replication initiation
contig00042-orf00007	integral to membrane	transporter activity	oligopeptide transport
contig00042-orf00013	#N/A	serine-type endopeptidase activity	proteolysis

Query	Cellular Component	Molecular Function	Biological Process
contig00042-orf00016	#N/A	ATP binding	DNA recombination
contig00042-orf00017	#N/A	hydrolase activity	#N/A
contig00042-orf00020	outer membrane	#N/A	#N/A
contig00044-orf00001	anchored to membrane	transferrin receptor activity	#N/A
contig00044-orf00003	cytoplasm	exodeoxyribonuclease VII activity	DNA catabolic process
contig00044-orf00006	#N/A	geranyltranstransferase activity	isoprenoid biosynthetic process
contig00044-orf00013	cytoplasm	GTP binding	tRNA modification
contig00044-orf00016	Holliday junction helicase complex	ATP binding	DNA recombination
contig00044-orf00020	#N/A	ATP binding	cobalamin biosynthetic process
contig00044-orf00021	#N/A	DNA binding	transposition, DNA-mediated
contig00044-orf00022	#N/A	aminopeptidase activity	cellular process
contig00044-orf00024	membrane	iron ion transmembrane transporter activity	iron ion transport
contig00044-orf00028	cytoplasm	D-sedoheptulose 7-phosphate isomerase activity	lipopolysaccharide core region biosynthetic...
contig00044-orf00030	#N/A	DNA binding	#N/A
contig00044-orf00031	#N/A	methyltransferase activity	metabolic process
contig00044-orf00037	intracellular	DNA binding	DNA repair
contig00044-orf00042	integral to membrane	metal ion transmembrane transporter activity	transmembrane transport
contig00044-orf00046	#N/A	sequence-specific DNA binding	#N/A
contig00044-orf00048	cytoplasm	ATP binding	valyl-tRNA aminoacylation
contig00044-orf00050	#N/A	indole-3-glycerol-phosphate synthase activity	tryptophan biosynthetic process
contig00044-orf00052	#N/A	DNA binding	DNA integration
contig00044-orf00053	#N/A	DNA binding	#N/A
contig00045-orf00005	#N/A	nicotinamidase activity	metabolic process
contig00045-orf00006	#N/A	transferase activity, transferring glycosyl...	lipopolysaccharide biosynthetic process
contig00045-orf00008	#N/A	electron carrier activity	#N/A
contig00045-orf00009	#N/A	electron carrier activity	#N/A
contig00045-orf00012	#N/A	ATP binding	purine base biosynthetic process
contig00045-orf00013	cytoplasm	RNA binding	rRNA processing
contig00045-orf00017	intracellular	ATP binding	DNA recombination
contig00045-orf00018	#N/A	DNA binding	DNA methylation
contig00045-orf00019	#N/A	methyltransferase activity	methylation
contig00045-orf00020	#N/A	ribonuclease activity	#N/A
contig00045-orf00025	#N/A	acyl-CoA dehydrogenase activity	oxidation reduction
contig00045-orf00028	#N/A	ATP binding	nucleobase, nucleoside, nucleotide and nucl...

Query	Cellular Component	Molecular Function	Biological Process
contig00045-orf00032	#N/A	sigma factor activity	regulation of transcription, DNA-dependent
contig00045-orf00036	#N/A	electron carrier activity	#N/A
contig00045-orf00042	#N/A	RNA binding	RNA processing
contig00045-orf00044	#N/A	#N/A	nucleoside metabolic process
contig00045-orf00048	membrane	transporter activity	sodium ion transport
contig00045-orf00069	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00045-orf00075	#N/A	(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imida...	IMP biosynthetic process
contig00045-orf00079	integral to membrane	amino acid transmembrane transporter activity	amino acid transport
contig00045-orf00081	outer membrane	#N/A	#N/A
contig00045-orf00083	membrane	#N/A	transmembrane transport
contig00045-orf00090	integral to membrane	#N/A	#N/A
contig00045-orf00092	plasma membrane	4 iron, 4 sulfur cluster binding	oxidation reduction
contig00045-orf00093	plasma membrane	NADH dehydrogenase (ubiquinone) activity	oxidation reduction
contig00045-orf00095	extrinsic to membrane	NAD or NADH binding	oxidation reduction
contig00045-orf00096	#N/A	NAD or NADH binding	oxidation reduction
contig00045-orf00097	#N/A	4 iron, 4 sulfur cluster binding	oxidation reduction
contig00045-orf00101	intracellular	nuclease activity	DNA repair
contig00045-orf00104	membrane	4 iron, 4 sulfur cluster binding	ATP synthesis coupled electron transport
contig00045-orf00105	integral to membrane	NADH dehydrogenase (quinone) activity	oxidation reduction
contig00045-orf00109	#N/A	NADH dehydrogenase (ubiquinone) activity	oxidation reduction
contig00045-orf00110	integral to membrane	NADH dehydrogenase (quinone) activity	ATP synthesis coupled electron transport
contig00045-orf00120	#N/A	chorismate mutase activity	chorismate metabolic process
contig00045-orf00123	integral to membrane	NADH dehydrogenase (ubiquinone) activity	mitochondrial electron transport, NADH to u...
contig00045-orf00125	integral to membrane	NADH dehydrogenase (ubiquinone) activity	ATP synthesis coupled electron transport
contig00045-orf00130	cytoplasm	ATP binding	proline biosynthetic process
contig00045-orf00140	integral to membrane	#N/A	#N/A
contig00045-orf00141	integral to membrane	#N/A	#N/A
contig00045-orf00145	cytoplasm	#N/A	translational termination
contig00045-orf00146	#N/A	di-trans,poly-cis-decaprenylcistransferase ...	cell cycle
contig00045-orf00148	integral to membrane	phosphatidate cytidylyltransferase activity	#N/A
contig00045-orf00157	outer membrane	#N/A	#N/A
contig00045-orf00159	#N/A	protein binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00045-orf00162	cytoplasm	hydro-lyase activity	fatty acid biosynthetic process
contig00045-orf00170	cytoplasm	4-hydroxythreonine-4-phosphate dehydrogenas...	oxidation reduction
contig00045-orf00174	#N/A	arsenate reductase (glutaredoxin) activity	oxidation reduction
contig00045-orf00178	#N/A	oxidoreductase activity	cell redox homeostasis
contig00045-orf00180	#N/A	ATP binding	cell division
contig00045-orf00181	integral to membrane	#N/A	cell cycle
contig00045-orf00184	#N/A	ATP binding	mismatch repair
contig00045-orf00196	intracellular	ATP binding	transport
contig00045-orf00199	intracellular	ATP binding	transport
contig00045-orf00203	#N/A	binding	oxidation reduction
contig00045-orf00204	membrane	#N/A	#N/A
contig00045-orf00206	#N/A	zinc ion binding	#N/A
contig00046-orf00003	#N/A	binding	regulation of transcription, DNA-dependent
contig00046-orf00006	#N/A	lactaldehyde dehydrogenase activity	oxidation reduction
contig00046-orf00010	cytoplasm	ATP binding	lysyl-tRNA aminoacylation
contig00046-orf00012	#N/A	#N/A	barrier septum formation
contig00046-orf00013	#N/A	ATPase activity	cobalamin biosynthetic process
contig00046-orf00015	#N/A	#N/A	cell cycle
contig00046-orf00017	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00046-orf00021	cytoplasm	binding	diaminopimelate biosynthetic process
contig00046-orf00022	outer membrane	#N/A	#N/A
contig00046-orf00023	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00046-orf00027	cytoplasm	acyltransferase activity	protein catabolic process
contig00046-orf00031	#N/A	peptidyl-prolyl cis-trans isomerase activity	protein folding
contig00046-orf00034	integral to membrane	#N/A	barrier septum formation
contig00046-orf00037	#N/A	#N/A	cell wall macromolecule catabolic process
contig00046-orf00039	#N/A	pseudouridine synthase activity	tRNA pseudouridine synthesis
contig00046-orf00043	#N/A	ribose-5-phosphate isomerase activity	carbohydrate metabolic process
contig00046-orf00052	chromosome	ATP binding	DNA topological change
contig00046-orf00055	#N/A	4 iron, 4 sulfur cluster binding	gluconeogenesis
contig00046-orf00058	#N/A	4 iron, 4 sulfur cluster binding	gluconeogenesis
contig00046-orf00060	cytoplasm	DNA binding	cell cycle

Query	Cellular Component	Molecular Function	Biological Process
contig00046-orf00063	#N/A	fructose-bisphosphate aldolase activity	glycolysis
contig00046-orf00067	#N/A	two-component response regulator activity	regulation of transcription, DNA-dependent
contig00046-orf00069	integral to membrane	protoheme IX farnesyltransferase activity	heme O biosynthetic process
contig00046-orf00070	#N/A	metalloendopeptidase activity	proteolysis
contig00046-orf00071	#N/A	N-acetyltransferase activity	N-terminal protein amino acid acetylation
contig00046-orf00080	integral to membrane	#N/A	#N/A
contig00046-orf00081	membrane	#N/A	#N/A
contig00047-orf00003	cell outer membrane	iron ion binding	siderophore transport
contig00047-orf00005	#N/A	#N/A	carbohydrate transport
contig00047-orf00007	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00047-orf00012	integral to membrane	voltage-gated chloride channel activity	chloride transport
contig00047-orf00019	#N/A	#N/A	Mo-molybdopterin cofactor biosynthetic process
contig00047-orf00023	#N/A	ATP binding	biosynthetic process
contig00047-orf00027	cytoplasm	ATP binding	coenzyme A biosynthetic process
contig00047-orf00033	#N/A	binding	#N/A
contig00047-orf00034	integral to membrane	sodium:hydrogen antiporter activity	regulation of pH
contig00047-orf00037	membrane	#N/A	transport
contig00047-orf00041	intracellular	catalytic activity	DNA repair
contig00048-orf00001	intracellular	GTP binding	translational elongation
contig00048-orf00003	small ribosomal subunit	rRNA binding	translation
contig00048-orf00004	small ribosomal subunit	rRNA binding	translation
contig00048-orf00007	#N/A	DNA binding	transcription, DNA-dependent
contig00048-orf00011	ribosome	structural constituent of ribosome	translation
contig00048-orf00012	ribosome	structural constituent of ribosome	ribosome biogenesis
contig00048-orf00013	large ribosomal subunit	rRNA binding	regulation of translation
contig00048-orf00015	#N/A	transcription elongation regulator activity	positive regulation of RNA elongation from ...
contig00048-orf00016	integral to membrane	P-P-bond-hydrolysis-driven protein transmem...	protein secretion
contig00049-orf00001	integral to plasma membrane	neurotransmitter:sodium symporter activity	neurotransmitter transport
contig00049-orf00003	#N/A	#N/A	thiamin biosynthetic process
contig00049-orf00005	cytoplasm	translation release factor activity, codon ...	translational termination
contig00049-orf00006	integral to membrane	transporter activity	transport
contig00049-orf00008	#N/A	ATP binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00049-orf00009	#N/A	cyanate hydratase activity	cyanate metabolic process
contig00049-orf00010	cytoplasm	coproporphyrinogen oxidase activity	oxidation reduction
contig00049-orf00011	cytoplasm	coproporphyrinogen oxidase activity	oxidation reduction
contig00049-orf00012	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00049-orf00014	#N/A	catalytic activity	cell division
contig00049-orf00021	intracellular	DNA binding	DNA repair
contig00049-orf00022	Gram-negative-bacterium-type cell wall	protein binding	barrier septum formation
contig00049-orf00023	#N/A	N-acetylmuramoyl-L-alanine amidase activity	peptidoglycan catabolic process
contig00049-orf00026	#N/A	5'-3' exonuclease activity	DNA recombination
contig00049-orf00035	membrane	transporter activity	transport
contig00049-orf00036	#N/A	#N/A	response to stress
contig00049-orf00039	#N/A	binding	metabolic process
contig00049-orf00041	integral to membrane	transporter activity	transport
contig00049-orf00043	cytoplasm	#N/A	cell cycle
contig00049-orf00046	integral to membrane	branched-chain aliphatic amino acid transme...	branched-chain aliphatic amino acid transport
contig00050-orf00002	cytoplasm	ATP binding	nucleotide-excision repair
contig00050-orf00003	#N/A	electron carrier activity	cell redox homeostasis
contig00050-orf00006	#N/A	ATP binding	peptide transport
contig00050-orf00008	#N/A	ligase activity	metabolic process
contig00050-orf00011	integral to membrane	transporter activity	transport
contig00050-orf00014	integral to membrane	transporter activity	transport
contig00050-orf00025	#N/A	diacylglycerol kinase activity	activation of protein kinase C activity by ...
contig00050-orf00031	integral to membrane	#N/A	#N/A
contig00050-orf00041	#N/A	FAD binding	#N/A
contig00050-orf00045	#N/A	isomerase activity	protein folding
contig00050-orf00049	#N/A	1,4-alpha-glucan branching enzyme activity	glycogen biosynthetic process
contig00051-orf00008	#N/A	nucleic acid binding	DNA metabolic process
contig00051-orf00009	membrane	#N/A	unidirectional conjugation
contig00051-orf00010	#N/A	single-stranded DNA binding	DNA replication
contig00051-orf00014	cytoplasm	ATP binding	pathogenesis
contig00051-orf00015	#N/A	#N/A	unidirectional conjugation
contig00051-orf00020	integral to membrane	#N/A	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00051-orf00021	outer membrane-bounded periplasmic space	transporter activity	transport
contig00051-orf00022	#N/A	#N/A	conjugation with cellular fusion
contig00051-orf00023	extracellular region	metalloendopeptidase activity	proteolysis
contig00051-orf00026	#N/A	ATP binding	#N/A
contig00051-orf00028	integral to membrane	#N/A	cobalamin biosynthetic process
contig00051-orf00034	intracellular	ATP binding	transport
contig00051-orf00040	#N/A	GTP binding	#N/A
contig00051-orf00041	integral to membrane	serine-type peptidase activity	proteolysis
contig00051-orf00044	plasma membrane	#N/A	#N/A
contig00051-orf00046	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00051-orf00049	integral to membrane	transporter activity	transport
contig00051-orf00051	#N/A	ATP binding	#N/A
contig00051-orf00054	#N/A	hydrolase activity	#N/A
contig00051-orf00060	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00051-orf00063	#N/A	L-threonine ammonia-lyase activity	isoleucine biosynthetic process
contig00051-orf00064	#N/A	L-threonine ammonia-lyase activity	isoleucine biosynthetic process
contig00051-orf00067	#N/A	serine-type D-Ala-D-Ala carboxypeptidase ac...	proteolysis
contig00051-orf00071	#N/A	DNA binding	transposition, DNA-mediated
contig00051-orf00073	cytoplasm	ATP binding	tRNA processing
contig00051-orf00075	integral to membrane	ATP binding	ATP biosynthetic process
contig00051-orf00078	membrane	ATP binding	ATP biosynthetic process
contig00051-orf00079	cytoplasm	nucleotide binding	regulation of transcription, DNA-dependent
contig00051-orf00080	#N/A	#N/A	response to stress
contig00051-orf00083	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00051-orf00084	#N/A	FMN binding	metabolic process
contig00051-orf00085	#N/A	FMN binding	metabolic process
contig00051-orf00087	#N/A	malate dehydrogenase (oxaloacetate-decarbox...	malate metabolic process
contig00051-orf00088	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00051-orf00090	#N/A	oxidoreductase activity	oxidation reduction
contig00051-orf00091	#N/A	morphine 6-dehydrogenase activity	oxidation reduction
contig00051-orf00092	#N/A	ferrous iron binding	cellular aromatic compound metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00051-orf00093	cytoplasm	dihydroorotate oxidase activity	de novo' pyrimidine base biosynthetic process
contig00051-orf00096	cytoplasm	N2-acetyl-L-ornithine:2-oxoglutarate 5-amin...	arginine biosynthetic process
contig00051-orf00102	#N/A	cofactor binding	phosphatidylethanolamine biosynthetic process
contig00051-orf00106	cytoplasm	ATP binding	nucleotide-excision repair
contig00051-orf00107	chromosome	ATP binding	#N/A
contig00052-orf00001	#N/A	glyceraldehyde-3-phosphate dehydrogenase (p...	glucose metabolic process
contig00052-orf00010	#N/A	acyltransferase activity	#N/A
contig00052-orf00013	#N/A	NADP or NADPH binding	D-gluconate metabolic process
contig00052-orf00018	#N/A	glycerate dehydrogenase activity	oxidation reduction
contig00052-orf00025	#N/A	transporter activity	transport
contig00052-orf00028	#N/A	#N/A	transmembrane transport
contig00052-orf00031	#N/A	#N/A	conjugation with cellular fusion
contig00052-orf00036	membrane	protein transporter activity	protein secretion
contig00052-orf00037	integral to membrane	ATP binding	proteolysis
contig00052-orf00039	integral to membrane	ATP binding	proteolysis
contig00052-orf00041	cytoplasm	ATP binding	glutamyl-tRNA aminoacylation
contig00052-orf00043	#N/A	iron ion transmembrane transporter activity	high-affinity iron ion transport
contig00052-orf00046	cytoplasm	ATP binding	glutamyl-tRNA aminoacylation
contig00052-orf00047	#N/A	metalloendopeptidase activity	proteolysis
contig00052-orf00049	#N/A	metalloendopeptidase activity	proteolysis
contig00052-orf00053	integral to membrane	ATP binding	transmembrane transport
contig00052-orf00057	#N/A	N-acetyltransferase activity	metabolic process
contig00052-orf00058	cell surface	magnesium ion binding	glycolysis
contig00052-orf00070	#N/A	ATP binding	#N/A
contig00052-orf00074	#N/A	hydrolase activity	#N/A
contig00052-orf00076	#N/A	carbonate dehydratase activity	carbon utilization
contig00052-orf00078	#N/A	ATP binding	NAD biosynthetic process
contig00052-orf00082	cytoplasm	rRNA (pseudouridine-N3-)-methyltransferase ...	rRNA methylation
contig00052-orf00090	#N/A	adenylate cyclase activity	cAMP biosynthetic process
contig00052-orf00094	outer membrane	hydrolase activity, hydrolyzing O-glycosyl ...	peptidoglycan turnover
contig00052-orf00095	outer membrane	hydrolase activity, hydrolyzing O-glycosyl ...	peptidoglycan turnover
contig00052-orf00096	membrane	#N/A	transmembrane transport
contig00052-orf00101	#N/A	iron ion binding	oxidation reduction
contig00053-orf00010	#N/A	ATP binding	folic acid and derivative biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00053-orf00011	polyphosphate kinase complex	ATP binding	polyphosphate biosynthetic process
contig00053-orf00016	#N/A	cation transmembrane transporter activity	cation transport
contig00053-orf00021	#N/A	#N/A	carbohydrate transport
contig00053-orf00025	#N/A	carbohydrate binding	carbohydrate metabolic process
contig00053-orf00028	#N/A	beta-phosphoglucomutase activity	carbohydrate metabolic process
contig00053-orf00030	plasma membrane	#N/A	#N/A
contig00053-orf00040	outer membrane-bounded periplasmic space	transporter activity	transport
contig00055-orf00007	membrane	transporter activity	transport
contig00055-orf00010	integral to membrane	#N/A	#N/A
contig00055-orf00013	integral to membrane	transporter activity	transmembrane transport
contig00055-orf00018	#N/A	1-acylglycerol-3-phosphate O-acyltransferas...	metabolic process
contig00055-orf00021	cytoplasm	ATP binding	protein refolding
contig00055-orf00023	cytoplasm	ATP binding	protein folding
contig00055-orf00026	cell outer membrane	iron ion binding	siderophore transport
contig00055-orf00028	#N/A	iron ion transmembrane transporter activity	high-affinity iron ion transport
contig00055-orf00029	#N/A	2,3-bisphosphoglycerate-dependent phosphogl...	glycolysis
contig00055-orf00032	#N/A	carboxy-lyase activity	#N/A
contig00055-orf00033	#N/A	pyridoxal phosphate binding	biosynthetic process
contig00055-orf00035	#N/A	catalase activity	hydrogen peroxide catabolic process
contig00055-orf00039	#N/A	5-amino-6-(5-phosphoribosylamino)uracil red...	oxidation reduction
contig00055-orf00040	#N/A	hydrolase activity	#N/A
contig00055-orf00042	#N/A	ATP binding	regulation of transcription
contig00055-orf00044	cytoplasm	3-deoxy-8-phosphooctulonate synthase activity	keto-3-deoxy-D-manno-octulosonic acid biosy...
contig00055-orf00045	cytoplasm	aspartate 1-decarboxylase activity	alanine biosynthetic process
contig00055-orf00047	#N/A	#N/A	response to metal ion
contig00055-orf00049	membrane	iron ion transmembrane transporter activity	iron ion transport
contig00055-orf00052	#N/A	phosphatase activity	metabolic process
contig00055-orf00062	outer membrane-bounded periplasmic space	transporter activity	transport
contig00055-orf00065	nitrate reductase complex	electron carrier activity	nitrate metabolic process
contig00055-orf00066	#N/A	#N/A	Mo-molybdopterin cofactor biosynthetic process
contig00055-orf00068	#N/A	nucleic acid binding	#N/A
contig00056-orf00005	outer membrane	#N/A	pathogenesis
contig00056-orf00008	#N/A	translation initiation factor activity	translational initiation

Query	Cellular Component	Molecular Function	Biological Process
contig00056-orf00009	intracellular	nuclease activity	DNA repair
contig00056-orf00011	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00056-orf00012	#N/A	binding	metabolic process
contig00056-orf00015	#N/A	NAD or NADH binding	oxidation reduction
contig00056-orf00018	membrane	#N/A	polysaccharide biosynthetic process
contig00056-orf00023	#N/A	#N/A	biosynthetic process
contig00056-orf00025	#N/A	#N/A	biosynthetic process
contig00056-orf00026	#N/A	transferase activity	#N/A
contig00056-orf00028	#N/A	ATP binding	#N/A
contig00056-orf00030	#N/A	methionyl-tRNA formyltransferase activity	translation
contig00056-orf00031	#N/A	pyridoxal phosphate binding	#N/A
contig00056-orf00034	#N/A	binding	biosynthetic process
contig00056-orf00037	membrane	polysaccharide transmembrane transporter ac...	polysaccharide transport
contig00056-orf00039	#N/A	protein tyrosine phosphatase activity	protein amino acid dephosphorylation
contig00056-orf00040	membrane	cobyrinic acid a,c-diamide synthase activity	capsule polysaccharide biosynthetic process
contig00056-orf00041	membrane	#N/A	#N/A
contig00056-orf00042	integral to membrane	hydrolase activity	#N/A
contig00056-orf00043	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00056-orf00045	#N/A	binding	oxidation reduction
contig00056-orf00046	#N/A	oxidoreductase activity	oxidation reduction
contig00056-orf00048	integral to membrane	phospho-N-acetylmuramoyl-pentapeptide-trans...	peptidoglycan biosynthetic process
contig00056-orf00050	cytoplasm	ATP binding	cell cycle
contig00056-orf00054	#N/A	metalloendopeptidase activity	proteolysis
contig00056-orf00057	cytoplasm	ATP binding	cell cycle
contig00056-orf00061	integral to membrane	#N/A	cell cycle
contig00056-orf00067	extrinsic to membrane	dihydroorotate oxidase activity	de novo' pyrimidine base biosynthetic process
contig00056-orf00068	#N/A	phosphoglycolate phosphatase activity	metabolic process
contig00056-orf00071	#N/A	iron ion transmembrane transporter activity	high-affinity iron ion transport
contig00056-orf00074	membrane	transporter activity	transport
contig00056-orf00077	#N/A	ATP binding	#N/A
contig00056-orf00078	#N/A	copper ion binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00056-orf00080	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00056-orf00083	#N/A	oxidoreductase activity	#N/A
contig00056-orf00085	#N/A	iron ion binding	#N/A
contig00056-orf00088	#N/A	binding	#N/A
contig00056-orf00094	membrane	#N/A	#N/A
contig00056-orf00096	#N/A	#N/A	Mo-molybdopterin cofactor biosynthetic process
contig00057-orf00010	integral to membrane	#N/A	#N/A
contig00057-orf00015	integral to membrane	sodium:hydrogen antiporter activity	regulation of pH
contig00057-orf00018	#N/A	protein binding	proteolysis
contig00057-orf00021	intracellular	4 iron, 4 sulfur cluster binding	base-excision repair
contig00057-orf00026	#N/A	ATP binding	DNA replication
contig00057-orf00027	#N/A	#N/A	cell redox homeostasis
contig00057-orf00031	#N/A	metallopeptidase activity	#N/A
contig00057-orf00034	cytoplasm	ATP binding	phenylalanyl-tRNA aminoacylation
contig00057-orf00035	#N/A	hydroxymethylbilane synthase activity	porphyrin biosynthetic process
contig00057-orf00037	#N/A	hydrolase activity	cellular amino acid metabolic
contig00057-orf00040	#N/A	dGTPase activity	GTP metabolic process
contig00057-orf00041	cytoplasm	magnesium ion binding	RNA catabolic process
contig00057-orf00044	cytoplasm	S-adenosylmethionine-dependent methyltransf...	response to tellurium ion
contig00057-orf00045	#N/A	DNA binding	transposition, DNA-mediated
contig00058-orf00002	#N/A	ATP binding	threonine biosynthetic process
contig00058-orf00008	riboflavin synthase complex	riboflavin synthase activity	riboflavin biosynthetic process
contig00058-orf00012	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00058-orf00013	#N/A	D-amino-acid dehydrogenase activity	alanine catabolic process
contig00058-orf00016	intracellular	GTP binding	#N/A
contig00058-orf00019	integral to membrane	#N/A	#N/A
contig00058-orf00023	#N/A	isocitrate dehydrogenase (NADP+) activity	oxidation reduction
contig00058-orf00024	#N/A	isocitrate dehydrogenase (NADP+) activity	oxidation reduction
contig00058-orf00026	intracellular	ATP binding	regulation of transcription, DNA-dependent
contig00058-orf00028	#N/A	phenol 2-monooxygenase activity	cellular aromatic compound metabolic process
contig00058-orf00029	#N/A	monooxygenase activity	cellular aromatic compound metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00058-orf00031	#N/A	phenol 2-monooxygenase activity	cellular aromatic compound metabolic process
contig00058-orf00033	#N/A	2 iron, 2 sulfur cluster binding	oxidation reduction
contig00058-orf00034	cytoplasm	acetaldehyde dehydrogenase (acetylating) ac...	aromatic compound catabolic process
contig00058-orf00035	#N/A	4-hydroxy-2-oxovalerate aldolase activity	aromatic compound catabolic process
contig00058-orf00036	#N/A	catalytic activity	metabolic process
contig00058-orf00038	#N/A	isomerase activity	cellular aromatic compound metabolic process
contig00058-orf00039	#N/A	2 iron, 2 sulfur cluster binding	#N/A
contig00058-orf00040	#N/A	catechol 2,3-dioxygenase activity	aromatic compound catabolic process
contig00058-orf00041	#N/A	oxidoreductase activity	oxidation reduction
contig00058-orf00042	#N/A	catalytic activity	metabolic process
contig00058-orf00043	cytoplasm	#N/A	cell cycle
contig00058-orf00044	#N/A	amidophosphoribosyltransferase activity	nucleoside metabolic process
contig00058-orf00045	#N/A	spermidine synthase activity	spermidine biosynthetic process
contig00058-orf00047	sulfite reductase complex (NADPH)	4 iron, 4 sulfur cluster binding	cysteine biosynthetic process
contig00058-orf00051	ribosome	structural constituent of ribosome	translation
contig00058-orf00056	#N/A	DNA binding	DNA recombination
contig00058-orf00058	cytoplasm	ATP binding	phenylalanyl-tRNA aminoacylation
contig00058-orf00059	#N/A	Type II site-specific deoxyribonuclease act...	#N/A
contig00058-orf00061	#N/A	DNA (cytosine-5-)-methyltransferase activity	DNA methylation
contig00058-orf00062	#N/A	DNA (cytosine-5-)-methyltransferase activity	DNA methylation
contig00058-orf00063	#N/A	DNA binding	mismatch repair
contig00058-orf00065	cytoplasm	ATP binding	phenylalanyl-tRNA aminoacylation
contig00058-orf00067	ribosome	rRNA binding	ribosomal large subunit assembly
contig00058-orf00068	ribosome	structural constituent of ribosome	translation
contig00058-orf00069	cytoplasm	translation initiation factor activity	translational initiation
contig00058-orf00070	cytoplasm	ATP binding	threonyl-tRNA aminoacylation
contig00058-orf00075	#N/A	electron carrier activity	#N/A
contig00058-orf00078	intracellular	nucleic acid binding	DNA methylation
contig00058-orf00081	membrane	#N/A	cellular response to starvation
contig00058-orf00085	#N/A	oxidoreductase activity	oxidation reduction
contig00058-orf00086	intracellular	4 iron, 4 sulfur cluster binding	base-excision repair
contig00058-orf00090	integral to membrane	transporter activity	transport

Query	Cellular Component	Molecular Function	Biological Process
contig00058-orf00093	#N/A	peptidase activity	proteolysis
contig00058-orf00102	#N/A	glycine dehydrogenase (decarboxylating) act...	glycine decarboxylation via glycine cleavag...
contig00058-orf00105	#N/A	DNA-3-methyladenine glycosylase I activity	base-excision repair
contig00058-orf00107	glycine cleavage complex	lipoic acid binding	glycine decarboxylation via glycine cleavag...
contig00058-orf00109	cytoplasm	aminomethyltransferase activity	glycine decarboxylation via glycine cleavag...
contig00058-orf00111	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00058-orf00112	#N/A	DNA binding	transposition, DNA-mediated
contig00058-orf00114	#N/A	ATP binding	#N/A
contig00058-orf00115	#N/A	acyl carrier activity	biosynthetic process
contig00058-orf00119	#N/A	electron carrier activity	#N/A
contig00058-orf00123	#N/A	amino acid binding	guanosine tetraphosphate metabolic process
contig00058-orf00124	#N/A	alcohol dehydrogenase (NAD) activity	oxidation reduction
contig00058-orf00127	#N/A	oxidoreductase activity	oxidation reduction
contig00058-orf00129	#N/A	transporter activity	transport
contig00058-orf00135	cytoplasm	3'-5' exonuclease activity	DNA replication
contig00058-orf00136	cytoplasm	acetate kinase activity	organic acid metabolic process
contig00058-orf00137	#N/A	ribokinase activity	D-ribose metabolic process
contig00058-orf00141	#N/A	DNA binding	DNA integration
contig00058-orf00159	#N/A	double-stranded DNA binding	DNA protection
contig00058-orf00165	#N/A	sequence-specific DNA binding	#N/A
contig00058-orf00179	#N/A	DNA binding	#N/A
contig00058-orf00184	provirus TAS:TIGR.	#N/A	#N/A
contig00058-orf00185	membrane	transporter activity	transport
contig00058-orf00187	#N/A	transporter activity	transport
contig00058-orf00194	integral to membrane	ATP binding	cell cycle
contig00058-orf00202	integral to membrane	#N/A	#N/A
contig00058-orf00204	#N/A	sugar binding	#N/A
contig00058-orf00208	#N/A	methyltransferase activity	#N/A
contig00058-orf00212	integral to membrane	#N/A	#N/A
contig00058-orf00218	#N/A	sequence-specific DNA binding	#N/A
contig00058-orf00227	#N/A	DNA binding	DNA methylation
contig00058-orf00228	#N/A	DNA binding	DNA methylation

Query	Cellular Component	Molecular Function	Biological Process
contig00058-orf00229	#N/A	ATP binding	#N/A
contig00058-orf00231	#N/A	ATP binding	DNA modification
contig00058-orf00233	#N/A	DNA binding	DNA modification
contig00058-orf00235	#N/A	DNA binding	DNA methylation
contig00058-orf00240	cytoplasm	4 iron, 4 sulfur cluster binding	NAD biosynthetic process
contig00058-orf00245	integral to membrane	#N/A	#N/A
contig00058-orf00247	#N/A	nicotinate-nucleotide diphosphorylase (carb...	NAD biosynthetic process
contig00058-orf00254	cytoplasm	NADP or NADPH binding	aromatic amino acid family biosynthetic pro...
contig00058-orf00256	cytoplasm	glutamate-ammonia ligase activity	glutamine biosynthetic process
contig00058-orf00258	#N/A	DNA binding	DNA repair
contig00058-orf00260	#N/A	oxidoreductase activity	oxidation reduction
contig00058-orf00261	cell outer membrane	iron ion binding	siderophore transport
contig00058-orf00264	cell outer membrane	iron ion binding	siderophore transport
contig00058-orf00267	#N/A	catalytic activity	#N/A
contig00058-orf00272	#N/A	6-pyruvoyltetrahydropterin synthase activity	tetrahydrobiopterin biosynthetic process
contig00058-orf00276	#N/A	hydrolase activity, acting on carbon-nitrog...	queuosine biosynthetic process
contig00058-orf00278	#N/A	catalytic activity	metabolic process
contig00058-orf00281	#N/A	phosphogluconate dehydratase activity	Entner-Doudoroff pathway
contig00058-orf00284	#N/A	binding	glucose metabolic process
contig00058-orf00288	#N/A	6-phosphogluconolactonase activity	pentose-phosphate shunt
contig00058-orf00289	cytoplasm	ATP binding	glycolysis
contig00058-orf00290	intracellular	sugar binding	carbohydrate metabolic process
contig00058-orf00293	cytoplasm	glucose-6-phosphate isomerase activity	gluconeogenesis
contig00058-orf00297	plasma membrane	#N/A	#N/A
contig00058-orf00298	#N/A	phosphoribosylanthranilate isomerase activity	tryptophan biosynthetic process
contig00058-orf00303	proton-transporting two-sector ATPase compl...	ATP binding	ATP synthesis coupled proton transport
contig00058-orf00305	#N/A	catalytic activity	#N/A
contig00058-orf00313	#N/A	ATP binding	biotin biosynthetic process
contig00058-orf00315	#N/A	adenosylmethionine-8-amino-7-oxononanoate t...	biotin biosynthetic process
contig00058-orf00317	#N/A	#N/A	cell wall macromolecule catabolic process
contig00058-orf00318	#N/A	DNA binding	transposition, DNA-mediated
contig00058-orf00319	membrane	lipid binding	transport
contig00058-orf00321	integral to membrane	transporter activity	transport

Query	Cellular Component	Molecular Function	Biological Process
contig00058-orf00323	membrane	protein transporter activity	protein secretion
contig00059-orf00004	#N/A	DNA binding	DNA recombination
contig00059-orf00007	#N/A	DNA binding	DNA methylation
contig00059-orf00008	#N/A	ATP binding	peptidyl-histidine phosphorylation
contig00059-orf00009	exodeoxyribonuclease V complex	exodeoxyribonuclease V activity	#N/A
contig00059-orf00011	#N/A	damaged DNA binding	DNA repair
contig00060-orf00001	#N/A	ATP binding	DNA repair
contig00060-orf00004	#N/A	hydrolase activity	#N/A
contig00060-orf00008	cytoplasm	3-phosphoshikimate 1-carboxyvinyltransferas...	aromatic amino acid family biosynthetic pro...
contig00060-orf00014	intracellular	nuclease activity	DNA repair
contig00060-orf00015	#N/A	ATP binding	de novo' IMP biosynthetic process
contig00060-orf00017	#N/A	N-acetyltransferase activity	metabolic process
contig00060-orf00022	#N/A	pyruvate dehydrogenase (acetyl-transferring...	oxidation reduction
contig00060-orf00024	pyruvate dehydrogenase complex	dihydrolipoyllysine-residue acetyltransfera...	glycolysis
contig00060-orf00027	cytoplasm	dihydrolipoyl dehydrogenase activity	cell redox homeostasis
contig00060-orf00029	#N/A	tRNA (guanine-N7-)-methyltransferase activity	tRNA modification
contig00060-orf00036	#N/A	ribulose-phosphate 3-epimerase activity	carbohydrate metabolic process
contig00060-orf00040	cytoplasm	ATP binding	histidine biosynthetic process
contig00060-orf00041	cytoplasm	adenylosuccinate synthase activity	purine nucleotide biosynthetic process
contig00060-orf00046	#N/A	DNA binding	transposition, DNA-mediated
contig00060-orf00047	#N/A	heat shock protein binding	protein folding
contig00060-orf00051	#N/A	aspartate ammonia-lyase activity	aspartate metabolic process
contig00061-orf00001	#N/A	transporter activity	transport
contig00061-orf00006	#N/A	electron carrier activity	negative regulation of transcription
contig00061-orf00009	integral to membrane	#N/A	#N/A
contig00061-orf00010	#N/A	clavaminate synthase activity	antibiotic biosynthetic process
contig00061-orf00015	Gram-negative-bacterium-type cell wall	galactose transmembrane transporter activity	galactose transport
contig00061-orf00018	#N/A	L-aspartate:2-oxoglutarate aminotransferase...	biosynthetic process
contig00062-orf00002	#N/A	DNA binding	#N/A
contig00062-orf00004	#N/A	ATP binding	protein metabolic process
contig00062-orf00010	plasma membrane	#N/A	#N/A
contig00062-orf00011	integral to membrane	#N/A	cytolysis
contig00062-orf00014	#N/A	[protein-PII] uridylyltransferase activity	nitrogen compound metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00062-orf00015	#N/A	sequence-specific DNA binding	#N/A
contig00062-orf00018	#N/A	kinase activity	nucleoside metabolic process
contig00062-orf00019	#N/A	4-(cytidine 5'-diphospho)-2-C-methyl-D-eryt...	phosphorylation
contig00062-orf00022	anchored to membrane	protein transporter activity	protein transport
contig00062-orf00023	#N/A	binding	#N/A
contig00062-orf00027	#N/A	hydrolase activity	#N/A
contig00062-orf00028	#N/A	UTglucose-1-phosphate uridylyltransferase...	biosynthetic process
contig00062-orf00029	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00062-orf00033	integral to membrane	4-hydroxybenzoate octaprenyltransferase act...	ubiquinone biosynthetic process
contig00062-orf00035	#N/A	kinase activity	phosphoenolpyruvate-dependent sugar phospho...
contig00062-orf00037	#N/A	ATP binding	regulation of carbohydrate metabolic process
contig00062-orf00039	#N/A	ATP binding	#N/A
contig00062-orf00044	intracellular	GTP binding	#N/A
contig00062-orf00045	#N/A	DNA binding	transposition, DNA-mediated
contig00062-orf00046	#N/A	cobalt ion binding	diaminopimelate biosynthetic process
contig00062-orf00047	#N/A	methylated-DNA-[protein]-cysteine S-methylt...	DNA repair
contig00063-orf00002	#N/A	DNA binding	DNA repair
contig00063-orf00007	#N/A	binding	metabolic process
contig00063-orf00008	integral to membrane	transporter activity	transport
contig00063-orf00013	cell outer membrane	receptor activity	transport
contig00063-orf00023	membrane	phosphatidylglycerophosphatase activity	#N/A
contig00063-orf00031	chromosome	ATP binding	chromosome organization
contig00063-orf00033	#N/A	acyltransferase activity	#N/A
contig00063-orf00036	integral to plasma membrane	neurotransmitter:sodium symporter activity	neurotransmitter transport
contig00063-orf00039	#N/A	N-acetylmuramoyl-L-alanine amidase activity	peptidoglycan catabolic process
contig00063-orf00041	cytoplasm	aspartate-semialdehyde dehydrogenase activity	lysine biosynthetic process via diaminopime...
contig00063-orf00044	#N/A	ATP binding	DNA recombination
contig00067-orf00001	#N/A	protein binding	proteolysis
contig00069-orf00003	#N/A	4 iron, 4 sulfur cluster binding	oxidation reduction
contig00069-orf00005	#N/A	oxidoreductase activity	oxidation reduction
contig00070-orf00002	integral to membrane	binding	transport
contig00070-orf00003	#N/A	DNA binding	DNA integration
contig00070-orf00004	membrane	ATP binding	ATP biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00070-orf00006	#N/A	ATP binding	#N/A
contig00070-orf00008	#N/A	ATP binding	#N/A
contig00070-orf00009	#N/A	ATP binding	#N/A
contig00070-orf00010	#N/A	ATP binding	#N/A
contig00071-orf00001	intracellular	DNA binding	DNA repair
contig00071-orf00003	#N/A	phosphorylase activity	carbohydrate metabolic process
contig00072-orf00002	#N/A	acyl-CoA dehydrogenase activity	oxidation reduction
contig00073-orf00002	#N/A	DNA binding	transposition, DNA-mediated
contig00073-orf00004	membrane	#N/A	#N/A
contig00074-orf00001	cytoplasm	GTP binding	translational elongation
contig00075-orf00002	membrane	transporter activity	transport
contig00075-orf00004	#N/A	carnitine O-acetyltransferase activity	#N/A
contig00075-orf00006	#N/A	kinase activity	#N/A
contig00075-orf00007	#N/A	iron ion binding	#N/A
contig00075-orf00008	cytoplasm	#N/A	DNA recombination
contig00075-orf00011	integral to membrane	ferrous iron transmembrane transporter acti...	ferrous iron transport
contig00075-orf00014	#N/A	DNA binding	DNA methylation
contig00075-orf00017	#N/A	ATP binding	biosynthetic process
contig00075-orf00018	#N/A	O-methyltransferase activity	#N/A
contig00075-orf00022	Gram-negative-bacterium-type cell wall	transporter activity	transport
contig00075-orf00029	membrane	electron carrier activity	respiratory electron transport chain
contig00075-orf00036	ATP-binding cassette (ABC) transporter complex	ATP binding	polyamine transport
contig00075-orf00039	integral to membrane	transporter activity	transport
contig00075-orf00041	#N/A	oxidoreductase activity	oxidation reduction
contig00075-orf00045	#N/A	2 iron, 2 sulfur cluster binding	#N/A
contig00075-orf00050	ribonucleoside-diphosphate reductase complex	ATP binding	DNA replication
contig00075-orf00051	#N/A	chaperone binding	protein folding
contig00075-orf00053	#N/A	iron ion binding	iron-sulfur cluster assembly
contig00075-orf00058	#N/A	iron ion binding	iron-sulfur cluster assembly
contig00075-orf00063	#N/A	cysteine desulfurase activity	cysteine metabolic process
contig00075-orf00064	#N/A	double-stranded DNA binding	regulation of transcription, DNA-dependent
contig00075-orf00066	#N/A	FMN binding	oxidation reduction
contig00075-orf00067	#N/A	RNA binding	RNA processing

Query	Cellular Component	Molecular Function	Biological Process
contig00075-orf00068	#N/A	protein binding	#N/A
contig00075-orf00069	#N/A	sigma factor activity	regulation of transcription, DNA-dependent
contig00075-orf00070	cytoplasm	ATP binding	translation
contig00075-orf00072	acetyl-CoA carboxylase complex	acetyl-CoA carboxylase activity	fatty acid biosynthetic process
contig00075-orf00075	#N/A	RNA binding	#N/A
contig00076-orf00005	integral to membrane	#N/A	#N/A
contig00076-orf00010	#N/A	2 iron, 2 sulfur cluster binding	biotin biosynthetic process
contig00076-orf00014	cytoplasm	fructose 1,6-bisphosphate 1-phosphatase act...	carbohydrate biosynthetic process
contig00076-orf00016	membrane	calcium ion binding	#N/A
contig00076-orf00019	#N/A	ATP binding	mRNA polyadenylation
contig00076-orf00020	#N/A	pseudouridine synthase activity	tRNA pseudouridine synthesis
contig00076-orf00022	cytoplasm	#N/A	rRNA processing
contig00076-orf00023	#N/A	binding	oxidation reduction
contig00076-orf00025	#N/A	[formate-C-acetyltransferase]-activating en...	oxidation reduction
contig00076-orf00028	cytoplasm	formate C-acetyltransferase activity	glucose metabolic process
contig00076-orf00031	#N/A	ferric iron binding	cellular iron ion homeostasis
contig00076-orf00035	intracellular	GTP binding	#N/A
contig00076-orf00037	#N/A	DNA binding	DNA integration
contig00076-orf00043	cytoplasm	4 iron, 4 sulfur cluster binding	lipoate biosynthetic process
contig00076-orf00044	cytoplasm	lipoyl(octanoyl) transferase activity	lipoate biosynthetic process
contig00076-orf00049	#N/A	ATP binding	proteolysis
contig00076-orf00051	#N/A	DNA binding	#N/A
contig00076-orf00053	#N/A	glutamate decarboxylase activity	glutamate metabolic process
contig00076-orf00054	cytoplasm	aminoacyl-tRNA hydrolase activity	translation
contig00076-orf00060	#N/A	binding	#N/A
contig00076-orf00061	#N/A	transferase activity	biosynthetic process
contig00076-orf00064	integral to membrane	#N/A	#N/A
contig00076-orf00065	#N/A	2-C-methyl-D-erythritol 4-phosphate cytidyl...	terpenoid biosynthetic process
contig00076-orf00066	intracellular	DNA binding	DNA replication
contig00077-orf00005	#N/A	DNA binding	DNA methylation
contig00078-orf00001	cell outer membrane	#N/A	#N/A
contig00078-orf00004	#N/A	branched-chain-amino-acid transaminase acti...	branched chain family amino acid metabolic ...
contig00078-orf00008	#N/A	binding	#N/A
contig00078-orf00011	flagellum	#N/A	#N/A
contig00078-orf00014	cytoplasm	thymidylate synthase activity	dTMP biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00078-orf00016	#N/A	binding	cellular amino acid metabolic
contig00078-orf00018	#N/A	metalloendopeptidase activity	proteolysis
contig00078-orf00019	#N/A	#N/A	lipid metabolic process
contig00078-orf00021	membrane	#N/A	respiratory chain complex IV assembly
contig00078-orf00026	#N/A	electron carrier activity	#N/A
contig00078-orf00027	intracellular	GTP binding	barrier septum formation
contig00078-orf00029	integral to membrane	transporter activity	protein transport
contig00078-orf00030	integral to membrane	protein transporter activity	protein transport
contig00078-orf00033	#N/A	DNA binding	#N/A
contig00078-orf00045	#N/A	DNA binding	#N/A
contig00079-orf00003	#N/A	metalloendopeptidase activity	cell wall macromolecule catabolic process
contig00079-orf00004	#N/A	CoA-transferase activity	metabolic process
contig00079-orf00006	integral to membrane	metalloendopeptidase activity	proteolysis
contig00079-orf00014	#N/A	ATP binding	mismatch repair
contig00079-orf00016	#N/A	hydrolase activity, acting on carbon-nitrog...	chromatin silencing
contig00080-orf00011	#N/A	DNA binding	transposition, DNA-mediated
contig00080-orf00012	#N/A	nicotinamidase activity	metabolic process
contig00080-orf00019	integral to membrane	protein transporter activity	protein secretion
contig00080-orf00020	integral to membrane	protein transporter activity	protein secretion
contig00080-orf00022	#N/A	catalytic activity	#N/A
contig00080-orf00023	cytoplasm	ATP binding	histidine biosynthetic process
contig00080-orf00027	cytoplasm	imidazoleglycerol-phosphate synthase activity	histidine biosynthetic process
contig00080-orf00028	proton-transporting two-sector ATPase compl...	hydrogen ion transmembrane transporter acti...	ATP synthesis coupled proton transport
contig00080-orf00030	cytoplasm	1-(5-phosphoribosyl)-5-[(5-phosphoribosylam...	histidine biosynthetic process
contig00080-orf00031	cytoplasm	imidazoleglycerol-phosphate synthase activity	glutamine metabolic process
contig00080-orf00035	#N/A	lactate transmembrane transporter activity	lactate transport
contig00080-orf00040	cytoplasm	RNA binding	translation
contig00080-orf00042	#N/A	ATP binding	DNA repair
contig00080-orf00044	#N/A	protein binding	proteolysis
contig00080-orf00048	#N/A	metalloendopeptidase activity	proteolysis
contig00080-orf00058	#N/A	hydrolase activity	#N/A
contig00080-orf00060	#N/A	dihydroneopterin aldolase activity	folic acid and derivative metabolic process
contig00080-orf00061	integral to membrane	#N/A	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00080-orf00063	#N/A	#N/A	lipid metabolic process
contig00080-orf00067	cytoplasm	amino acid binding	L-phenylalanine biosynthetic process
contig00080-orf00071	#N/A	DNA binding	regulation of transcription, DNA-dependent
contig00080-orf00072	integral to membrane	ATP binding	peptidyl-histidine phosphorylation
contig00080-orf00074	#N/A	binding	metabolic process
contig00080-orf00076	ribosome	ribosome binding	ribosomal small subunit biogenesis
contig00080-orf00077	cytoplasm	RNA binding	tRNA modification
contig00080-orf00079	membrane	#N/A	toxin biosynthetic process
contig00080-orf00081	#N/A	#N/A	cell division
contig00080-orf00082	#N/A	ATP binding	folic acid and derivative biosynthetic process
contig00080-orf00085	#N/A	ATP binding	#N/A
contig00080-orf00089	cytoplasm	RNA binding	response to antibiotic
contig00080-orf00091	#N/A	FMN binding	metabolic process
contig00080-orf00094	#N/A	acyltransferase activity	signal transduction
contig00080-orf00095	#N/A	acyltransferase activity	metabolic process
contig00080-orf00098	#N/A	sigma factor activity	regulation of transcription, DNA-dependent
contig00080-orf00102	alpha DNA polymerase:primase complex	DNA binding	DNA replication, synthesis of RNA primer
contig00080-orf00105	integral to membrane	transporter activity	transmembrane transport
contig00080-orf00109	#N/A	binding	#N/A
contig00080-orf00114	cell outer membrane	receptor activity	transport
contig00080-orf00122	#N/A	succinate-semialdehyde dehydrogenase [NAD(P...	oxidation reduction
contig00080-orf00128	integral to membrane	P-P-bond-hydrolysis-driven protein transmem...	intracellular protein transport
contig00080-orf00130	integral to membrane	P-P-bond-hydrolysis-driven protein transmem...	intracellular protein transport
contig00080-orf00134	membrane	transferrin receptor activity	#N/A
contig00080-orf00136	#N/A	heme oxygenase (decyclizing) activity	heme oxidation
contig00080-orf00139	#N/A	transferase activity	#N/A
contig00080-orf00140	cytoplasm	#N/A	#N/A
contig00080-orf00142	#N/A	binding	cellular amino acid metabolic
contig00080-orf00146	cytoplasm	#N/A	regulation of DNA repair
contig00080-orf00156	cytoplasm	dihydrolipoyl dehydrogenase activity	cell redox homeostasis
contig00080-orf00158	#N/A	electron carrier activity	cell redox homeostasis
contig00080-orf00160	membrane	1-acylglycerol-3-phosphate O-acyltransferas...	phospholipid biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00080-orf00161	#N/A	damaged DNA binding	base-excision repair
contig00080-orf00163	#N/A	methyltransferase activity	metabolic process
contig00080-orf00166	#N/A	pyridoxal phosphate binding	tryptophan biosynthetic process
contig00080-orf00169	#N/A	fumarate hydratase activity	generation of precursor metabolites and energy
contig00080-orf00172	#N/A	electron carrier activity	oxidation reduction
contig00080-orf00173	#N/A	electron carrier activity	oxidation reduction
contig00080-orf00175	#N/A	4 iron, 4 sulfur cluster binding	#N/A
contig00080-orf00180	membrane	transporter activity	sodium ion transport
contig00080-orf00182	#N/A	catalytic activity	metabolic process
contig00080-orf00186	#N/A	catalytic activity	metabolic process
contig00080-orf00188	cell outer membrane	transporter activity	I-kappaB kinase/NF-kappaB cascade EXReactome.
contig00080-orf00191	#N/A	CTP synthase activity	pyrimidine nucleotide biosynthetic process
contig00080-orf00195	#N/A	cation transmembrane transporter activity	cation transport
contig00081-orf00003	cytoplasm	ATP binding	prolyl-tRNA aminoacylation
contig00081-orf00006	cytoplasmic membrane-bounded vesicle	carboxylesterase activity	#N/A
contig00081-orf00010	#N/A	2 iron, 2 sulfur cluster binding	oxidation reduction
contig00081-orf00013	plasma membrane	#N/A	#N/A
contig00081-orf00017	#N/A	binding	transport
contig00081-orf00020	integral to membrane	ATP binding	transmembrane transport
contig00081-orf00022	membrane	ATP binding	transport
contig00081-orf00024	#N/A	oxidoreductase activity, acting on single d...	#N/A
contig00086-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00088-orf00001	cytoplasm	serine O-acetyltransferase activity	cysteine biosynthetic process from serine
contig00088-orf00003	mitochondrion	adenyl-nucleotide exchange factor activity	protein folding
contig00088-orf00013	#N/A	ATP binding	#N/A
contig00088-orf00016	#N/A	acetolactate synthase activity	branched chain family amino acid biosynthet...
contig00088-orf00018	#N/A	acetolactate synthase activity	branched chain family amino acid biosynthet...
contig00088-orf00021	cytoplasm	oxidoreductase activity	antibiotic biosynthetic process
contig00088-orf00023	#N/A	binding	isoleucine biosynthetic process
contig00088-orf00027	integral to membrane	ATP binding	peptidyl-histidine phosphorylation

Query	Cellular Component	Molecular Function	Biological Process
contig00088-orf00028	membrane	#N/A	transmembrane transport
contig00088-orf00033	#N/A	metalloendopeptidase activity	proteolysis
contig00089-orf00001	outer membrane-bounded periplasmic space	transporter activity	transport
contig00089-orf00003	integral to membrane	transporter activity	transport
contig00089-orf00004	#N/A	ATP binding	#N/A
contig00089-orf00006	#N/A	ATP binding	#N/A
contig00089-orf00010	#N/A	GTP cyclohydrolase I activity	#N/A
contig00089-orf00014	#N/A	cystathionine gamma-synthase activity	cellular amino acid metabolic
contig00089-orf00019	intracellular	GTP binding	#N/A
contig00089-orf00026	integral to membrane	ATP binding	ATP biosynthetic process
contig00089-orf00029	#N/A	DNA binding	transposition, DNA-mediated
contig00092-orf00003	integral to membrane	NAD(P)+ transhydrogenase (AB-specific) acti...	oxidation reduction
contig00092-orf00005	integral to membrane	#N/A	amino acid transport
contig00092-orf00010	#N/A	binding	oxidation reduction
contig00092-orf00011	#N/A	lactoylglutathione lyase activity	#N/A
contig00092-orf00013	#N/A	methyltransferase activity	methylation
contig00092-orf00016	tricarboxylic acid cycle enzyme complex	fumarate hydratase activity	fumarate metabolic process
contig00092-orf00019	#N/A	3'-5'-exoribonuclease activity	tRNA processing
contig00092-orf00020	ATP-binding cassette (ABC) transporter complex	ATP binding	transport
contig00092-orf00022	#N/A	amino acid binding	cellular amino acid biosynthetic process
contig00092-orf00034	#N/A	glutathione transferase activity	#N/A
contig00092-orf00035	integral to membrane	two-component sensor activity	two-component signal transduction system (p...
contig00092-orf00036	cytoplasm	argininosuccinate lyase activity	arginine biosynthetic process via ornithine
contig00092-orf00037	cytoplasm	ATP binding	pyrimidine nucleotide metabolic process
contig00092-orf00039	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00092-orf00041	ribosome	RNA binding	translation
contig00092-orf00042	chromosome	DNA binding	DNA recombination
contig00092-orf00046	#N/A	ATP binding	#N/A
contig00092-orf00048	cytoplasm	ATP binding	CTP biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00092-orf00049	cytoplasm	4 iron, 4 sulfur cluster binding	rRNA processing
contig00092-orf00050	#N/A	binding	#N/A
contig00092-orf00051	#N/A	sequence-specific DNA binding	#N/A
contig00092-orf00053	#N/A	4-hydroxy-3-methylbut-2-en-1-yl diphosphate...	oxidation reduction
contig00092-orf00060	#N/A	copper ion binding	nitrogen compound metabolic process
contig00092-orf00062	integral to membrane	electron carrier activity	aerobic respiration
contig00092-orf00067	cell outer membrane	receptor activity	transport
contig00092-orf00068	cell outer membrane	receptor activity	transport
contig00092-orf00070	#N/A	1-deoxy-D-xylulose-5-phosphate reductoisome...	oxidation reduction
contig00092-orf00073	#N/A	DNA binding	regulation of transcription, DNA-dependent
contig00092-orf00074	ribosome	rRNA binding	translation
contig00092-orf00076	integral to membrane	electron carrier activity	electron transport chain
contig00092-orf00077	membrane	sodium:amino acid symporter activity	sodium ion transport
contig00094-orf00007	#N/A	#N/A	metabolic process
contig00094-orf00010	#N/A	iron ion binding	iron-sulfur cluster assembly
contig00094-orf00011	#N/A	DNA binding	#N/A
contig00094-orf00013	chromosome	ATP binding	DNA topological change
contig00094-orf00016	membrane	ATP binding	peptidyl-histidine phosphorylation
contig00094-orf00017	intracellular	ATP binding	regulation of transcription, DNA-dependent
contig00094-orf00021	#N/A	glucose-1-phosphate thymidylyltransferase a...	extracellular polysaccharide biosynthetic p...
contig00095-orf00007	#N/A	transporter activity	transport
contig00095-orf00011	integral to membrane	#N/A	#N/A
contig00096-orf00001	#N/A	sequence-specific DNA binding	#N/A
contig00096-orf00003	#N/A	DNA topoisomerase activity	DNA replication initiation
contig00096-orf00010	#N/A	sigma factor activity	regulation of transcription, DNA-dependent
contig00097-orf00001	#N/A	DNA binding	DNA integration
contig00099-orf00002	#N/A	#N/A	cell redox homeostasis
contig00099-orf00003	#N/A	protein tyrosine phosphatase activity	protein amino acid dephosphorylation
contig00099-orf00007	#N/A	GTP binding	riboflavin biosynthetic process
contig00099-orf00009	#N/A	DNA binding	DNA integration

Query	Cellular Component	Molecular Function	Biological Process
contig00099-orf00013	#N/A	S-methyl-5-thioribose-1-phosphate isomerase...	L-methionine biosynthetic process from S-ad...
contig00099-orf00015	#N/A	#N/A	DNA packaging
contig00099-orf00017	integral to membrane	#N/A	phosphoenolpyruvate-dependent sugar phospho...
contig00099-orf00019	#N/A	DNA primase activity	#N/A
contig00099-orf00023	#N/A	DNA primase activity	DNA metabolic process
contig00099-orf00025	cytoplasm	kinase activity	phosphoenolpyruvate-dependent sugar phospho...
contig00099-orf00027	#N/A	DNA binding	DNA integration
contig00099-orf00028	membrane	lipid binding	transport
contig00099-orf00029	membrane	lipid binding	transport
contig00101-orf00002	cytoplasm	glucosamine-1-phosphate N-acetyltransferase...	cell morphogenesis
contig00101-orf00008	outer membrane-bounded periplasmic space	transporter activity	transport
contig00101-orf00010	#N/A	5'-3' exonuclease activity	DNA repair
contig00101-orf00012	anchored to membrane	protein binding	cell adhesion
contig00102-orf00003	outer membrane	#N/A	pathogenesis
contig00106-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00106-orf00002	pilus	#N/A	cell adhesion
contig00106-orf00006	#N/A	#N/A	biosynthetic process
contig00106-orf00007	intracellular	GTP binding	#N/A
contig00106-orf00022	cytoplasm	ATP binding	DNA replication initiation
contig00106-orf00023	cytoplasm	3'-5' exonuclease activity	DNA replication
contig00106-orf00030	#N/A	#N/A	biosynthetic process
contig00106-orf00032	#N/A	FAD binding	oxidation reduction
contig00106-orf00034	#N/A	protein tyrosine phosphatase activity	dephosphorylation
contig00107-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00107-orf00010	#N/A	ATP binding	sulfate reduction
contig00107-orf00012	#N/A	carbonate dehydratase activity	one-carbon metabolic process
contig00107-orf00013	cytoplasm	unfolded protein binding	protein refolding
contig00107-orf00014	cytoplasm	nickel ion binding	nitrogen compound metabolic process
contig00107-orf00015	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00107-orf00018	#N/A	phosphoadenylyl-sulfate reductase (thioredo...	cysteine biosynthetic process
contig00107-orf00023	exodeoxyribonuclease V complex	ATP binding	#N/A

Query	Cellular Component	Molecular Function	Biological Process
contig00108-orf00001	extrinsic to membrane	ATP binding	lipoprotein transport
contig00108-orf00002	Gram-negative-bacterium-type cell wall	#N/A	transport
contig00108-orf00004	#N/A	DNA binding	DNA recombination
contig00108-orf00005	#N/A	isomerase activity	#N/A
contig00108-orf00007	cytoplasm	aminomethyltransferase activity	glycine catabolic process
contig00108-orf00010	#N/A	DNA binding	DNA integration
contig00108-orf00014	cytoplasm	homoserine O-acetyltransferase activity	methionine biosynthetic process
contig00108-orf00019	#N/A	1-aminocyclopropane-1-carboxylate synthase ...	biosynthetic process
contig00108-orf00021	#N/A	methyltransferase activity	menaquinone biosynthetic process
contig00108-orf00028	integral to membrane	C4-dicarboxylate transmembrane transporter ...	C4-dicarboxylate transport
contig00108-orf00030	#N/A	O-methyltransferase activity	#N/A
contig00108-orf00033	#N/A	phosphoribosylaminoimidazole carboxylase ac...	de novo' IMP biosynthetic process
contig00108-orf00035	#N/A	ATP binding	#N/A
contig00108-orf00036	#N/A	IMP dehydrogenase activity	GMP biosynthetic process
contig00108-orf00039	cell surface	magnesium ion binding	glycolysis
contig00108-orf00040	integral to membrane	#N/A	cell cycle
contig00108-orf00047	#N/A	ATP binding	#N/A
contig00108-orf00049	cytoplasm	rRNA (guanine-N2-)-methyltransferase activity	rRNA methylation
contig00108-orf00054	cytoplasm	translation elongation factor activity	translational elongation
contig00108-orf00058	chromosome	ATP binding	DNA topological change
contig00108-orf00059	#N/A	O-acetylhomoserine aminocarboxypropyltransf...	cellular amino acid metabolic
contig00108-orf00061	#N/A	ATP binding	DNA repair
contig00108-orf00065	cytoplasm	#N/A	DNA recombination
contig00108-orf00069	#N/A	dCTP deaminase activity	dUTP biosynthetic process
contig00108-orf00075	integral to membrane	hydrolase activity	establishment of competence for transformation
contig00108-orf00079	#N/A	ligase activity	#N/A
contig00108-orf00081	#N/A	3-isopropylmalate dehydratase activity	leucine biosynthetic process
contig00108-orf00083	membrane	#N/A	response to toxin
contig00108-orf00090	cytoplasm	3-isopropylmalate dehydrogenase activity	leucine biosynthetic process
contig00108-orf00095	integral to membrane	#N/A	#N/A
contig00108-orf00100	integral to membrane	#N/A	#N/A
contig00108-orf00102	#N/A	adenosylmethionine decarboxylase activity	spermidine biosynthetic process
contig00108-orf00104	integral to membrane	#N/A	#N/A
contig00108-orf00107	#N/A	DNA binding	DNA replication
contig00108-orf00109	membrane	peptidyl-prolyl cis-trans isomerase activity	protein folding

Query	Cellular Component	Molecular Function	Biological Process
contig00108-orf00114	#N/A	phosphoribosylglycinamide formyltransferase...	de novo' IMP biosynthetic process
contig00108-orf00117	#N/A	nuclease activity	#N/A
contig00108-orf00121	#N/A	2-C-methyl-D-erythritol 2,4-cyclodiphosphat...	terpenoid biosynthetic process
contig00108-orf00124	#N/A	4 iron, 4 sulfur cluster binding	oxidation reduction
contig00108-orf00129	integral to membrane	tetracycline:hydrogen antiporter activity	response to antibiotic
contig00109-orf00002	#N/A	DNA binding	DNA integration
contig00113-orf00006	integral to membrane	ATP binding	transport
contig00113-orf00008	#N/A	ATP binding	#N/A
contig00113-orf00011	cell outer membrane	transporter activity	ion transport
contig00113-orf00012	#N/A	transporter activity	transport
contig00113-orf00015	#N/A	aminopeptidase activity	cellular process
contig00113-orf00019	integral to membrane	transporter activity	transport
contig00113-orf00022	integral to membrane	transporter activity	transport
contig00113-orf00024	#N/A	ATP binding	peptide transport
contig00113-orf00026	#N/A	catalytic activity	biosynthetic process
contig00113-orf00027	integral to membrane	#N/A	#N/A
contig00113-orf00029	#N/A	ATP binding	tricarboxylic acid cycle
contig00113-orf00036	cytoplasm	dihydrolipoyl dehydrogenase activity	cell redox homeostasis
contig00113-orf00044	oxoglutarate dehydrogenase	dihydrolipoyllysine-residue succinyltransfe...	tricarboxylic acid cycle
contig00113-orf00049	#N/A	oxoglutarate dehydrogenase (succinyl-transf...	glycolysis
contig00113-orf00050	cytoplasm	acyltransferase activity	cellular carbohydrate metabolic process
contig00113-orf00052	#N/A	electron carrier activity	oxidation reduction
contig00113-orf00053	#N/A	electron carrier activity	electron transport chain
contig00113-orf00054	membrane	electron carrier activity	tricarboxylic acid cycle
contig00113-orf00055	membrane	electron carrier activity	tricarboxylic acid cycle
contig00113-orf00062	#N/A	cysteine synthase activity	cysteine biosynthetic process from serine
contig00113-orf00066	cytoplasm	diaminopimelate epimerase activity	lysine biosynthetic process via diaminopime...
contig00113-orf00067	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00113-orf00068	cytoplasm	FAD binding	cell cycle
contig00113-orf00075	#N/A	enzyme regulator activity	regulation of nitrogen utilization
contig00113-orf00079	cytoplasm	ATP binding	de novo' IMP biosynthetic process
contig00113-orf00083	#N/A	dihydroorotase activity	pyrimidine base biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00113-orf00086	cytoplasm	protein binding	tRNA processing
contig00113-orf00089	#N/A	endodeoxyribonuclease activity, producing 5...	#N/A
contig00113-orf00092	#N/A	3'-5' exonuclease activity	DNA replication
contig00113-orf00093	#N/A	GTP binding	#N/A
contig00113-orf00103	cytoplasm	coproporphyrinogen oxidase activity	oxidation reduction
contig00113-orf00104	cell outer membrane	porin activity	#N/A
contig00113-orf00107	#N/A	bis(5'-nucleosyl)-tetraphosphatase (symmetr...	#N/A
contig00113-orf00108	cytoplasm	transaldolase activity	pentose-phosphate shunt
contig00113-orf00133	#N/A	copper ion binding	#N/A
contig00113-orf00138	cytoplasm	ATP binding	intracellular protein transmembrane transport
contig00113-orf00141	cytoplasm	ATP binding	glutaminyl-tRNA aminoacylation
contig00113-orf00144	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00113-orf00146	#N/A	oxidoreductase activity	#N/A
contig00113-orf00157	#N/A	#N/A	cell redox homeostasis
contig00113-orf00170	integral to membrane	sulfate transmembrane transporter activity	sulfate transport
contig00113-orf00174	#N/A	oxidoreductase activity	#N/A
contig00113-orf00182	exodeoxyribonuclease V complex	exodeoxyribonuclease V activity	#N/A
contig00113-orf00184	cell outer membrane	receptor activity	transport
contig00113-orf00185	cell outer membrane	receptor activity	transport
contig00115-orf00001	#N/A	transcription factor activity	regulation of transcription, DNA-dependent
contig00115-orf00002	cell outer membrane	receptor activity	transport
contig00115-orf00006	#N/A	phosphoserine phosphatase activity	L-serine biosynthetic process
contig00115-orf00008	#N/A	DNA binding	DNA replication
contig00115-orf00013	#N/A	RNA binding	#N/A
contig00115-orf00015	cell outer membrane	iron ion binding	siderophore transport
contig00115-orf00019	integral to membrane	ATP binding	transmembrane transport
contig00115-orf00022	#N/A	DNA binding	transposition, DNA-mediated
contig00115-orf00024	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00115-orf00027	#N/A	lactate transmembrane transporter activity	lactate transport
contig00115-orf00033	#N/A	aminopeptidase activity	proteolysis
contig00116-orf00001	#N/A	DNA (cytosine-5-)-methyltransferase activity	DNA methylation
contig00116-orf00005	cytoplasm	alanine-tRNA ligase activity	alanyl-tRNA aminoacylation

Query	Cellular Component	Molecular Function	Biological Process
contig00116-orf00006	outer membrane-bounded periplasmic space	transporter activity	transport
contig00116-orf00008	#N/A	catalytic activity	metabolic process
contig00116-orf00010	#N/A	adenosine deaminase activity	purine ribonucleoside monophosphate biosynt...
contig00116-orf00013	cytoplasm	ATP binding	tryptophanyl-tRNA aminoacylation
contig00116-orf00016	cytoplasm	ATP binding	protein metabolic process
contig00116-orf00021	#N/A	hydrolase activity	#N/A
contig00116-orf00029	#N/A	metallocarboxypeptidase activity	proteolysis
contig00116-orf00032	cytoplasm	acetylglutamate kinase activity	arginine biosynthetic process
contig00116-orf00033	#N/A	exopolyphosphatase activity	#N/A
contig00116-orf00036	membrane	transporter activity	transmembrane transport
contig00116-orf00037	#N/A	single-stranded DNA binding	DNA replication
contig00116-orf00038	#N/A	DNA binding	DNA integration
contig00116-orf00039	#N/A	DNA binding	DNA integration
contig00116-orf00043	#N/A	binding	#N/A
contig00116-orf00045	#N/A	binding	#N/A
contig00117-orf00003	#N/A	exonuclease activity	RNA metabolic process
contig00117-orf00006	integral to membrane	ATP binding	two-component signal transduction system (p...
contig00117-orf00007	intracellular	sequence-specific DNA binding	regulation of transcription, DNA-dependent
contig00117-orf00009	integral to membrane	electron carrier activity	cell redox homeostasis
contig00117-orf00012	cytoplasm	uracil DNA N-glycosylase activity	base-excision repair
contig00117-orf00014	#N/A	calcium ion binding	proteolysis
contig00117-orf00015	membrane	calcium ion binding	#N/A
contig00117-orf00017	#N/A	alcohol dehydrogenase (NAD) activity	ethanol oxidation
contig00117-orf00018	cytoplasmic membrane-bounded vesicle	carboxylesterase activity	#N/A
contig00117-orf00020	#N/A	peptidyl-prolyl cis-trans isomerase activity	protein folding
contig00117-orf00022	membrane	transporter activity	sodium ion transport
contig00117-orf00023	#N/A	3-dehydroquinate dehydratase activity	aromatic amino acid family biosynthetic pro...
contig00117-orf00025	integral to membrane	#N/A	#N/A
contig00117-orf00027	integral to membrane	#N/A	#N/A
contig00117-orf00035	cell outer membrane	receptor activity	transport
contig00117-orf00037	#N/A	catalytic activity	carbohydrate metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00118-orf00001	#N/A	sequence-specific DNA binding	#N/A
contig00119-orf00004	#N/A	endonuclease activity	RNA catabolic process
contig00119-orf00016	#N/A	DNA binding	DNA integration
contig00120-orf00001	#N/A	binding	#N/A
contig00122-orf00004	#N/A	calcium ion binding	#N/A
contig00123-orf00001	cytoplasm	ATP binding	methionyl-tRNA aminoacylation
contig00123-orf00004	#N/A	#N/A	transmembrane transport
contig00124-orf00001	extrinsic to membrane	ATP binding	plasma membrane ATP synthesis coupled proto...
contig00124-orf00002	extrinsic to membrane	ATP binding	plasma membrane ATP synthesis coupled proto...
contig00124-orf00006	extrinsic to membrane	ATP binding	plasma membrane ATP synthesis coupled proto...
contig00124-orf00007	extrinsic to membrane	hydrogen ion transporting ATP synthase acti...	ATP synthesis coupled proton transport
contig00124-orf00008	integral to membrane	hydrogen ion transporting ATP synthase acti...	ATP synthesis coupled proton transport
contig00124-orf00009	integral to membrane	hydrogen ion transporting ATP synthase acti...	ATP synthesis coupled proton transport
contig00124-orf00010	integral to membrane	hydrogen ion transmembrane transporter acti...	ATP synthesis coupled proton transport
contig00124-orf00014	#N/A	ATP binding	protein amino acid phosphorylation
contig00124-orf00015	membrane	inorganic phosphate transmembrane transport...	phosphate transport
contig00124-orf00016	#N/A	ATP binding	amino sugar metabolic process
contig00124-orf00017	#N/A	cytochrome-c oxidase activity	oxidation reduction
contig00124-orf00019	#N/A	electron carrier activity	#N/A
contig00124-orf00021	integral to membrane	cytochrome-c oxidase activity	aerobic respiration
contig00124-orf00023	#N/A	protein binding	#N/A
contig00124-orf00024	#N/A	hydrolase activity	#N/A
contig00124-orf00025	#N/A	hydrolase activity, acting on carbon-nitrog...	nitrogen compound metabolic process
contig00124-orf00027	#N/A	1-deoxy-D-xylulose-5-phosphate synthase act...	terpenoid biosynthetic process
contig00124-orf00029	#N/A	binding	oxidation reduction
contig00124-orf00031	#N/A	transferase activity	metabolic process
contig00124-orf00032	integral to membrane	#N/A	#N/A
contig00124-orf00033	#N/A	crossover junction endodeoxyribonuclease ac...	DNA recombination

Query	Cellular Component	Molecular Function	Biological Process
contig00124-orf00034	integral to membrane	acyltransferase activity	lipopolysaccharide core region biosynthetic...
contig00124-orf00036	#N/A	DNA binding	DNA integration
contig00125-orf00001	integral to membrane	inorganic phosphate transmembrane transport...	phosphate transport
contig00125-orf00003	membrane	acyltransferase activity	#N/A
contig00128-orf00001	#N/A	DNA binding	DNA integration
contig00131-orf00001	cytoplasm	DNA binding	nucleotide-excision repair
contig00131-orf00002	#N/A	binding	oxidation reduction
contig00131-orf00004	mitochondrial respiratory chain	electron carrier activity	electron transport chain
contig00131-orf00008	#N/A	isomerase activity	cellular aromatic compound metabolic process
contig00131-orf00011	#N/A	hydrolase activity	#N/A
contig00131-orf00013	#N/A	transferase activity, transferring glycosyl...	carbohydrate metabolic process
contig00131-orf00015	#N/A	endonuclease activity	#N/A
contig00131-orf00016	#N/A	4 iron, 4 sulfur cluster binding	#N/A
contig00131-orf00019	#N/A	oxidoreductase activity	oxidation reduction
contig00131-orf00021	membrane	transporter activity	transmembrane transport
contig00131-orf00024	membrane	lipid binding	transport
contig00131-orf00026	membrane	lipid binding	transport
contig00131-orf00027	membrane	ATP binding	transport
contig00132-orf00004	chromosome	ATP binding	chromosome organization
contig00134-orf00001	#N/A	electron carrier activity	#N/A
contig00134-orf00002	#N/A	aromatic-amino-acid:2-oxoglutarate aminotra...	biosynthetic process
contig00134-orf00005	#N/A	magnesium ion binding	carbohydrate metabolic process
contig00134-orf00010	#N/A	asparaginase activity	cellular amino acid metabolic
contig00134-orf00011	#N/A	endodeoxyribonuclease activity, producing 5...	#N/A
contig00134-orf00015	#N/A	thiamin phosphate kinase activity	thiamin biosynthetic process
contig00134-orf00016	#N/A	phosphatidylglycerophosphatase activity	lipid metabolic process
contig00134-orf00019	#N/A	DNA binding	transposition, DNA-mediated
contig00135-orf00003	cytoplasm	4 iron, 4 sulfur cluster binding	tRNA modification
contig00135-orf00007	cytoplasm	glutamate-1-semialdehyde 2,1-aminomutase ac...	porphyrin biosynthetic process
contig00135-orf00011	integral to membrane	#N/A	transmembrane transport
contig00136-orf00001	outer membrane-bounded periplasmic space	transporter activity	transport
contig00136-orf00003	ribosome	rRNA binding	translation
contig00136-orf00006	membrane	phospholipase activity	lipid metabolic process
contig00136-orf00013	cytoplasm	pyrophosphatase activity	lipid A biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00136-orf00015	#N/A	serine-type D-Ala-D-Ala carboxypeptidase ac...	proteolysis
contig00136-orf00017	#N/A	histidinol-phosphate transaminase activity	histidine biosynthetic process
contig00136-orf00026	cell outer membrane	iron ion binding	siderophore transport
contig00136-orf00029	#N/A	hydrolase activity	#N/A
contig00138-orf00001	#N/A	ATP binding	lipid A biosynthetic process
contig00138-orf00009	cytoplasm	3-deoxy-manno-octulosonate cytidylyltransfe...	keto-3-deoxy-D-manno-octulosonic acid biosy...
contig00138-orf00014	cytoplasm	adenylate kinase activity	nucleobase, nucleoside, nucleotide and nucl...
contig00138-orf00015	#N/A	orotidine-5'-phosphate decarboxylase activity	de novo' pyrimidine base biosynthetic process
contig00138-orf00016	#N/A	binding	metabolic process
contig00138-orf00017	#N/A	kinase activity	carbohydrate metabolic process
contig00138-orf00019	#N/A	ADP-glyceromanno-heptose 6-epimerase activity	carbohydrate metabolic process
contig00138-orf00020	#N/A	pyridoxal phosphate binding	biosynthetic process
contig00138-orf00021	#N/A	2-nitropropane dioxygenase activity	oxidation reduction
contig00138-orf00022	#N/A	carbohydrate binding	hexose metabolic process
contig00138-orf00025	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00138-orf00029	#N/A	dUTP diphosphatase activity	dUTP metabolic process
contig00138-orf00031	integral to membrane	transporter activity	transmembrane transport
contig00139-orf00001	#N/A	DNA binding	DNA integration
contig00141-orf00002	#N/A	metalloendopeptidase activity	proteolysis
contig00141-orf00004	#N/A	3-deoxy-7-phosphoheptulonate synthase activity	aromatic amino acid family biosynthetic pro...
contig00141-orf00008	#N/A	sugar binding	biosynthetic process
contig00141-orf00010	outer membrane	#N/A	pathogenesis
contig00141-orf00012	cell outer membrane	#N/A	#N/A
contig00141-orf00014	intracellular	ATP binding	pilus assembly
contig00141-orf00015	integral to membrane	protein transporter activity	protein secretion by the type II secretion ...
contig00141-orf00016	integral to membrane	aspartic-type endopeptidase activity	#N/A
contig00141-orf00017	cytoplasm	ATP binding	coenzyme A biosynthetic process
contig00141-orf00019	#N/A	FMN adenylyltransferase activity	riboflavin biosynthetic process
contig00141-orf00020	#N/A	FMN adenylyltransferase activity	riboflavin biosynthetic process
contig00141-orf00022	#N/A	3 iron, 4 sulfur cluster binding	isopentenyl diphosphate biosynthetic proces...
contig00141-orf00023	integral to membrane	aspartic-type endopeptidase activity	proteolysis

Query	Cellular Component	Molecular Function	Biological Process
contig00141-orf00028	#N/A	binding	#N/A
contig00141-orf00029	outer membrane-bounded periplasmic space	iron ion transmembrane transporter activity	iron ion transport
contig00141-orf00032	integral to membrane	citrate transmembrane transporter activity	citrate transport
contig00141-orf00040	Gram-negative-bacterium-type cell wall	FMN binding	oxidation reduction
contig00141-orf00041	integral to membrane	oxidoreductase activity, acting on NADH or ...	oxidation reduction
contig00141-orf00043	Gram-negative-bacterium-type cell wall	oxidoreductase activity, acting on NADH or ...	respiratory electron transport chain
contig00141-orf00045	Gram-negative-bacterium-type cell wall	2 iron, 2 sulfur cluster binding	oxidation reduction
contig00141-orf00047	#N/A	FMN binding	coenzyme A biosynthetic process
contig00142-orf00001	#N/A	DNA binding	transposition, DNA-mediated
contig00142-orf00009	#N/A	ATP binding	metabolic process
contig00142-orf00010	integral to membrane	#N/A	#N/A
contig00142-orf00011	acetyl-CoA carboxylase complex	acetyl-CoA carboxylase activity	fatty acid biosynthetic process
contig00143-orf00001	#N/A	DNA binding	DNA integration
contig00143-orf00002	#N/A	nucleic acid binding	#N/A
contig00145-orf00001	#N/A	binding	#N/A
contig00145-orf00004	cytoplasm	aspartate-tRNA ligase activity	aspartyl-tRNA aminoacylation
contig00145-orf00007	#N/A	binding	#N/A
contig00148-orf00005	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00148-orf00007	#N/A	methyltransferase activity	methylation
contig00148-orf00012	#N/A	ATP binding	translation
contig00148-orf00014	#N/A	ATP binding	regulation of translational fidelity
contig00148-orf00016	#N/A	ATP binding	cell morphogenesis
contig00148-orf00017	#N/A	#N/A	regulation of cell shape
contig00148-orf00018	integral to membrane	#N/A	regulation of cell shape
contig00148-orf00019	#N/A	penicillin binding	peptidoglycan-based cell wall biogenesis
contig00148-orf00022	integral to membrane	#N/A	cell cycle
contig00148-orf00026	#N/A	FMN binding	cysteine biosynthetic process
contig00148-orf00028	#N/A	magnesium ion binding	alginic acid biosynthetic process
contig00148-orf00034	#N/A	amino acid binding	isoleucine biosynthetic process
contig00148-orf00041	#N/A	thioredoxin peroxidase activity	cell redox homeostasis
contig00148-orf00044	cytoplasm	coproporphyrinogen oxidase activity	oxidation reduction
contig00148-orf00046	cytoplasm	glycine hydroxymethyltransferase activity	glycine metabolic process

Query	Cellular Component	Molecular Function	Biological Process
contig00148-orf00048	#N/A	ATP binding	cell division
contig00148-orf00050	integral to membrane	carbohydrate transmembrane transporter acti...	carbohydrate transport
contig00148-orf00052	#N/A	ATP binding	DNA recombination
contig00148-orf00057	membrane	signal transducer activity	chemotaxis
contig00148-orf00062	#N/A	pyridoxal phosphate binding	threonine biosynthetic process
contig00148-orf00064	#N/A	RNA binding	#N/A
contig00148-orf00065	cytoplasm	nucleic acid binding	rRNA methylation
contig00148-orf00067	integral to membrane	ATP binding	proteolysis
contig00148-orf00068	cytoplasm	FAD binding	oxidation reduction
contig00148-orf00072	#N/A	metal ion binding	porphyrin biosynthetic process
contig00148-orf00076	#N/A	ATP binding	#N/A
contig00148-orf00077	#N/A	#N/A	transmembrane transport
contig00149-orf00001	#N/A	4 iron, 4 sulfur cluster binding	#N/A
contig00149-orf00002	#N/A	methyltransferase activity	methylation
contig00149-orf00009	chromosome	ATP binding	DNA topological change
contig00149-orf00011	#N/A	#N/A	DNA mediated transformation
contig00149-orf00013	#N/A	#N/A	DNA mediated transformation
contig00149-orf00016	intracellular	ATP binding	regulation of transcription, DNA-dependent
contig00149-orf00017	integral to membrane	ATP binding	peptidyl-histidine phosphorylation
contig00149-orf00019	cytoplasm	RNA binding	regulation of transcription, DNA-dependent
contig00149-orf00022	extracellular region	metallopeptidase activity	proteolysis
contig00149-orf00029	#N/A	#N/A	cell wall macromolecule catabolic process
contig00149-orf00033	#N/A	catalytic activity	cellular metabolic process
contig00149-orf00035	#N/A	catalytic activity	metabolic process
contig00149-orf00036	cell outer membrane	receptor activity	transport
contig00149-orf00038	#N/A	catalytic activity	biosynthetic process
contig00149-orf00041	cytoplasm	acyl carrier activity	fatty acid biosynthetic process
contig00149-orf00042	#N/A	3-oxoacyl-[acyl-carrier-protein] synthase a...	fatty acid biosynthetic process
contig00149-orf00050	#N/A	magnesium ion binding	glycolysis
contig00149-orf00051	#N/A	hypoxanthine phosphoribosyltransferase acti...	nucleoside metabolic process
contig00149-orf00052	integral to membrane	protein-N(PI)-phosphohistidine-sugar phosph...	phosphoenolpyruvate-dependent sugar phospho...
contig00149-orf00054	cytoplasm	kinase activity	phosphoenolpyruvate-dependent sugar phospho...

Query	Cellular Component	Molecular Function	Biological Process
contig00149-orf00056	cytoplasm	kinase activity	phosphoenolpyruvate-dependent sugar phospho...
contig00149-orf00061	#N/A	ATP binding	#N/A
contig00150-orf00001	#N/A	beta-phosphoglucomutase activity	metabolic process
contig00150-orf00004	#N/A	ATP binding	peptidyl-histidine phosphorylation
contig00151-orf00003	integral to membrane	#N/A	transmembrane transport
contig00151-orf00004	#N/A	dATP pyrophosphohydrolase activity	DNA repair
contig00151-orf00007	cytoplasm	inorganic diphosphatase activity	phosphate metabolic process
contig00151-orf00009	intracellular	DNA binding	DNA replication
contig00151-orf00010	#N/A	hydrolase activity	metabolic process
contig00151-orf00012	#N/A	phosphomethylpyrimidine kinase activity	thiamin biosynthetic process
contig00151-orf00016	#N/A	alanine racemase activity	alanine metabolic process
contig00151-orf00018	#N/A	amino acid binding	metabolic process
contig00151-orf00023	#N/A	#N/A	response to stress
contig00151-orf00026	intracellular	transcription factor activity	regulation of transcription, DNA-dependent
contig00151-orf00028	#N/A	tRNA (uracil-5-)-methyltransferase activity	tRNA modification
contig00151-orf00030	integral to membrane	#N/A	#N/A
contig00151-orf00032	#N/A	chorismate synthase activity	aromatic amino acid family biosynthetic pro...
contig00151-orf00041	cell outer membrane	calcium ion binding	pathogenesis
contig00151-orf00044	#N/A	ATP binding	#N/A
contig00151-orf00050	membrane	calcium ion binding	oxidation reduction
contig00151-orf00053	membrane	DNA binding	positive regulation of transcription
contig00151-orf00054	acetyl-CoA carboxylase complex	acetyl-CoA carboxylase activity	fatty acid biosynthetic process
contig00151-orf00060	integral to membrane	hydrolase activity, acting on carbon-nitrog...	lipoprotein biosynthetic process
contig00151-orf00061	#N/A	sigma factor activity	regulation of transcription, DNA-dependent
contig00151-orf00064	ribosome	structural constituent of ribosome	translation
contig00151-orf00065	#N/A	electron carrier activity	cell redox homeostasis
contig00152-orf00003	integral to membrane	CDP-diacylglycerol-glycerol-3-phosphate 3-p...	phospholipid biosynthetic process
contig00152-orf00008	#N/A	electron carrier activity	#N/A
contig00152-orf00014	#N/A	transketolase activity	metabolic process
contig00152-orf00018	#N/A	sulfuric ester hydrolase activity	metabolic process
contig00155-orf00001	pilus	#N/A	cell adhesion
contig00157-orf00001	#N/A	DNA binding	DNA integration
contig00158-orf00001	#N/A	antioxidant activity	cell redox homeostasis

Query	Cellular Component	Molecular Function	Biological Process
contig00161-orf00001	#N/A	RNA binding	rRNA processing
contig00161-orf00005	cytoplasm	dihydrodipicolinate synthase activity	diaminopimelate biosynthetic process
contig00161-orf00010	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00162-orf00007	#N/A	RNA binding	RNA processing
contig00162-orf00008	#N/A	inositol-1(or 4)-monophosphatase activity	#N/A
contig00162-orf00010	membrane	transporter activity	signal transduction
contig00162-orf00011	integral to membrane	ATP binding	proteolysis
contig00162-orf00012	Gram-negative-bacterium-type cell wall	protein transporter activity	protein secretion
contig00162-orf00014	#N/A	ATP binding	#N/A
contig00162-orf00020	#N/A	#N/A	transmembrane transport
contig00162-orf00022	cell outer membrane	iron ion binding	siderophore transport
contig00162-orf00024	#N/A	specific transcriptional repressor activity	negative regulation of transcription
contig00162-orf00029	integral to membrane	calcium ion binding	cell communication
contig00162-orf00032	cytoplasm	glutamate-5-semialdehyde dehydrogenase acti...	oxidation reduction
contig00162-orf00037	#N/A	transferase activity, transferring glycosyl...	lipopolysaccharide biosynthetic process
contig00162-orf00038	#N/A	DNA binding	regulation of transcription, DNA-dependent
contig00162-orf00040	cytoplasm	methyltransferase activity	oxidation reduction
contig00162-orf00041	cytoplasm	ATP binding	metabolic process
contig00162-orf00043	#N/A	binding	metabolic process
contig00162-orf00046	#N/A	hydroxyacylglutathione hydrolase activity	#N/A
contig00162-orf00049	membrane	protein transporter activity	protein secretion
contig00165-orf00001	#N/A	nucleic acid binding	#N/A
contig00167-orf00001	#N/A	ATP binding	nucleobase, nucleoside, nucleotide and nucl...
contig00167-orf00004	#N/A	2-amino-4-hydroxy-6-hydroxymethyldihydropte...	folic acid and derivative biosynthetic process
contig00167-orf00009	#N/A	RNA binding	regulation of transcription, DNA-dependent
contig00167-orf00015	#N/A	binding	#N/A
contig00167-orf00016	cytoplasm	ATP binding	histidyl-tRNA aminoacylation
contig00167-orf00019	#N/A	pseudouridine synthase activity	pseudouridine synthesis
contig00167-orf00021	#N/A	transferase activity	metabolic process
contig00167-orf00024	cytoplasm	uroporphyrinogen decarboxylase activity	porphyrin biosynthetic process

Query	Cellular Component	Molecular Function	Biological Process
contig00167-orf00026	#N/A	binding	#N/A
contig00167-orf00028	#N/A	uroporphyrinogen-III synthase activity	tetrapyrrole biosynthetic process
contig00167-orf00032	#N/A	heat shock protein binding	protein folding
contig00167-orf00035	membrane	cobalt ion transmembrane transporter activity	cobalt ion transport
contig00167-orf00036	membrane	cobalt ion transmembrane transporter activity	cobalt ion transport
contig00167-orf00038	#N/A	hydrolase activity	#N/A
contig00167-orf00041	#N/A	DNA binding	transposition, DNA-mediated
contig00168-orf00001	#N/A	DNA binding	DNA integration
contig00169-orf00001	#N/A	DNA binding	DNA integration

Appendix E

Pfam domain annotation of identified *N. sicca* 4320 ORFs.

The amino acid sequences of the identified *N. sicca* 4320 ORFs were used to search the Pfam domain database. Query: *N. sicca* 4320 ORF. Pfam subject: Pfam match to *N. sicca* 4320 ORF. Pfam ID: Pfam match identification number.

Query	Pfam Subject	Pfam ID
contig00001-orf00001	GSH-S_N	PF02951.7
contig00001-orf00001	Pfam-B_1558	PB001558
contig00001-orf00001	GSH-S_ATP	PF02955.9
contig00001-orf00001	Pfam-B_195	PB000195
contig00001-orf00003	DAGK_prokar	PF01219.12
contig00001-orf00004	DUF461	PF04314.6
contig00001-orf00005	tRNA_Me_trans	PF03054.9
contig00001-orf00008	AMP-binding	PF00501.21
contig00001-orf00010	PhoH	PF02562.9
contig00001-orf00012	HD	PF01966.15
contig00001-orf00012	RelA_SpoT	PF04607.10
contig00001-orf00012	TGS	PF02824.14
contig00001-orf00012	ACT	PF01842.18
contig00001-orf00013	RNA_pol_Rpb6	PF01192.15
contig00001-orf00015	Guanylate_kin	PF00625.14
contig00001-orf00015	Strep_his_triad	PF04270.6
contig00001-orf00016	Pribosyltran	PF00156.20
contig00001-orf00019	Pfam-B_852	PB000852
contig00001-orf00019	TPR_2	PF07719.10
contig00001-orf00019	Pfam-B_14450	PB014450
contig00001-orf00019	SLT	PF01464.13
contig00001-orf00020	rve	PF00665.19
contig00001-orf00020	NPH3	PF03000.7
contig00002-orf00001	CBFD_NFYB_HMF	PF00808.16
contig00002-orf00003	Pfam-B_9471	PB009471
contig00002-orf00003	Rep_trans	PF02486.12
contig00002-orf00005	Pfam-B_4866	PB004866
contig00002-orf00006	Pfam-B_13759	PB013759
contig00002-orf00007	Pfam-B_17119	PB017119
contig00002-orf00007	CoatB	PF10389.2
contig00002-orf00008	Pfam-B_7376	PB007376
contig00003-orf00001	Phage_integrase	PF00589.15
contig00004-orf00003	BCCT	PF02028.10
contig00004-orf00003	Pfam-B_1007	PB001007
contig00004-orf00003	Pfam-B_324	PB000324
contig00004-orf00006	NAD_synthase	PF02540.10
contig00004-orf00008	ATPase-cat_bd	PF12156.1
contig00004-orf00009	SpecificRecomb	PF10136.2
contig00004-orf00009	Form_Nir_trans	PF01226.10
contig00004-orf00009	DUF373	PF04123.6
contig00005-orf00001	SMC_N	PF02463.12
contig00005-orf00001	NTPase_P4	PF11602.1

Query	Pfam Subject	Pfam ID
contig00005-orf00001	Pfam-B_13372	PB013372
contig00005-orf00001	Syntaxin-6_N	PF09177.4
contig00005-orf00001	Laminin_II	PF06009.5
contig00005-orf00002	Acetate_kinase	PF00871.10
contig00005-orf00002	Lact_bio_phlase	PF09508.3
contig00005-orf00006	DUF3608	PF12257.1
contig00005-orf00007	CcoS	PF03597.8
contig00005-orf00008	MFS_1	PF07690.9
contig00006-orf00001	CLP_protease	PF00574.16
contig00006-orf00001	Pfam-B_420	PB000420
contig00006-orf00003	Trigger_N	PF05697.6
contig00006-orf00003	Trigger_C	PF05698.7
contig00006-orf00003	Turandot	PF07240.4
contig00006-orf00003	FKBP_C	PF00254.21
contig00006-orf00003	Trigger_C	PF05698.7
contig00006-orf00007	Peptidase_M23	PF01551.15
contig00006-orf00009	PPDK_N	PF01326.12
contig00006-orf00009	PEP-utilizers	PF00391.16
contig00006-orf00009	PEP-utilizers_C	PF02896.11
contig00006-orf00010	DUF299	PF03618.7
contig00006-orf00013	Pfam-B_15386	PB015386
contig00006-orf00013	NikM	PF10670.2
contig00007-orf00001	Phage_integr_N	PF02899.10
contig00007-orf00001	Phage_integrase	PF00589.15
contig00007-orf00001	Pfam-B_17331	PB017331
contig00008-orf00001	Exonuc_X-T	PF00929.17
contig00008-orf00005	adh_short	PF00106.18
contig00008-orf00008	MscL	PF01741.11
contig00008-orf00011	HSP33	PF01430.12
contig00008-orf00011	TraQ	PF09679.3
contig00008-orf00014	ABC1	PF03109.9
contig00008-orf00014	WaaY	PF06176.4
contig00008-orf00014	DUF1678	PF07913.4
contig00008-orf00016	Pfam-B_15229	PB015229
contig00008-orf00016	NLPC_P60	PF00877.12
contig00008-orf00017	Pfam-B_12713	PB012713
contig00008-orf00017	GIT1_C	PF12205.1
contig00008-orf00017	HTH_Mga	PF08280.4
contig00008-orf00022	Na_Ala_symp	PF01235.10
contig00008-orf00026	GidB	PF02527.8
contig00008-orf00032	S4	PF01479.18
contig00008-orf00032	PseudoU_synth_2	PF00849.15

Query	Pfam Subject	Pfam ID
contig00008-orf00032	TraY	PF05509.4
contig00008-orf00032	DUF1127	PF06568.4
contig00008-orf00039	S1	PF00575.16
contig00008-orf00039	RNase_E_G	PF10150.2
contig00008-orf00039	Pfam-B_17400	PB017400
contig00008-orf00043	MFS_1	PF07690.9
contig00008-orf00043	IGPD	PF00475.11
contig00008-orf00046	MFS_1	PF07690.9
contig00008-orf00048	Ribosomal_L3	PF00297.15
contig00008-orf00048	IalB	PF06776.5
contig00008-orf00049	Ribosomal_L4	PF00573.15
contig00008-orf00050	Ribosomal_L23	PF00276.13
contig00008-orf00052	Ribosomal_L2	PF00181.16
contig00008-orf00052	Ribosomal_L2_C	PF03947.11
contig00008-orf00053	Ribosomal_S19	PF00203.14
contig00008-orf00054	Ribosomal_L22	PF00237.12
contig00008-orf00055	Ribosomal_S3_N	PF00417.12
contig00008-orf00055	DUF2092	PF09865.2
contig00008-orf00055	KH_2	PF07650.10
contig00008-orf00055	Ribosomal_S3_C	PF00189.13
contig00008-orf00056	Ribosomal_L16	PF00252.11
contig00008-orf00056	HlyD	PF00529.13
contig00008-orf00057	Ribosomal_L29	PF00831.16
contig00008-orf00059	Ribosomal_L5_C	PF00673.14
contig00008-orf00060	Ribosomal_S14	PF00253.14
contig00008-orf00062	Ribosomal_L6	PF00347.16
contig00008-orf00064	Ribosomal_L18e	PF00828.12
contig00008-orf00065	SecY	PF00344.13
contig00008-orf00067	RNA_pol_L	PF01193.17
contig00008-orf00067	RNA_pol_A_bac	PF01000.19
contig00008-orf00067	RNA_pol_A_CTD	PF03118.8
contig00008-orf00070	DAO	PF01266.17
contig00008-orf00071	Exosortase_EpsH	PF09721.3
contig00008-orf00071	DUF1469	PF07332.4
contig00008-orf00071	DUF3180	PF11377.1
contig00008-orf00071	ICMT	PF04140.7
contig00008-orf00072	NERD	PF08378.4
contig00008-orf00072	Pfam-B_8634	PB008634
contig00008-orf00075	TMP-TENI	PF02581.10
contig00008-orf00075	DUF2865	PF11064.1
contig00008-orf00075	AAT	PF03417.9
contig00008-orf00076	ADH_N	PF08240.5

Query	Pfam Subject	Pfam ID
contig00008-orf00076	ADH_zinc_N	PF00107.19
contig00008-orf00077	HxlR	PF01638.10
contig00008-orf00080	ThiS	PF02597.13
contig00008-orf00081	ThiG	PF05690.7
contig00008-orf00083	5_3_exonuc_N	PF02739.9
contig00008-orf00083	5_3_exonuc	PF01367.13
contig00008-orf00083	3_5_exonuc	PF01612.13
contig00008-orf00083	DNA_pol_A	PF00476.13
contig00008-orf00086	Na_H_antiporter	PF03553.7
contig00008-orf00087	Dynamitin	PF04912.7
contig00008-orf00087	Hemagglutinin	PF00509.11
contig00008-orf00087	Striatin	PF08232.5
contig00008-orf00087	DUF2968	PF11180.1
contig00008-orf00087	Pfam-B_5463	PB005463
contig00008-orf00087	XhlA	PF10779.2
contig00008-orf00087	SlyX	PF04102.5
contig00008-orf00090	Rhodanese	PF00581.13
contig00008-orf00091	PCMT	PF01135.12
contig00008-orf00094	GAF	PF01590.19
contig00008-orf00094	Pfam-B_2535	PB002535
contig00008-orf00094	Pfam-B_7306	PB007306
contig00008-orf00096	TIM	PF00121.11
contig00008-orf00097	SecG	PF03840.7
contig00008-orf00097	DUF3278	PF11683.1
contig00008-orf00098	AP2	PF00847.13
contig00008-orf00100	PseudoU_synth_2	PF00849.15
contig00008-orf00102	UPF0016	PF01169.12
contig00008-orf00102	UPF0016	PF01169.12
contig00008-orf00103	DUF218	PF02698.10
contig00008-orf00104	SRP54_N	PF02881.12
contig00008-orf00104	SRP54	PF00448.15
contig00008-orf00104	TPP_enzyme_M	PF00205.15
contig00008-orf00104	Peptidase_C23	PF05379.4
contig00008-orf00104	Pfam-B_13277	PB013277
contig00008-orf00104	SRP_SPB	PF02978.12
contig00008-orf00106	Cytochrom_C_asm	PF01578.13
contig00009-orf00001	Transposase_11	PF01609.14
contig00009-orf00003	Pfam-B_76	PB000076
contig00009-orf00003	SWIM	PF04434.10
contig00009-orf00003	Pfam-B_15608	PB015608
contig00009-orf00004	DUF2828	PF11443.1
contig00009-orf00004	VWA_CoxE	PF05762.7

Query	Pfam Subject	Pfam ID
contig00009-orf00005	AAA_5	PF07728.7
contig00009-orf00005	Pfam-B_112	PB000112
contig00009-orf00006	DUF3418	PF11898.1
contig00010-orf00003	Pfam-B_141	PB000141
contig00010-orf00004	FtsK_SpoIIIE	PF01580.11
contig00010-orf00004	Pfam-B_3932	PB003932
contig00010-orf00004	Ftsk_gamma	PF09397.3
contig00010-orf00007	GreA_GreB_N	PF03449.8
contig00010-orf00007	GreA_GreB	PF01272.12
contig00010-orf00009	RNase_PH	PF01138.14
contig00010-orf00009	RNase_PH_C	PF03725.8
contig00010-orf00009	PNPase	PF03726.7
contig00010-orf00009	RNase_PH	PF01138.14
contig00010-orf00009	RNase_PH_C	PF03725.8
contig00010-orf00009	KH_1	PF00013.22
contig00010-orf00009	S1	PF00575.16
contig00010-orf00012	Lipase_GDSL	PF00657.15
contig00010-orf00012	Pfam-B_2673	PB002673
contig00010-orf00013	Pfam-B_16958	PB016958
contig00010-orf00013	DUF459	PF04311.6
contig00010-orf00015	MBOAT	PF03062.12
contig00010-orf00015	Transposase_7	PF01526.10
contig00010-orf00018	Phosphorylase	PF00343.13
contig00010-orf00020	CBM_48	PF02922.11
contig00010-orf00020	Alpha-amylase	PF00128.17
contig00010-orf00020	Pfam-B_375	PB000375
contig00010-orf00020	SBP_bac_9	PF01297.10
contig00010-orf00020	Pfam-B_2479	PB002479
contig00010-orf00022	HlyD	PF00529.13
contig00010-orf00022	Pfam-B_8630	PB008630
contig00010-orf00025	Glycos_trans_3N	PF02885.10
contig00010-orf00025	Glycos_transf_3	PF00591.14
contig00010-orf00027	GATase	PF00117.21
contig00010-orf00030	Phage_AlpA	PF05930.5
contig00010-orf00032	PRA-PH	PF01503.10
contig00010-orf00035	DNA_methylase	PF00145.10
contig00010-orf00035	DNA_methylase	PF00145.10
contig00010-orf00039	SSB	PF00436.18
contig00010-orf00040	DUF2271	PF10029.2
contig00010-orf00041	DUF1153	PF06627.4
contig00010-orf00041	LTXXQ	PF07813.5
contig00010-orf00047	DUF3366	PF11846.1

Query	Pfam Subject	Pfam ID
contig00010-orf00047	KaiC	PF06745.6
contig00010-orf00050	PRA-PH	PF01503.10
contig00010-orf00053	UPF0150	PF03681.8
contig00010-orf00055	Peptidase_S24	PF00717.16
contig00010-orf00058	Pfam-B_5588	PB005588
contig00010-orf00058	TFIIE_beta	PF02186.8
contig00010-orf00058	HTH_DeoR	PF08220.5
contig00010-orf00061	IstB	PF01695.10
contig00010-orf00067	RusA	PF05866.4
contig00010-orf00068	Pfam-B_4921	PB004921
contig00010-orf00068	NinB	PF05772.5
contig00010-orf00069	UPF0122	PF04297.7
contig00010-orf00071	Pfam-B_1215	PB001215
contig00010-orf00071	Phage_Nu1	PF07471.5
contig00010-orf00072	Pfam-B_334	PB000334
contig00010-orf00072	Terminase_6	PF03237.8
contig00010-orf00073	Phage_portal	PF04860.5
contig00010-orf00073	Pfam-B_1002	PB001002
contig00010-orf00073	Phage_Mu_F	PF04233.7
contig00010-orf00074	Peptidase_U35	PF04586.10
contig00010-orf00074	SAB	PF04382.6
contig00010-orf00076	RR_TM4-6	PF06459.5
contig00010-orf00077	Phage_QLRG	PF05135.6
contig00010-orf00078	DUF646	PF04883.5
contig00010-orf00078	Pfam-B_12524	PB012524
contig00010-orf00078	Pfam-B_1106	PB001106
contig00010-orf00081	Big_1	PF02369.9
contig00010-orf00084	DUF3670	PF12419.1
contig00010-orf00085	DUF2460	PF09343.3
contig00010-orf00086	DUF2163	PF09931.2
contig00010-orf00086	DUF2163	PF09931.2
contig00010-orf00086	Phage_BR0599	PF09356.3
contig00010-orf00087	NLPC_P60	PF00877.12
contig00010-orf00087	Pfam-B_7683	PB007683
contig00010-orf00088	DUF390	PF04094.7
contig00010-orf00088	H_lectin	PF09458.3
contig00010-orf00090	Pfam-B_413	PB000413
contig00010-orf00090	Pfam-B_17	PB000017
contig00010-orf00090	Pfam-B_572	PB000572
contig00010-orf00090	Pfam-B_725	PB000725
contig00010-orf00090	DUF1983	PF09327.4
contig00010-orf00090	DUF3672	PF12421.1

Query	Pfam Subject	Pfam ID
contig00010-orf00092	Pfam-B_15693	PB015693
contig00010-orf00092	Pfam-B_763	PB000763
contig00010-orf00092	Pfam-B_15546	PB015546
contig00010-orf00095	YhhN	PF07947.7
contig00010-orf00095	DUF3176	PF11374.1
contig00010-orf00095	Rick_17kDa_Anti	PF05433.8
contig00010-orf00096	Peptidase_M15_3	PF08291.4
contig00010-orf00100	HTH_3	PF01381.15
contig00010-orf00101	OGG_N	PF07934.5
contig00010-orf00102	DUF845	PF05820.4
contig00010-orf00103	Phage_integrase	PF00589.15
contig00010-orf00103	HTH_8	PF02954.12
contig00010-orf00106	Cupin_4	PF08007.5
contig00010-orf00107	Hormone_3	PF00159.11
contig00010-orf00107	Tropomyosin	PF00261.13
contig00010-orf00107	ATP-synt_DE	PF00401.13
contig00010-orf00107	PKK	PF12474.1
contig00010-orf00109	7TM_GPCR_Srz	PF10325.2
contig00010-orf00111	ABC_tran	PF00005.20
contig00010-orf00111	Pfam-B_154	PB000154
contig00010-orf00111	Pfam-B_11182	PB011182
contig00010-orf00111	Pfam-B_11162	PB011162
contig00010-orf00111	Pfam-B_13170	PB013170
contig00010-orf00111	Pfam-B_1712	PB001712
contig00010-orf00111	Pfam-B_6903	PB006903
contig00010-orf00111	Pfam-B_18493	PB018493
contig00010-orf00111	Pfam-B_16279	PB016279
contig00010-orf00111	ABC_tran	PF00005.20
contig00010-orf00111	Pfam-B_11182	PB011182
contig00010-orf00113	Sod_Fe_N	PF00081.15
contig00010-orf00113	Sod_Fe_C	PF02777.11
contig00010-orf00114	DnaB	PF00772.14
contig00010-orf00114	DnaB_C	PF03796.8
contig00010-orf00115	Shufflon_N	PF04917.5
contig00010-orf00115	N_methyl	PF07963.5
contig00010-orf00115	GspH	PF12019.1
contig00010-orf00116	Pfam-B_262	PB000262
contig00010-orf00116	N_methyl	PF07963.5
contig00010-orf00116	TSGP1	PF07771.4
contig00010-orf00117	N_methyl	PF07963.5
contig00010-orf00120	Pilin_PilX	PF11530.1
contig00010-orf00123	Pantoate_ligase	PF02569.8

Query	Pfam Subject	Pfam ID
contig00010-orf00126	Phage_Cox	PF10743.2
contig00010-orf00126	Pantoate_transf	PF02548.8
contig00010-orf00127	Spermine_synth	PF01564.10
contig00010-orf00127	DUF2581	PF10756.2
contig00010-orf00128	GlutR_N	PF05201.8
contig00010-orf00128	Shikimate_DH	PF01488.13
contig00010-orf00128	GlutR_dimer	PF00745.13
contig00010-orf00128	EntA_Immun	PF08951.3
contig00010-orf00137	Pfam-B_15619	PB015619
contig00010-orf00137	Atrophin-1	PF03154.8
contig00010-orf00137	DUF1311	PF07007.5
contig00010-orf00137	PBP_GOBP	PF01395.15
contig00010-orf00138	HTH_3	PF01381.15
contig00010-orf00138	DUF1904	PF08921.4
contig00010-orf00138	DUF3450	PF11932.1
contig00010-orf00138	Sec2p	PF06428.4
contig00010-orf00138	ATP-synt_E_2	PF08112.4
contig00011-orf00001	Sec63	PF02889.9
contig00011-orf00002	Glycos_transf_2	PF00535.19
contig00011-orf00002	Pfam-B_13403	PB013403
contig00011-orf00003	MVIN	PF03023.7
contig00011-orf00004	MVIN	PF03023.7
contig00011-orf00008	DSBA	PF01323.13
contig00011-orf00008	DUF1139	PF06599.4
contig00011-orf00010	GTP1_OBG	PF01018.15
contig00011-orf00010	DUF3602	PF12223.1
contig00011-orf00010	MMR_HSR1	PF01926.16
contig00011-orf00010	Gon7	PF08738.3
contig00011-orf00011	tRNA-synt_1e	PF01406.12
contig00011-orf00011	DALR_2	PF09190.4
contig00011-orf00012	Hexapep	PF00132.17
contig00011-orf00012	Pfam-B_16490	PB016490
contig00011-orf00012	Hexapep	PF00132.17
contig00011-orf00012	Hexapep	PF00132.17
contig00011-orf00014	Ribosomal_L31	PF01197.11
contig00011-orf00019	Redoxin	PF08534.3
contig00011-orf00020	4HBT	PF03061.15
contig00011-orf00022	TonB_dep_Rec	PF00593.17
contig00011-orf00024	Plug	PF07715.8
contig00011-orf00026	CTP_transf_2	PF01467.19
contig00011-orf00028	UPF0005	PF01027.13
contig00011-orf00028	TauE	PF01925.12

Query	Pfam Subject	Pfam ID
contig00011-orf00030	Pfam-B_9648	PB009648
contig00011-orf00030	Lipoprotein_5	PF01298.11
contig00011-orf00030	Bacteriocin_IIc	PF10439.2
contig00011-orf00031	Pribosyltran	PF00156.20
contig00011-orf00031	DHBP_synthase	PF00926.12
contig00011-orf00033	TF_Zn_Ribbon	PF08271.5
contig00011-orf00033	Pfam-B_742	PB000742
contig00011-orf00033	Pfam-B_11855	PB011855
contig00011-orf00033	Pfam-B_1983	PB001983
contig00011-orf00033	MAP7	PF05672.4
contig00011-orf00033	DUF2058	PF09831.2
contig00011-orf00033	DUF607	PF04678.6
contig00011-orf00033	DUF3708	PF12501.1
contig00011-orf00033	Clusterin	PF01093.10
contig00011-orf00033	Pfam-B_18365	PB018365
contig00011-orf00033	Macoilin	PF09726.2
contig00011-orf00033	DUF912	PF06024.5
contig00011-orf00034	AA_kinase	PF00696.21
contig00011-orf00034	Acetyltransf_1	PF00583.17
contig00011-orf00036	KAP_NTPase	PF07693.7
contig00011-orf00036	RNase_E_G	PF10150.2
contig00011-orf00036	DUF3516	PF12029.1
contig00011-orf00036	CbiG_mid	PF11761.1
contig00011-orf00036	GspM_II	PF10741.2
contig00011-orf00038	GIDA	PF01134.15
contig00011-orf00041	AA_kinase	PF00696.21
contig00011-orf00043	UBA	PF00627.24
contig00011-orf00043	EF_TS	PF00889.12
contig00011-orf00045	Ribosomal_S2	PF00318.13
contig00011-orf00045	BLOC1_2	PF10046.2
contig00011-orf00047	Pfam-B_5296	PB005296
contig00011-orf00047	7tm_7	PF08395.5
contig00011-orf00047	FtsL	PF04999.6
contig00011-orf00047	MscL	PF01741.11
contig00011-orf00047	Bac_small_YrzI	PF09501.3
contig00011-orf00048	5-FTHF_cyc-lig	PF01812.13
contig00011-orf00049	Acetyltransf_1	PF00583.17
contig00011-orf00051	Adeno_E3_14_5	PF04834.5
contig00011-orf00052	Mqo	PF06039.8
contig00011-orf00055	APH	PF01636.16
contig00011-orf00057	OstA	PF03968.7
contig00011-orf00057	OstA_C	PF04453.7

Query	Pfam Subject	Pfam ID
contig00011-orf00058	SurA_N	PF09312.4
contig00011-orf00058	SurA_N	PF09312.4
contig00011-orf00058	Rotamase	PF00639.14
contig00011-orf00068	PAP2	PF01569.14
contig00011-orf00068	Pfam-B_2977	PB002977
contig00011-orf00068	BPD_transp_2	PF02653.9
contig00011-orf00069	Torsin	PF06309.4
contig00011-orf00069	Abhydrolase_1	PF00561.13
contig00011-orf00070	Peptidase_S49	PF01343.11
contig00011-orf00072	DnaJ	PF00226.24
contig00011-orf00072	DUF1311	PF07007.5
contig00011-orf00072	DnaJ_C	PF01556.11
contig00011-orf00072	DnaJ_CXXCXGXG	PF00684.12
contig00011-orf00072	DnaJ_C	PF01556.11
contig00011-orf00072	DnaJ_C	PF01556.11
contig00011-orf00075	tRNA-synt_1	PF00133.15
contig00011-orf00075	tRNA-synt_1	PF00133.15
contig00011-orf00075	tRNA-synt_1	PF00133.15
contig00011-orf00075	Anticodon_1	PF08264.6
contig00011-orf00078	DRP	PF06044.5
contig00011-orf00078	DUF1407	PF07191.5
contig00011-orf00078	FdhE	PF04216.5
contig00011-orf00078	CK_II_beta	PF01214.11
contig00011-orf00082	N6_N4_Mtase	PF01555.11
contig00011-orf00083	N6_N4_Mtase	PF01555.11
contig00011-orf00084	Pfam-B_13706	PB013706
contig00011-orf00084	Pfam-B_2974	PB002974
contig00011-orf00084	HTH_AraC	PF00165.16
contig00011-orf00084	HTH_AraC	PF00165.16
contig00011-orf00087	Aldedh	PF00171.15
contig00011-orf00087	Aldedh	PF00171.15
contig00011-orf00087	Fe-ADH	PF00465.12
contig00011-orf00088	Pfam-B_5612	PB005612
contig00011-orf00090	DUF1311	PF07007.5
contig00011-orf00090	Med15_fungi	PF05397.5
contig00011-orf00094	Glt_symporter	PF03616.7
contig00011-orf00095	SBF	PF01758.9
contig00011-orf00095	Birna_VP4	PF01768.9
contig00011-orf00097	Pfam-B_110	PB000110
contig00011-orf00097	Pfam-B_345	PB000345
contig00011-orf00097	Pfam-B_2161	PB002161
contig00011-orf00097	Methyltransf_11	PF08241.5

Query	Pfam Subject	Pfam ID
contig00011-orf00097	Pfam-B_1802	PB001802
contig00011-orf00097	Pfam-B_225	PB000225
contig00011-orf00101	mRNA_cap_enzyme	PF01331.12
contig00011-orf00102	Ribosomal_S10	PF00338.15
contig00011-orf00102	PRP3	PF08572.3
contig00012-orf00001	FAD_binding_3	PF01494.12
contig00012-orf00002	DUF441	PF04284.6
contig00012-orf00003	polyprenyl_synt	PF00348.10
contig00012-orf00003	DUF3486	PF11985.1
contig00012-orf00005	Ribosomal_L21p	PF00829.14
contig00012-orf00007	Ribosomal_L27	PF01016.12
contig00012-orf00009	ThiC	PF01964.11
contig00012-orf00010	Lpp-LpqN	PF10738.2
contig00012-orf00010	CCP_MauG	PF03150.7
contig00012-orf00010	Cytochrom_C	PF00034.14
contig00012-orf00012	NAD_Gly3P_dh_N	PF01210.16
contig00012-orf00012	NAD_Gly3P_dh_C	PF07479.7
contig00012-orf00013	PspA_IM30	PF04012.5
contig00012-orf00013	DUF904	PF06005.5
contig00012-orf00013	Baculo_PEP_C	PF04513.5
contig00012-orf00013	Vac_Fusion	PF02346.9
contig00012-orf00013	DUF3584	PF12128.1
contig00012-orf00013	Apolipoprotein	PF01442.11
contig00012-orf00013	THOC7	PF05615.6
contig00012-orf00013	Mnd1	PF03962.8
contig00012-orf00013	HOOK	PF05622.5
contig00012-orf00013	DUF1465	PF07323.5
contig00012-orf00013	DUF1875	PF08961.3
contig00012-orf00013	bZIP_1	PF00170.14
contig00012-orf00013	FtsL	PF04999.6
contig00012-orf00013	DivIVA	PF05103.6
contig00012-orf00013	DUF3482	PF11981.1
contig00012-orf00013	Prefoldin_2	PF01920.13
contig00012-orf00013	DUF1640	PF07798.4
contig00012-orf00013	DUF342	PF03961.6
contig00012-orf00013	Gp-FAR-1	PF05823.5
contig00012-orf00013	Phage_GP20	PF06810.4
contig00012-orf00013	Syntaxin	PF00804.18
contig00012-orf00013	ApoLp-III	PF07464.4
contig00012-orf00013	Bap31	PF05529.5
contig00012-orf00013	Seryl_tRNA_N	PF02403.15
contig00012-orf00013	HALZ	PF02183.11

Query	Pfam Subject	Pfam ID
contig00012-orf00013	DUF3086	PF11285.1
contig00012-orf00013	ADIP	PF11559.1
contig00012-orf00013	DUF2508	PF10704.2
contig00012-orf00013	Jnk-SapK_ap_N	PF09744.2
contig00012-orf00013	Ribosomal_S30AE	PF02482.12
contig00012-orf00013	RmuC	PF02646.9
contig00012-orf00013	Laminin_II	PF06009.5
contig00012-orf00013	DUF904	PF06005.5
contig00012-orf00013	TPR_MLP1_2	PF07926.5
contig00012-orf00013	DUF1241	PF06840.4
contig00012-orf00013	bZIP_1	PF00170.14
contig00012-orf00013	FlaC_arch	PF05377.4
contig00012-orf00013	PEP-utilisers_N	PF05524.6
contig00012-orf00013	BING4CT	PF08149.4
contig00012-orf00015	ZapA	PF05164.6
contig00012-orf00017	Ribosomal_L13	PF00572.11
contig00012-orf00018	Ribosomal_S9	PF00380.12
contig00012-orf00020	Pfam-B_424	PB000424
contig00012-orf00020	CW_binding_1	PF01473.13
contig00012-orf00020	SEC-C	PF02810.8
contig00012-orf00022	Na_H_Exchanger	PF00999.14
contig00012-orf00022	TrkA_N	PF02254.11
contig00012-orf00022	TrkA_C	PF02080.14
contig00013-orf00002	rve	PF00665.19
contig00013-orf00002	DUF461	PF04314.6
contig00013-orf00004	Pro_isomerase	PF00160.14
contig00013-orf00006	YceI	PF04264.6
contig00013-orf00009	Proteasom_Rpn13	PF04683.6
contig00013-orf00009	FtsK_SpoIIIE	PF01580.11
contig00013-orf00009	Ftsk_gamma	PF09397.3
contig00013-orf00012	SNF	PF00209.11
contig00013-orf00012	SNF	PF00209.11
contig00013-orf00013	FxsA	PF04186.6
contig00013-orf00014	Entericidin	PF08085.4
contig00013-orf00014	DUF3373	PF11853.1
contig00013-orf00014	DUF2076	PF09849.2
contig00013-orf00014	Hira	PF07569.4
contig00013-orf00014	Rick_17kDa_Anti	PF05433.8
contig00014-orf00002	Zot	PF05707.5
contig00014-orf00002	Pfam-B_14715	PB014715
contig00014-orf00004	DUF2523	PF10734.2
contig00015-orf00001	Transposase_11	PF01609.14

Query	Pfam Subject	Pfam ID
contig00016-orf00001	Lipoprotein_9	PF03180.7
contig00016-orf00003	HTH_1	PF00126.20
contig00016-orf00003	LysR_substrate	PF03466.13
contig00016-orf00004	Pfam-B_18398	PB018398
contig00016-orf00004	OmpA	PF00691.13
contig00016-orf00004	Pilus_CpaD	PF09476.3
contig00016-orf00004	DUF561	PF04481.5
contig00016-orf00006	Seryl_tRNA_N	PF02403.15
contig00016-orf00006	HlyD	PF00529.13
contig00016-orf00006	Mnd1	PF03962.8
contig00016-orf00006	BLOC1_2	PF10046.2
contig00016-orf00006	Spc7	PF08317.4
contig00016-orf00006	LUC7	PF03194.8
contig00016-orf00006	Plasmid_RAQPRD	PF09686.3
contig00016-orf00006	tRNA-synt_2b	PF00587.18
contig00016-orf00007	Ribosomal_S6	PF01250.10
contig00016-orf00009	Ribosomal_S18	PF01084.13
contig00016-orf00010	Ribosomal_L9_N	PF01281.12
contig00016-orf00010	Phage_lysis	PF03245.6
contig00016-orf00010	Pilus_CpaD	PF09476.3
contig00016-orf00010	Ribosomal_L9_C	PF03948.7
contig00016-orf00013	Glucosaminidase	PF01832.13
contig00016-orf00015	Aldose_epim	PF01263.13
contig00016-orf00017	AAA	PF00004.22
contig00016-orf00017	Pfam-B_12262	PB012262
contig00016-orf00017	DNA_pol3_gamma3	PF12169.1
contig00016-orf00017	Pfam-B_678	PB000678
contig00016-orf00019	EAP30	PF04157.9
contig00016-orf00019	DUF149	PF02575.9
contig00016-orf00019	Pfam-B_15337	PB015337
contig00016-orf00019	DUF3300	PF11737.1
contig00016-orf00021	RecO_N	PF11967.1
contig00016-orf00021	RecO_C	PF02565.8
contig00016-orf00024	Pfam-B_7227	PB007227
contig00016-orf00024	Pfam-B_5638	PB005638
contig00016-orf00025	zf-CHCC	PF10276.2
contig00016-orf00026	MliC	PF09864.2
contig00016-orf00029	UPF0154	PF03672.6
contig00016-orf00029	FeoB_C	PF07664.5
contig00016-orf00029	DUF539	PF04400.6
contig00016-orf00030	ApbE	PF02424.8
contig00016-orf00033	S-AdoMet_synt_N	PF00438.13

Query	Pfam Subject	Pfam ID
contig00016-orf00033	S-AdoMet_synt_M	PF02772.9
contig00016-orf00033	S-AdoMet_synt_C	PF02773.9
contig00016-orf00035	PdxJ	PF03740.6
contig00016-orf00035	DUF849	PF05853.5
contig00016-orf00038	ACPS	PF01648.13
contig00017-orf00002	THF_DHG_CYH	PF00763.16
contig00017-orf00002	SLBB	PF10531.2
contig00017-orf00002	THF_DHG_CYH_C	PF02882.12
contig00017-orf00006	Isochorismatase	PF00857.13
contig00017-orf00007	Acetyltransf_1	PF00583.17
contig00017-orf00008	SspB	PF04386.6
contig00017-orf00009	GST_N	PF02798.13
contig00017-orf00009	GST_C	PF00043.18
contig00017-orf00011	Pfam-B_724	PB000724
contig00017-orf00011	Hexapep	PF00132.17
contig00017-orf00016	GlnE	PF03710.8
contig00017-orf00016	GlnD_UR_UTase	PF08335.4
contig00017-orf00016	GlnE	PF03710.8
contig00017-orf00016	GlnD_UR_UTase	PF08335.4
contig00017-orf00019	Lip_A_acyltrans	PF03279.6
contig00017-orf00021	HTH_5	PF01022.13
contig00017-orf00024	Exo_endo_phos	PF03372.16
contig00018-orf00002	Ala_racemase_N	PF01168.13
contig00018-orf00002	BolA	PF01722.11
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Pfam-B_8974	PB008974
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
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contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7

Query	Pfam Subject	Pfam ID
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Pfam-B_19018	PB019018
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Pfam-B_19505	PB019505
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Pfam-B_19018	PB019018
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	Hep_Hag	PF05658.7
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	Pfam-B_19505	PB019505
contig00018-orf00010	Pfam-B_4382	PB004382
contig00018-orf00010	Phage_T7_tail	PF03906.7
contig00018-orf00010	Pfam-B_9545	PB009545
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	Pfam-B_9545	PB009545
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	Cpn10	PF00166.14
contig00018-orf00010	HIM	PF05662.7
contig00018-orf00010	HIM	PF05662.7
contig00019-orf00001	Cas_Cas1	PF01867.9
contig00020-orf00001	SAICAR_synt	PF01259.11
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	Pfam-B_639	PB000639
contig00020-orf00005	Pfam-B_9305	PB009305
contig00020-orf00005	Pfam-B_12469	PB012469
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	Pfam-B_7705	PB007705
contig00020-orf00005	Pfam-B_9305	PB009305
contig00020-orf00005	Pfam-B_639	PB000639
contig00020-orf00005	Pfam-B_12469	PB012469
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	Pfam-B_7705	PB007705

Query	Pfam Subject	Pfam ID
contig00020-orf00005	Pfam-B_12469	PB012469
contig00020-orf00005	Pfam-B_639	PB000639
contig00020-orf00005	Pfam-B_9305	PB009305
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	HemolysinCabind	PF00353.12
contig00020-orf00005	RTX_C	PF08339.3
contig00020-orf00005	HCBP_related	PF06594.4
contig00020-orf00007	RmlD_sub_bind	PF04321.10
contig00020-orf00009	DUF836	PF05768.7
contig00020-orf00010	Fer2_BFD	PF04324.8
contig00020-orf00010	V-SNARE_C	PF12352.1
contig00021-orf00002	Inhibitor_I34	PF10466.2
contig00021-orf00003	DUF3606	PF12244.1
contig00021-orf00003	TPR_2	PF07719.10
contig00021-orf00003	Sel1	PF08238.5
contig00021-orf00003	Sel1	PF08238.5
contig00021-orf00003	Sel1	PF08238.5
contig00021-orf00003	Sel1	PF08238.5
contig00021-orf00003	Sel1	PF08238.5
contig00021-orf00004	Pfam-B_4654	PB004654
contig00021-orf00004	SBF	PF01758.9
contig00021-orf00005	RNase_HII	PF01351.11
contig00021-orf00009	LpxB	PF02684.8
contig00021-orf00010	VacJ	PF04333.6
contig00021-orf00011	Pfam-B_2305	PB002305
contig00021-orf00011	Pfam-B_915	PB000915
contig00021-orf00014	Tol_Tol_Ttg2	PF05494.5
contig00021-orf00016	MCE	PF02470.13
contig00021-orf00016	MreC	PF04085.7
contig00021-orf00019	DUF140	PF02405.9
contig00021-orf00019	DDDD	PF10161.2
contig00021-orf00022	Pfam-B_6541	PB006541
contig00021-orf00022	Pfam-B_5069	PB005069
contig00021-orf00022	ABC_tran	PF00005.20
contig00021-orf00026	TAT_signal	PF10518.2
contig00021-orf00027	Tubulin	PF00091.18
contig00021-orf00027	FtsZ_C	PF12327.1
contig00021-orf00028	FtsA	PF02491.13
contig00021-orf00028	SrfB	PF07520.4
contig00021-orf00028	FtsA	PF02491.13
contig00021-orf00028	DRTGG	PF07085.5

Query	Pfam Subject	Pfam ID
contig00021-orf00030	POTRA_1	PF08478.3
contig00021-orf00030	FtsQ	PF03799.8
contig00021-orf00032	Dala_Dala_lig_N	PF01820.14
contig00021-orf00032	Dala_Dala_lig_N	PF01820.14
contig00021-orf00032	Dala_Dala_lig_C	PF07478.6
contig00021-orf00032	Pfam-B_1558	PB001558
contig00021-orf00035	Mur_ligase	PF01225.18
contig00021-orf00035	Mur_ligase_M	PF08245.5
contig00021-orf00035	Mur_ligase_C	PF02875.14
contig00021-orf00037	LCM	PF04072.7
contig00021-orf00040	Glyco_transf_28	PF03033.13
contig00021-orf00040	Pfam-B_946	PB000946
contig00021-orf00040	Glyco_tran_28_C	PF04101.9
contig00021-orf00042	FTSW_RODA_SPOVE	PF01098.12
contig00021-orf00047	Amidase	PF01425.14
contig00021-orf00049	RHH_2	PF03693.7
contig00021-orf00049	Amidase	PF01425.14
contig00021-orf00051	TLC	PF03219.7
contig00021-orf00052	2-Hacid_dh_C	PF02826.12
contig00021-orf00052	Mur_ligase_M	PF08245.5
contig00021-orf00052	Mur_ligase_C	PF02875.14
contig00021-orf00054	Sel1	PF08238.5
contig00021-orf00054	Arc_PepC	PF06819.4
contig00021-orf00054	Sel1	PF08238.5
contig00021-orf00054	Transposase_Tn5	PF02281.9
contig00021-orf00054	Sel1	PF08238.5
contig00021-orf00054	Glu_syn_central	PF04898.7
contig00021-orf00054	Sel1	PF08238.5
contig00021-orf00055	Bac_globin	PF01152.14
contig00021-orf00055	Pfam-B_1247	PB001247
contig00022-orf00001	Ribosomal_L33	PF00471.13
contig00022-orf00002	Ribosomal_L28	PF00830.12
contig00022-orf00005	MFS_1	PF07690.9
contig00022-orf00007	DUF3290	PF11694.1
contig00022-orf00007	HlyD	PF00529.13
contig00022-orf00009	Acetate_kinase	PF00871.10
contig00022-orf00009	FAD_binding_4	PF01565.16
contig00022-orf00011	PrpF	PF04303.6
contig00022-orf00011	Virul_Fac	PF10139.2
contig00022-orf00011	Ribosomal_60s	PF00428.12
contig00022-orf00013	Aconitase	PF00330.13
contig00022-orf00013	Aconitase_C	PF00694.12

Query	Pfam Subject	Pfam ID
contig00022-orf00014	Aconitase	PF00330.13
contig00022-orf00016	EamA	PF00892.13
contig00022-orf00016	EamA	PF00892.13
contig00022-orf00019	TauE	PF01925.12
contig00022-orf00019	Na_Pi_cotrans	PF02690.8
contig00022-orf00019	Ndr	PF03096.7
contig00022-orf00020	TauD	PF02668.9
contig00022-orf00021	Citrate_synt	PF00285.14
contig00022-orf00025	ICL	PF00463.14
contig00022-orf00025	ComA	PF02679.8
contig00022-orf00031	MFS_1	PF07690.9
contig00023-orf00001	Pfam-B_18818	PB018818
contig00023-orf00001	PTA_PTB	PF01515.12
contig00023-orf00003	Trp_Tyr_perm	PF03222.6
contig00023-orf00004	Pro_CA	PF00484.12
contig00023-orf00005	Pro_CA	PF00484.12
contig00023-orf00007	Sulfate_transp	PF00916.13
contig00023-orf00013	dTDP_sugar_isom	PF00908.10
contig00023-orf00014	Orn_Arg_deC_N	PF02784.9
contig00023-orf00014	Orn_DAP_Arg_deC	PF00278.15
contig00023-orf00015	Pfam-B_70	PB000070
contig00023-orf00016	Frataxin_Cyay	PF01491.9
contig00023-orf00018	LuxS	PF02664.8
contig00023-orf00018	DUF2540	PF10802.1
contig00023-orf00019	EamA	PF00892.13
contig00023-orf00019	EamA	PF00892.13
contig00023-orf00020	NTP_transferase	PF00483.16
contig00023-orf00020	NTP_transferase	PF00483.16
contig00023-orf00022	Flavin_Reduct	PF01613.11
contig00023-orf00023	RNA12	PF10443.2
contig00023-orf00023	MarR	PF01047.15
contig00023-orf00025	Redoxin	PF08534.3
contig00023-orf00026	Gp_dh_N	PF00044.17
contig00023-orf00026	Gp_dh_C	PF02800.13
contig00023-orf00029	AsmA	PF05170.7
contig00023-orf00029	Pfam-B_2548	PB002548
contig00023-orf00029	Pfam-B_6191	PB006191
contig00023-orf00030	DAHP_synth_1	PF00793.13
contig00023-orf00034	Aconitase_B_N	PF11791.1
contig00023-orf00034	Aconitase_2_N	PF06434.6
contig00023-orf00034	Aconitase	PF00330.13
contig00023-orf00034	DUF521	PF04412.6

Query	Pfam Subject	Pfam ID
contig00023-orf00034	Aconitase	PF00330.13
contig00023-orf00036	zf-C4_ClpX	PF06689.6
contig00023-orf00036	Pfam-B_14	PB000014
contig00023-orf00036	AAA_2	PF07724.7
contig00023-orf00036	ClpB_D2-small	PF10431.2
contig00023-orf00040	Peptidase_S11	PF00768.13
contig00023-orf00041	Peptidase_M48	PF01435.11
contig00024-orf00005	tRNA-synt_1	PF00133.15
contig00024-orf00005	Anticodon_1	PF08264.6
contig00024-orf00005	zf-FPG_IleRS	PF06827.7
contig00024-orf00007	HemS	PF05171.5
contig00024-orf00010	Peripla_BP_2	PF01497.11
contig00024-orf00012	PSI_PsaJ	PF01701.11
contig00024-orf00012	FecCD	PF01032.11
contig00024-orf00014	SMC_N	PF02463.12
contig00024-orf00014	ABC_tran	PF00005.20
contig00024-orf00016	tRNA_lig_kinase	PF08303.4
contig00024-orf00016	SKI	PF01202.15
contig00024-orf00019	GntP_permease	PF02447.9
contig00024-orf00019	DUF1240	PF06836.5
contig00024-orf00021	Ribosomal_S30AE	PF02482.12
contig00024-orf00021	Spore_GerAC	PF05504.4
contig00024-orf00023	Sigma54_CBD	PF04963.6
contig00024-orf00023	CUE	PF02845.9
contig00024-orf00023	Sigma54_DBD	PF04552.6
contig00024-orf00024	Sigma54_AID	PF00309.13
contig00024-orf00026	ABC_tran	PF00005.20
contig00024-orf00026	BCA_ABC_TP_C	PF12399.1
contig00024-orf00028	OstA	PF03968.7
contig00024-orf00029	DUF1239	PF06835.6
contig00024-orf00031	Hydrolase_3	PF08282.5
contig00024-orf00031	Hydrolase_3	PF08282.5
contig00024-orf00032	HTH_1	PF00126.20
contig00024-orf00032	LysR_substrate	PF03466.13
contig00024-orf00033	NIF3	PF01784.11
contig00024-orf00034	UCR_Fe-S_N	PF10399.2
contig00024-orf00034	CytB6-F_Fe-S	PF08802.3
contig00024-orf00034	Rieske	PF00355.19
contig00024-orf00035	Cytochrom_B_N	PF00033.12
contig00024-orf00035	Cytochrom_B_C	PF00032.10
contig00024-orf00036	Cytochrom_C1	PF02167.8
contig00024-orf00037	ThiF	PF00899.14

Query	Pfam Subject	Pfam ID
contig00024-orf00037	MoeZ_MoeB	PF05237.6
contig00024-orf00038	Glyco_hydro_65C	PF03633.8
contig00024-orf00040	FecCD	PF01032.11
contig00024-orf00042	FecCD	PF01032.11
contig00024-orf00042	TPPK_C	PF12555.1
contig00024-orf00042	Bac_export_3	PF01313.12
contig00024-orf00043	Acyl_transf_3	PF01757.15
contig00024-orf00043	Pfam-B_150	PB000150
contig00024-orf00043	Pfam-B_1658	PB001658
contig00024-orf00044	Pfam-B_1290	PB001290
contig00024-orf00044	FmdE	PF02663.7
contig00024-orf00045	ABC_tran	PF00005.20
contig00024-orf00045	ABC_ATPase	PF09818.2
contig00024-orf00047	DUF788	PF05620.4
contig00024-orf00049	Queuosine_synth	PF02547.8
contig00024-orf00051	Fer4_NifH	PF00142.11
contig00024-orf00051	ParA	PF10609.2
contig00025-orf00003	CarD_TRCF	PF02559.9
contig00025-orf00003	HemY_N	PF07219.6
contig00025-orf00003	DEAD	PF00270.22
contig00025-orf00003	Helicase_C	PF00271.24
contig00025-orf00003	Pfam-B_8434	PB008434
contig00025-orf00003	TRCF	PF03461.8
contig00026-orf00001	DUF28	PF01709.13
contig00026-orf00003	SBP_bac_9	PF01297.10
contig00026-orf00014	Pfam-B_1684	PB001684
contig00026-orf00014	DUF3335	PF11814.1
contig00026-orf00014	Peptidase_C39	PF03412.8
contig00026-orf00014	Pfam-B_1781	PB001781
contig00026-orf00016	DAO	PF01266.17
contig00026-orf00016	DAO	PF01266.17
contig00026-orf00016	ETF_QO	PF05187.6
contig00026-orf00019	DUF3683	PF12447.1
contig00026-orf00019	FAD_binding_4	PF01565.16
contig00026-orf00019	FAD-oxidase_C	PF02913.12
contig00026-orf00019	FAD-oxidase_C	PF02913.12
contig00026-orf00019	Fer4	PF00037.20
contig00026-orf00019	CCG	PF02754.9
contig00026-orf00019	CCG	PF02754.9
contig00026-orf00019	DUF3400	PF11880.1
contig00026-orf00020	Sugar_tr	PF00083.17
contig00026-orf00021	FAD_binding_4	PF01565.16

Query	Pfam Subject	Pfam ID
contig00026-orf00021	AcylCoA_dehyd_C	PF12186.1
contig00026-orf00021	Lact-deh-memb	PF09330.4
contig00026-orf00024	CMD	PF02627.13
contig00026-orf00024	Glycos_trans_3N	PF02885.10
contig00026-orf00026	Acyl-CoA_dh_N	PF02771.9
contig00026-orf00026	Acyl-CoA_dh_M	PF02770.12
contig00026-orf00026	Acyl-CoA_dh_2	PF08028.4
contig00026-orf00029	Rubredoxin	PF00301.13
contig00026-orf00029	ADK_lid	PF05191.7
contig00026-orf00029	DUF2296	PF10058.2
contig00026-orf00029	XPA_N	PF01286.11
contig00026-orf00029	TF_Zn_Ribbon	PF08271.5
contig00026-orf00031	Acyltransferase	PF01553.14
contig00026-orf00032	PP-binding	PF00550.18
contig00026-orf00034	DUF340	PF03956.6
contig00027-orf00001	Pfam-B_13759	PB013759
contig00027-orf00002	Pfam-B_4866	PB004866
contig00027-orf00003	Pfam-B_9471	PB009471
contig00027-orf00003	Rep_trans	PF02486.12
contig00027-orf00005	Pfam-B_12083	PB012083
contig00027-orf00005	TIP41	PF04176.6
contig00027-orf00005	LolA	PF03548.8
contig00027-orf00005	DUF2092	PF09865.2
contig00027-orf00005	DUF2092	PF09865.2
contig00027-orf00008	DUF455	PF04305.7
contig00027-orf00011	Cation_efflux	PF01545.14
contig00027-orf00014	Hydrolase	PF00702.19
contig00027-orf00015	Malate_DH	PF12434.1
contig00027-orf00015	malic	PF00390.12
contig00027-orf00015	Malic_M	PF03949.8
contig00027-orf00016	Thymidylate_kin	PF02223.10
contig00027-orf00018	SCPU	PF05229.8
contig00027-orf00019	Pfam-B_16886	PB016886
contig00027-orf00019	Pili_assembly_N	PF00345.13
contig00027-orf00020	Usher	PF00577.13
contig00027-orf00023	SCPU	PF05229.8
contig00027-orf00024	NAD_binding_2	PF03446.8
contig00027-orf00026	GumN	PF07446.4
contig00027-orf00026	RepB	PF07506.4
contig00027-orf00027	Peptidase_S15	PF02129.11
contig00027-orf00031	HATPase_c	PF02518.19
contig00027-orf00031	DNA_gyraseB	PF00204.18

Query	Pfam Subject	Pfam ID
contig00027-orf00031	DNA_gyraseB_C	PF00986.14
contig00027-orf00033	NUDIX	PF00293.21
contig00027-orf00035	Form_Nir_trans	PF01226.10
contig00027-orf00036	Pfam-B_7357	PB007357
contig00027-orf00036	Abhydrolase_3	PF07859.6
contig00027-orf00036	Peptidase_S9	PF00326.14
contig00027-orf00038	Na_Ala_symp	PF01235.10
contig00027-orf00038	DUF2569	PF10754.2
contig00027-orf00039	Pfam-B_261	PB000261
contig00027-orf00039	HTH_11	PF08279.5
contig00027-orf00039	Transposase_5	PF01498.11
contig00027-orf00039	rve	PF00665.19
contig00028-orf00001	rve	PF00665.19
contig00028-orf00002	SecB	PF02556.7
contig00028-orf00003	Glutaredoxin	PF00462.17
contig00028-orf00006	S1	PF00575.16
contig00028-orf00006	RNase_E_G	PF10150.2
contig00028-orf00008	Response_reg	PF00072.17
contig00028-orf00008	Trans_reg_C	PF00486.21
contig00028-orf00011	Pfam-B_5488	PB005488
contig00028-orf00011	Pfam-B_4864	PB004864
contig00028-orf00011	HAMP	PF00672.18
contig00028-orf00011	HisKA	PF00512.18
contig00028-orf00011	BCS1_N	PF08740.4
contig00028-orf00011	HATPase_c	PF02518.19
contig00028-orf00013	adh_short	PF00106.18
contig00028-orf00013	Pfam-B_822	PB000822
contig00028-orf00017	Glycos_transf_2	PF00535.19
contig00028-orf00018	Glycos_transf_2	PF00535.19
contig00028-orf00018	DUF2862	PF11061.1
contig00028-orf00018	GlcNAc	PF11397.1
contig00028-orf00019	ABC_membrane	PF00664.16
contig00028-orf00019	ABC_tran	PF00005.20
contig00028-orf00019	Pfam-B_11559	PB011559
contig00028-orf00019	Pfam-B_26	PB000026
contig00028-orf00020	Acyl_transf_1	PF00698.14
contig00028-orf00020	BMC	PF00936.12
contig00028-orf00023	CSD	PF00313.15
contig00028-orf00023	CSD	PF00313.15
contig00028-orf00023	DUF1294	PF06961.6
contig00028-orf00027	ACP_syn_III	PF08545.3
contig00028-orf00027	ACP_syn_III_C	PF08541.3

Query	Pfam Subject	Pfam ID
contig00028-orf00029	Methyltrans_RNA	PF04452.7
contig00028-orf00030	Inositol_P	PF00459.18
contig00028-orf00033	GST_N	PF02798.13
contig00028-orf00033	GST_C	PF00043.18
contig00028-orf00035	HTH_11	PF08279.5
contig00028-orf00035	Pfam-B_344	PB000344
contig00028-orf00035	Death	PF00531.15
contig00028-orf00037	MGS	PF02142.15
contig00028-orf00037	AICARFT_IMPCHas	PF01808.11
contig00028-orf00039	Pilin_PilX	PF11530.1
contig00028-orf00040	CsgG	PF03783.7
contig00028-orf00040	Pfam-B_16879	PB016879
contig00028-orf00040	Pfam-B_5873	PB005873
contig00028-orf00041	Pfam-B_785	PB000785
contig00028-orf00041	YkyA	PF10368.2
contig00028-orf00041	Pfam-B_720	PB000720
contig00028-orf00043	DUF799	PF05643.4
contig00028-orf00043	Pfam-B_1798	PB001798
contig00028-orf00043	PQQ	PF01011.14
contig00028-orf00045	EamA	PF00892.13
contig00028-orf00045	SPC25	PF06703.4
contig00028-orf00045	EamA	PF00892.13
contig00028-orf00045	DASH_Dad1	PF08649.3
contig00028-orf00047	HTH_8	PF02954.12
contig00028-orf00047	Phage_NinH	PF06322.4
contig00028-orf00050	Dus	PF01207.10
contig00028-orf00052	Peptidase_M50	PF02163.15
contig00028-orf00055	DNA_pol3_delta	PF06144.6
contig00028-orf00055	Pfam-B_4606	PB004606
contig00028-orf00055	Pfam-B_4838	PB004838
contig00028-orf00056	LPAM_1	PF08139.5
contig00028-orf00056	Rz1	PF06085.4
contig00028-orf00056	RplB	PF04390.5
contig00028-orf00058	Abhydrolase_1	PF00561.13
contig00028-orf00059	Pfam-B_5612	PB005612
contig00028-orf00060	DUF571	PF04600.5
contig00028-orf00060	DUF1469	PF07332.4
contig00028-orf00060	CcoS	PF03597.8
contig00028-orf00062	RDD	PF06271.5
contig00028-orf00066	Pro_dh	PF01619.11
contig00028-orf00066	Aldedh	PF00171.15
contig00028-orf00067	SSF	PF00474.10

Query	Pfam Subject	Pfam ID
contig00028-orf00070	ABC1	PF03109.9
contig00028-orf00070	Pkinase	PF00069.18
contig00028-orf00075	DUF526	PF04380.6
contig00028-orf00075	Spc7	PF08317.4
contig00028-orf00075	Dynamitin	PF04912.7
contig00028-orf00075	ISG65-75	PF11727.1
contig00028-orf00075	Transposase_30	PF04740.5
contig00028-orf00075	Pfam-B_10308	PB010308
contig00028-orf00075	DUF1875	PF08961.3
contig00028-orf00075	IL6	PF00489.10
contig00028-orf00075	COG2	PF06148.4
contig00028-orf00075	Med25_SD1	PF11235.1
contig00028-orf00079	Pfam-B_4703	PB004703
contig00028-orf00079	Mg_chelatase	PF01078.14
contig00028-orf00081	6PF2K	PF01591.11
contig00028-orf00082	Pfam-B_3	PB000003
contig00028-orf00086	DUF2078	PF09851.2
contig00028-orf00086	SPOR	PF05036.6
contig00028-orf00087	DSBA	PF01323.13
contig00028-orf00089	BacA	PF02673.11
contig00028-orf00091	TP_methylase	PF00590.13
contig00028-orf00092	Maf	PF02545.7
contig00028-orf00093	DUF177	PF02620.10
contig00028-orf00094	Ribosomal_L32p	PF01783.16
contig00028-orf00095	Pribosyltran	PF00156.20
contig00028-orf00098	FA_synthesis	PF02504.8
contig00028-orf00101	tRNA_synt_2f	PF02092.10
contig00028-orf00101	Rb-bdg_C_Cenp-F	PF10490.2
contig00028-orf00101	DALR_1	PF05746.8
contig00028-orf00102	tRNA-synt_2e	PF02091.8
contig00028-orf00105	Pfam-B_650	PB000650
contig00028-orf00105	Exon_PolB	PF10108.2
contig00029-orf00003	SUFU	PF05076.6
contig00029-orf00006	DUF1557	PF07591.4
contig00029-orf00006	Pfam-B_190	PB000190
contig00029-orf00010	Pfam-B_44	PB000044
contig00029-orf00010	Pfam-B_45	PB000045
contig00029-orf00010	FUSC	PF04632.5
contig00029-orf00010	Pfam-B_7778	PB007778
contig00029-orf00010	Pfam-B_835	PB000835
contig00029-orf00014	OTCace_N	PF02729.14
contig00029-orf00014	OTCace	PF00185.17

Query	Pfam Subject	Pfam ID
contig00029-orf00016	PyrI	PF01948.11
contig00029-orf00016	PyrI_C	PF02748.8
contig00029-orf00016	zf-BED	PF02892.8
contig00029-orf00018	Toluene_X	PF03349.9
contig00029-orf00021	DHFR_1	PF00186.12
contig00029-orf00025	DegV	PF02645.9
contig00029-orf00028	Pfam-B_13961	PB013961
contig00029-orf00028	Pfam-B_8477	PB008477
contig00029-orf00028	PCRF	PF03462.11
contig00029-orf00028	MIR	PF02815.12
contig00029-orf00028	RF-1	PF00472.13
contig00029-orf00032	EPSP_synthase	PF00275.13
contig00029-orf00035	Acetyltransf_1	PF00583.17
contig00029-orf00037	tRNA_bind	PF01588.13
contig00030-orf00002	UvrD-helicase	PF00580.14
contig00030-orf00002	Pfam-B_6611	PB006611
contig00030-orf00002	Pfam-B_15539	PB015539
contig00030-orf00002	Viral_helicase1	PF01443.11
contig00030-orf00002	Pfam-B_9137	PB009137
contig00030-orf00002	Pfam-B_11590	PB011590
contig00030-orf00002	Pfam-B_16230	PB016230
contig00030-orf00002	Pfam-B_2627	PB002627
contig00030-orf00008	Pentapeptide	PF00805.15
contig00030-orf00008	Pentapeptide	PF00805.15
contig00030-orf00008	Pentapeptide	PF00805.15
contig00030-orf00008	Pentapeptide	PF00805.15
contig00030-orf00008	Pentapeptide	PF00805.15
contig00030-orf00008	Laminin_II	PF06009.5
contig00030-orf00008	TMPIT	PF07851.6
contig00030-orf00008	DUF342	PF03961.6
contig00030-orf00008	DUF883	PF05957.6
contig00030-orf00008	SWI-SNF_Ssr4	PF08549.3
contig00030-orf00008	DUF2207	PF09972.2
contig00030-orf00008	DUF2157	PF09925.2
contig00031-orf00002	OTCace_N	PF02729.14
contig00031-orf00002	OTCace	PF00185.17
contig00031-orf00005	Arg_tRNA_synt_N	PF03485.9
contig00031-orf00005	tRNA-synt_1d	PF00750.12
contig00031-orf00005	DALR_1	PF05746.8
contig00031-orf00007	TauE	PF01925.12
contig00031-orf00010	CDP-OH_P_transf	PF01066.14
contig00031-orf00011	Pfam-B_5612	PB005612

Query	Pfam Subject	Pfam ID
contig00031-orf00014	tRNA_anti	PF01336.18
contig00031-orf00014	Exonuc_VII_L	PF02601.8
contig00031-orf00014	BRE1	PF08647.4
contig00031-orf00021	Bacteriocin_IIc	PF10439.2
contig00031-orf00023	LpxK	PF02606.7
contig00032-orf00002	Sugar_tr	PF00083.17
contig00032-orf00005	ABC_tran	PF00005.20
contig00032-orf00006	Retrotrans_gag	PF03732.10
contig00032-orf00008	Ferric_reduct	PF01794.12
contig00032-orf00008	FAD_binding_8	PF08022.5
contig00032-orf00008	DUF3465	PF11948.1
contig00032-orf00009	LysR_substrate	PF03466.13
contig00032-orf00011	Pfam-B_284	PB000284
contig00032-orf00011	Viral_helicase1	PF01443.11
contig00032-orf00011	Viral_helicase1	PF01443.11
contig00032-orf00011	Pfam-B_6611	PB006611
contig00032-orf00012	C4dic_mal_tran	PF03595.10
contig00032-orf00013	C4dic_mal_tran	PF03595.10
contig00032-orf00016	Methyltransf_11	PF08241.5
contig00032-orf00016	Transposase_17	PF01797.9
contig00033-orf00003	Haemagg_act	PF05860.6
contig00033-orf00003	Pfam-B_5549	PB005549
contig00033-orf00003	Fil_haemagg	PF05594.7
contig00033-orf00003	Pfam-B_6070	PB006070
contig00033-orf00003	Fil_haemagg	PF05594.7
contig00033-orf00003	Pfam-B_6070	PB006070
contig00033-orf00003	Pfam-B_5549	PB005549
contig00033-orf00003	Pfam-B_5549	PB005549
contig00033-orf00003	Pfam-B_11830	PB011830
contig00033-orf00003	Pfam-B_313	PB000313
contig00033-orf00003	Pfam-B_665	PB000665
contig00033-orf00003	Pfam-B_313	PB000313
contig00033-orf00010	POTRA_2	PF08479.4
contig00033-orf00010	ShlB	PF03865.6
contig00036-orf00002	Pfam-B_3313	PB003313
contig00036-orf00005	DUF1436	PF07262.4
contig00036-orf00006	adh_short	PF00106.18
contig00036-orf00008	Amino_oxidase	PF01593.17
contig00036-orf00008	Pfam-B_942	PB000942
contig00036-orf00010	SQS_PSY	PF00494.12
contig00036-orf00011	HSP70	PF00012.13
contig00036-orf00011	DUF1686	PF07937.4

Query	Pfam Subject	Pfam ID
contig00036-orf00013	Pyr_excise	PF03013.7
contig00036-orf00014	Fer2	PF00111.20
contig00036-orf00016	DUF528	PF04384.6
contig00036-orf00018	MTHFR	PF02219.10
contig00036-orf00018	Radical_SAM	PF04055.14
contig00036-orf00020	Meth_synt_1	PF08267.5
contig00036-orf00020	Meth_synt_2	PF01717.11
contig00036-orf00022	PNP_UDP_1	PF01048.13
contig00036-orf00025	UPF0118	PF01594.9
contig00036-orf00026	AIRS	PF00586.17
contig00036-orf00026	AIRS_C	PF02769.15
contig00037-orf00002	Abi	PF02517.9
contig00037-orf00003	DUF504	PF04457.5
contig00037-orf00006	SCP2	PF02036.10
contig00037-orf00008	Na_Ala_symp	PF01235.10
contig00037-orf00009	Aldedh	PF00171.15
contig00037-orf00012	DHDPS	PF00701.15
contig00037-orf00013	DAO	PF01266.17
contig00037-orf00014	Pro_racemase	PF05544.4
contig00037-orf00016	PAS_4	PF08448.3
contig00037-orf00016	DRMBL	PF07522.7
contig00037-orf00016	Phage_integrase	PF00589.15
contig00037-orf00016	HTH_AraC	PF00165.16
contig00037-orf00016	Lysyl_oxidase	PF01186.10
contig00037-orf00016	DUF2802	PF10975.1
contig00037-orf00016	HTH_AraC	PF00165.16
contig00039-orf00001	Pfam-B_19018	PB019018
contig00039-orf00001	Pfam-B_4382	PB004382
contig00039-orf00001	HIM	PF05662.7
contig00039-orf00001	Pfam-B_4382	PB004382
contig00039-orf00001	HIM	PF05662.7
contig00039-orf00001	YadA	PF03895.8
contig00039-orf00005	zf-Sec23_Sec24	PF04810.8
contig00039-orf00007	Pfam-B_126	PB000126
contig00039-orf00007	OapA	PF04225.5
contig00039-orf00007	DUF2845	PF11006.1
contig00039-orf00007	HrpB_C	PF08482.3
contig00039-orf00007	Peptidase_M23	PF01551.15
contig00039-orf00010	DUF165	PF02592.8
contig00039-orf00011	GTP_cyclohydroI	PF01227.15
contig00039-orf00012	MarR	PF01047.15
contig00039-orf00012	DUF2984	PF11203.1

Query	Pfam Subject	Pfam ID
contig00039-orf00013	OEP	PF02321.11
contig00039-orf00013	OEP	PF02321.11
contig00039-orf00014	Transgly	PF00912.15
contig00039-orf00014	Transpeptidase	PF00905.15
contig00039-orf00015	Competence_A	PF11104.1
contig00039-orf00016	PilN	PF05137.6
contig00039-orf00018	PilP	PF04351.6
contig00039-orf00019	STN	PF07660.7
contig00039-orf00019	Secretin_N	PF03958.10
contig00039-orf00019	Secretin	PF00263.14
contig00039-orf00021	DHQ_synthase	PF01761.13
contig00039-orf00021	DUF1042	PF06294.4
contig00039-orf00023	Semialdhyde_dh	PF01118.17
contig00039-orf00023	Semialdhyde_dhC	PF02774.11
contig00039-orf00024	YkuD	PF03734.7
contig00039-orf00026	TRAM	PF01938.13
contig00039-orf00026	tRNA_U5-meth_tr	PF05958.4
contig00039-orf00028	DUF2154	PF09922.2
contig00039-orf00028	Neur_chan_memb	PF02932.9
contig00039-orf00028	Pfam-B_210	PB000210
contig00039-orf00028	Pfam-B_137	PB000137
contig00039-orf00029	Response_reg	PF00072.17
contig00039-orf00029	Pfam-B_13704	PB013704
contig00039-orf00030	Ras	PF00071.15
contig00039-orf00030	UPF0139	PF03669.6
contig00039-orf00032	Robl_LC7	PF03259.10
contig00039-orf00034	MTS	PF05175.7
contig00040-orf00001	RuvB_N	PF05496.5
contig00040-orf00001	PEPCK_ATP	PF01293.13
contig00040-orf00001	RuvB_C	PF05491.6
contig00040-orf00003	Cache_2	PF08269.4
contig00040-orf00005	PolyA_pol	PF01743.13
contig00040-orf00005	HD	PF01966.15
contig00040-orf00006	Band_7	PF01145.18
contig00040-orf00008	NfeD	PF01957.11
contig00040-orf00008	RseC_MucC	PF04246.5
contig00040-orf00011	Pfam-B_4511	PB004511
contig00040-orf00011	DUF2130	PF09903.2
contig00040-orf00011	Pfam-B_4511	PB004511
contig00040-orf00012	ABC_membrane_2	PF06472.8
contig00040-orf00012	ABC_tran	PF00005.20
contig00040-orf00014	Plug	PF07715.8

Query	Pfam Subject	Pfam ID
contig00040-orf00015	FAD_binding_6	PF00970.17
contig00040-orf00015	NAD_binding_1	PF00175.14
contig00041-orf00001	Pfam-B_665	PB000665
contig00041-orf00004	Guanylate_cyc_2	PF09778.2
contig00041-orf00004	Pfam-B_6109	PB006109
contig00041-orf00006	Pfam-B_18851	PB018851
contig00041-orf00010	Pfam-B_665	PB000665
contig00041-orf00010	Pfam-B_11049	PB011049
contig00041-orf00010	Pfam-B_18851	PB018851
contig00042-orf00001	Pfam-B_13759	PB013759
contig00042-orf00001	DUF1330	PF07045.4
contig00042-orf00002	Pfam-B_4866	PB004866
contig00042-orf00004	Pfam-B_9471	PB009471
contig00042-orf00004	Rep_trans	PF02486.12
contig00042-orf00007	PTR2	PF00854.14
contig00042-orf00007	Arif-1	PF06770.4
contig00042-orf00009	CinA	PF02464.10
contig00042-orf00013	Peptidase_S9_N	PF02897.8
contig00042-orf00013	Peptidase_S9	PF00326.14
contig00042-orf00014	Lsm_interact	PF05391.4
contig00042-orf00016	DNA_ligase_A_M	PF01068.14
contig00042-orf00017	Lactamase_B	PF00753.20
contig00042-orf00020	DUF1757	PF08560.3
contig00042-orf00020	SmpA_OmlA	PF04355.6
contig00042-orf00022	YkuD	PF03734.7
contig00042-orf00022	Pfam-B_15758	PB015758
contig00044-orf00001	Caldesmon	PF02029.8
contig00044-orf00001	Pfam-B_1520	PB001520
contig00044-orf00001	DUF303	PF03629.11
contig00044-orf00001	Lipoprotein_5	PF01298.11
contig00044-orf00001	Pfam-B_9648	PB009648
contig00044-orf00003	Exonuc_VII_S	PF02609.9
contig00044-orf00003	TBCA	PF02970.9
contig00044-orf00003	PspA_IM30	PF04012.5
contig00044-orf00003	MAD	PF05557.6
contig00044-orf00003	HR1	PF02185.9
contig00044-orf00003	Matrilin_ccoil	PF10393.2
contig00044-orf00006	polyprenyl_synt	PF00348.10
contig00044-orf00008	Pfam-B_4622	PB004622
contig00044-orf00008	Cu_bind_like	PF02298.10
contig00044-orf00010	PGK	PF00162.12
contig00044-orf00013	TrmE_N	PF10396.2

Query	Pfam Subject	Pfam ID
contig00044-orf00013	Pfam-B_229	PB000229
contig00044-orf00013	MMR_HSR1	PF01926.16
contig00044-orf00013	Pfam-B_102	PB000102
contig00044-orf00016	RuvA_N	PF01330.14
contig00044-orf00016	HHH	PF00633.16
contig00044-orf00016	HHH	PF00633.16
contig00044-orf00016	RuvA_C	PF07499.6
contig00044-orf00018	Pfam-B_6419	PB006419
contig00044-orf00020	Pfam-B_5349	PB005349
contig00044-orf00020	CbiA	PF01656.16
contig00044-orf00022	Peptidase_M24	PF00557.17
contig00044-orf00026	DUF2613	PF11021.1
contig00044-orf00026	BON	PF04972.10
contig00044-orf00026	BON	PF04972.10
contig00044-orf00028	SIS	PF01380.15
contig00044-orf00030	UPF0102	PF02021.10
contig00044-orf00031	TP_methylase	PF00590.13
contig00044-orf00033	DUF488	PF04343.6
contig00044-orf00037	Exo_endo_phos	PF03372.16
contig00044-orf00040	DUF1234	PF06821.6
contig00044-orf00040	DrsE	PF02635.8
contig00044-orf00042	Zip	PF02535.15
contig00044-orf00042	Zip	PF02535.15
contig00044-orf00042	DUF2975	PF11188.1
contig00044-orf00042	YqhR	PF11085.1
contig00044-orf00046	HTH_3	PF01381.15
contig00044-orf00048	tRNA-synt_1	PF00133.15
contig00044-orf00048	Anticodon_1	PF08264.6
contig00044-orf00048	Cas6	PF09559.3
contig00044-orf00048	DUF3214	PF11499.1
contig00044-orf00048	Val_tRNA-synt_C	PF10458.2
contig00044-orf00048	Cob_adeno_trans	PF01923.11
contig00044-orf00050	IGPS	PF00218.14
contig00044-orf00051	Pfam-B_18168	PB018168
contig00044-orf00051	Mnd1	PF03962.8
contig00044-orf00051	DUF883	PF05957.6
contig00044-orf00051	CRISPR_Cse1	PF09481.3
contig00044-orf00051	Tape_meas_lam_C	PF09718.3
contig00044-orf00052	Phage_integrase	PF00589.15
contig00044-orf00052	Csm1	PF12539.1
contig00044-orf00053	DUF1133	PF06576.4
contig00045-orf00002	UPF0066	PF01980.9

Query	Pfam Subject	Pfam ID
contig00045-orf00005	Isochorismatase	PF00857.13
contig00045-orf00006	Glyco_transf_9	PF01075.10
contig00045-orf00006	TraW_N	PF12477.1
contig00045-orf00008	ETF	PF01012.14
contig00045-orf00009	ETF	PF01012.14
contig00045-orf00009	ETF_alpha	PF00766.12
contig00045-orf00010	UPF0029	PF01205.12
contig00045-orf00011	Pfam-B_4182	PB004182
contig00045-orf00011	ParBc_2	PF08857.4
contig00045-orf00012	GARS_N	PF02844.8
contig00045-orf00012	GARS_A	PF01071.12
contig00045-orf00012	GARS_C	PF02843.9
contig00045-orf00012	Corona_3	PF04694.5
contig00045-orf00013	Sua5_yciO_yrdC	PF01300.11
contig00045-orf00017	DEAD	PF00270.22
contig00045-orf00017	Helicase_C	PF00271.24
contig00045-orf00017	Pfam-B_5988	PB005988
contig00045-orf00017	RQC	PF09382.3
contig00045-orf00017	HRDC	PF00570.16
contig00045-orf00017	HRDC	PF00570.16
contig00045-orf00017	HRDC	PF00570.16
contig00045-orf00018	N6_N4_Mtase	PF01555.11
contig00045-orf00020	RNB	PF00773.12
contig00045-orf00020	RNB	PF00773.12
contig00045-orf00020	Pfam-B_2493	PB002493
contig00045-orf00025	Acyl-CoA_dh_N	PF02771.9
contig00045-orf00025	Acyl-CoA_dh_M	PF02770.12
contig00045-orf00025	Acyl-CoA_dh_1	PF00441.17
contig00045-orf00025	Pfam-B_46	PB000046
contig00045-orf00028	Pfam-B_13448	PB013448
contig00045-orf00028	Pfam-B_9448	PB009448
contig00045-orf00028	DEAD	PF00270.22
contig00045-orf00028	DEAD_2	PF06733.8
contig00045-orf00028	Pfam-B_3344	PB003344
contig00045-orf00028	Helicase_C	PF00271.24
contig00045-orf00030	DUF3079	PF11278.1
contig00045-orf00032	Sigma70_r2	PF04542.7
contig00045-orf00032	NDUFB10	PF10249.2
contig00045-orf00032	Sigma70_r4_2	PF08281.5
contig00045-orf00036	Pfam-B_18168	PB018168
contig00045-orf00036	Mitofilin	PF09731.2
contig00045-orf00036	Borrelia_P83	PF05262.4

Query	Pfam Subject	Pfam ID
contig00045-orf00036	Cytochrom_C	PF00034.14
contig00045-orf00038	PhnA_Zn_Ribbon	PF08274.5
contig00045-orf00038	PADR1	PF08063.5
contig00045-orf00038	zf-B_box	PF00643.17
contig00045-orf00038	PhnA	PF03831.7
contig00045-orf00039	DPBB_1	PF03330.11
contig00045-orf00039	SPOR	PF05036.6
contig00045-orf00042	SpoU_methylase	PF00588.12
contig00045-orf00042	OTCace	PF00185.17
contig00045-orf00042	Malate_DH	PF12434.1
contig00045-orf00044	Pribosyltran	PF00156.20
contig00045-orf00046	Abhydrolase_1	PF00561.13
contig00045-orf00048	Na_sulph_symp	PF00939.12
contig00045-orf00051	Methyltransf_11	PF08241.5
contig00045-orf00054	Redoxin	PF08534.3
contig00045-orf00054	PMSR	PF01625.14
contig00045-orf00054	SelR	PF01641.11
contig00045-orf00057	Pfam-B_12843	PB012843
contig00045-orf00057	Apolipoprotein	PF01442.11
contig00045-orf00057	Mnd1	PF03962.8
contig00045-orf00057	Phasin	PF05597.4
contig00045-orf00057	ApoLp-III	PF07464.4
contig00045-orf00057	DUF2359	PF10151.2
contig00045-orf00057	DUF1664	PF07889.5
contig00045-orf00057	DUF883	PF05957.6
contig00045-orf00057	Prominin	PF05478.4
contig00045-orf00057	RB_A	PF01858.10
contig00045-orf00057	Perilipin	PF03036.9
contig00045-orf00057	SRP54_N	PF02881.12
contig00045-orf00057	SRP54	PF00448.15
contig00045-orf00060	DUF2063	PF09836.2
contig00045-orf00061	DUF692	PF05114.6
contig00045-orf00062	Pfam-B_11267	PB011267
contig00045-orf00065	DoxX	PF07681.5
contig00045-orf00065	Abi	PF02517.9
contig00045-orf00066	DUF258	PF03193.9
contig00045-orf00068	Lysine_decarbox	PF03641.7
contig00045-orf00068	KNTase_C	PF07827.4
contig00045-orf00069	PseudoU_synth_2	PF00849.15
contig00045-orf00069	TruB_N	PF01509.11
contig00045-orf00069	Plasmid_stab_B	PF10784.2
contig00045-orf00075	Lyase_1	PF00206.13

Query	Pfam Subject	Pfam ID
contig00045-orf00075	ASL_C	PF08328.4
contig00045-orf00076	DUF218	PF02698.10
contig00045-orf00079	SDF	PF00375.11
contig00045-orf00081	Surf_Ag_VNR	PF07244.8
contig00045-orf00081	Bac_surface_Ag	PF01103.16
contig00045-orf00083	TM_helix	PF05552.5
contig00045-orf00083	MS_channel	PF00924.11
contig00045-orf00086	DUF336	PF03928.7
contig00045-orf00089	Pfam-B_218	PB000218
contig00045-orf00089	DUF490	PF04357.6
contig00045-orf00089	DUF490	PF04357.6
contig00045-orf00090	DUF3318	PF11780.1
contig00045-orf00090	DUF533	PF04391.5
contig00045-orf00090	Glycos_trans_3N	PF02885.10
contig00045-orf00090	Sigma70_r3	PF04539.9
contig00045-orf00091	Oxidored_q4	PF00507.12
contig00045-orf00092	Oxidored_q6	PF01058.15
contig00045-orf00093	Complex1_30kDa	PF00329.12
contig00045-orf00093	Pfam-B_11290	PB011290
contig00045-orf00095	NiFeSe_Hases	PF00374.12
contig00045-orf00095	Complex1_49kDa	PF00346.12
contig00045-orf00095	Complex1_49kDa	PF00346.12
contig00045-orf00096	Complex1_24kDa	PF01257.12
contig00045-orf00096	DUF1636	PF07845.4
contig00045-orf00097	Complex1_51K	PF01512.10
contig00045-orf00097	SLBB	PF10531.2
contig00045-orf00097	NADH_4Fe-4S	PF10589.2
contig00045-orf00098	Pfam-B_5652	PB005652
contig00045-orf00101	GIY-YIG	PF01541.17
contig00045-orf00104	Fer2	PF00111.20
contig00045-orf00104	TGS	PF02824.14
contig00045-orf00104	NADH-G_4Fe-4S_3	PF10588.2
contig00045-orf00104	DUF1271	PF06902.4
contig00045-orf00104	Molybdopterin	PF00384.15
contig00045-orf00104	Molydop_binding	PF01568.14
contig00045-orf00105	NADHdh	PF00146.14
contig00045-orf00108	c-SKI_SMAD_bind	PF08782.3
contig00045-orf00108	Fer4	PF00037.20
contig00045-orf00108	Pfam-B_13121	PB013121
contig00045-orf00108	Fer4	PF00037.20
contig00045-orf00109	Oxidored_q3	PF00499.13
contig00045-orf00110	Oxidored_q2	PF00420.17

Query	Pfam Subject	Pfam ID
contig00045-orf00110	Herpes_LMP1	PF05297.4
contig00045-orf00113	Fic	PF02661.11
contig00045-orf00113	DUF2131	PF09904.2
contig00045-orf00113	SPC22	PF04573.5
contig00045-orf00117	Oxidored_q1_N	PF00662.13
contig00045-orf00117	Oxidored_q1	PF00361.13
contig00045-orf00117	Oxidored_q1_C	PF01010.12
contig00045-orf00120	Osmo_CC	PF08946.3
contig00045-orf00120	CM_2	PF01817.14
contig00045-orf00120	DUF349	PF03993.5
contig00045-orf00121	Cupin_2	PF07883.4
contig00045-orf00123	Oxidored_q5_N	PF01059.10
contig00045-orf00123	Oxidored_q1	PF00361.13
contig00045-orf00123	Pfam-B_19727	PB019727
contig00045-orf00125	Oxidored_q1	PF00361.13
contig00045-orf00127	Phage_integr_N	PF02899.10
contig00045-orf00128	DUF2818	PF10993.1
contig00045-orf00128	NicO	PF03824.9
contig00045-orf00130	AA_kinase	PF00696.21
contig00045-orf00130	PUA	PF01472.13
contig00045-orf00133	DNA_photolyase	PF00875.11
contig00045-orf00133	FAD_binding_7	PF03441.7
contig00045-orf00137	FUSC	PF04632.5
contig00045-orf00138	CopD	PF05425.6
contig00045-orf00138	DUF1516	PF07457.4
contig00045-orf00140	AA_permease	PF00324.14
contig00045-orf00140	DUF3382	PF11862.1
contig00045-orf00140	OST3_OST6	PF04756.6
contig00045-orf00141	TerC	PF03741.9
contig00045-orf00141	PHO4	PF01384.13
contig00045-orf00145	RRF	PF01765.12
contig00045-orf00145	DUF883	PF05957.6
contig00045-orf00145	TBCA	PF02970.9
contig00045-orf00146	Prenyltransf	PF01255.12
contig00045-orf00146	Spc97_Spc98	PF04130.6
contig00045-orf00146	Dor1	PF04124.5
contig00045-orf00148	CTP_transf_1	PF01148.13
contig00045-orf00151	DXP_reductoisom	PF02670.9
contig00045-orf00151	DUF1999	PF09390.3
contig00045-orf00151	DXP_redisom_C	PF08436.5
contig00045-orf00154	Peptidase_M50	PF02163.15
contig00045-orf00154	IU_nuc_hydro	PF01156.12

Query	Pfam Subject	Pfam ID
contig00045-orf00154	PDZ	PF00595.17
contig00045-orf00154	Pfam-B_3163	PB003163
contig00045-orf00154	PDZ	PF00595.17
contig00045-orf00157	Surf_Ag_VNR	PF07244.8
contig00045-orf00157	Surf_Ag_VNR	PF07244.8
contig00045-orf00157	Surf_Ag_VNR	PF07244.8
contig00045-orf00157	Surf_Ag_VNR	PF07244.8
contig00045-orf00157	Surf_Ag_VNR	PF07244.8
contig00045-orf00157	Bac_surface_Ag	PF01103.16
contig00045-orf00159	OmpH	PF03938.7
contig00045-orf00159	IncA	PF04156.7
contig00045-orf00159	IMD	PF08397.4
contig00045-orf00159	DUF3490	PF11995.1
contig00045-orf00159	Spectrin	PF00435.14
contig00045-orf00159	zf-C4H2	PF10146.2
contig00045-orf00159	DUF342	PF03961.6
contig00045-orf00159	Erythro_esteras	PF05139.7
contig00045-orf00159	Seryl_tRNA_N	PF02403.15
contig00045-orf00160	LpxD	PF04613.7
contig00045-orf00160	Pfam-B_5771	PB005771
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00160	Pfam-B_16490	PB016490
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00160	Pfam-B_16490	PB016490
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00160	Hexapep	PF00132.17
contig00045-orf00162	FabA	PF07977.6
contig00045-orf00162	DNA_gyraseB	PF00204.18
contig00045-orf00164	Abi_2	PF07751.4
contig00045-orf00164	CH	PF00307.24
contig00045-orf00165	Pfam-B_16490	PB016490
contig00045-orf00165	Hexapep	PF00132.17
contig00045-orf00165	Hexapep	PF00132.17
contig00045-orf00165	Hexapep	PF00132.17
contig00045-orf00165	Pfam-B_2350	PB002350
contig00045-orf00165	Pfam-B_16490	PB016490
contig00045-orf00170	PdxA	PF04166.5
contig00045-orf00172	DUF218	PF02698.10
contig00045-orf00174	ArsC	PF03960.8
contig00045-orf00178	Redoxin	PF08534.3

Query	Pfam Subject	Pfam ID
contig00045-orf00180	Pfam-B_5069	PB005069
contig00045-orf00180	Pfam-B_6541	PB006541
contig00045-orf00180	ABC_tran	PF00005.20
contig00045-orf00181	FtsX	PF02687.14
contig00045-orf00184	MutS_I	PF01624.13
contig00045-orf00184	MutS_II	PF05188.10
contig00045-orf00184	MutS_III	PF05192.11
contig00045-orf00184	MutS_IV	PF05190.11
contig00045-orf00184	MutS_V	PF00488.14
contig00045-orf00184	Pfam-B_15024	PB015024
contig00045-orf00185	Pfam-B_11819	PB011819
contig00045-orf00185	WW	PF00397.19
contig00045-orf00186	NLPC_P60	PF00877.12
contig00045-orf00189	Pfam-B_376	PB000376
contig00045-orf00189	DUF481	PF04338.5
contig00045-orf00193	Pfam-B_176	PB000176
contig00045-orf00193	DUF2074	PF09847.2
contig00045-orf00193	DUF2755	PF10954.1
contig00045-orf00193	DUF3522	PF12036.1
contig00045-orf00193	LAB_N	PF07578.4
contig00045-orf00196	GSPII_E	PF00437.13
contig00045-orf00199	GSPII_E	PF00437.13
contig00045-orf00199	TFIIA_gamma_N	PF02268.9
contig00045-orf00201	Ala_racemase_N	PF01168.13
contig00045-orf00203	F420_oxidored	PF03807.10
contig00045-orf00204	YGGT	PF02325.10
contig00045-orf00204	YGGT	PF02325.10
contig00045-orf00206	DUF2093	PF09866.2
contig00045-orf00206	zf-dskA_traR	PF01258.10
contig00046-orf00003	Rotamase	PF00639.14
contig00046-orf00003	SMP_2	PF10144.2
contig00046-orf00006	Aldedh	PF00171.15
contig00046-orf00010	Pfam-B_11388	PB011388
contig00046-orf00010	tRNA_anti	PF01336.18
contig00046-orf00010	tRNA-synt_2	PF00152.13
contig00046-orf00012	MinC_N	PF05209.6
contig00046-orf00012	MinC_C	PF03775.9
contig00046-orf00012	DUF342	PF03961.6
contig00046-orf00013	CbiA	PF01656.16
contig00046-orf00013	Mur_ligase_M	PF08245.5
contig00046-orf00015	MinE	PF03776.7
contig00046-orf00017	HTH_1	PF00126.20

Query	Pfam Subject	Pfam ID
contig00046-orf00017	LysR_substrate	PF03466.13
contig00046-orf00018	DUF1021	PF06257.4
contig00046-orf00021	DapB_N	PF01113.13
contig00046-orf00021	DapB_C	PF05173.7
contig00046-orf00022	SmpA_OmlA	PF04355.6
contig00046-orf00023	FUR	PF01475.12
contig00046-orf00023	Benyvirus_14KDa	PF07255.4
contig00046-orf00027	Leu_Phe_trans	PF03588.7
contig00046-orf00029	Tyr_Deacylase	PF02580.9
contig00046-orf00031	Rotamase	PF00639.14
contig00046-orf00032	BolA	PF01722.11
contig00046-orf00033	YCII	PF03795.7
contig00046-orf00033	Pfam-B_3260	PB003260
contig00046-orf00034	MerC	PF03203.7
contig00046-orf00034	IspA	PF04279.8
contig00046-orf00034	Pfam-B_271	PB000271
contig00046-orf00034	MerC	PF03203.7
contig00046-orf00037	LysM	PF01476.13
contig00046-orf00039	PseudoU_synth_1	PF01416.13
contig00046-orf00039	DUF2344	PF10105.2
contig00046-orf00039	PseudoU_synth_1	PF01416.13
contig00046-orf00040	Porin_1	PF00267.14
contig00046-orf00040	Pfam-B_631	PB000631
contig00046-orf00040	Phage-tail_2	PF09096.3
contig00046-orf00043	LacAB_rpiB	PF02502.11
contig00046-orf00052	HATPase_c	PF02518.19
contig00046-orf00052	DNA_gyraseB	PF00204.18
contig00046-orf00052	Toprim	PF01751.15
contig00046-orf00052	Pfam-B_11111	PB011111
contig00046-orf00052	DNA_gyraseB_C	PF00986.14
contig00046-orf00055	SDH_alpha	PF03313.8
contig00046-orf00058	SDH_beta	PF03315.8
contig00046-orf00060	Phage_integr_N	PF02899.10
contig00046-orf00060	Phage_integrase	PF00589.15
contig00046-orf00060	DIL	PF01843.12
contig00046-orf00061	4HBT	PF03061.15
contig00046-orf00063	F_bP_aldolase	PF01116.13
contig00046-orf00067	Response_reg	PF00072.17
contig00046-orf00067	LytTR	PF04397.8
contig00046-orf00068	tRNA-synt_1c	PF00749.14
contig00046-orf00070	Peptidase_M22	PF00814.18
contig00046-orf00071	Acetyltransf_1	PF00583.17

Query	Pfam Subject	Pfam ID
contig00046-orf00072	UDG	PF03167.12
contig00046-orf00077	ArgJ	PF01960.11
contig00046-orf00080	LrgA	PF03788.7
contig00046-orf00080	DUF2545	PF10810.1
contig00046-orf00080	MF_alpha_N	PF05436.4
contig00046-orf00081	LrgB	PF04172.9
contig00046-orf00081	DUF2456	PF10445.2
contig00047-orf00001	Esterase	PF00756.13
contig00047-orf00003	Plug	PF07715.8
contig00047-orf00003	TonB_dep_Rec	PF00593.17
contig00047-orf00005	MFS_1	PF07690.9
contig00047-orf00005	COX7C	PF02935.9
contig00047-orf00005	DUF3087	PF11286.1
contig00047-orf00007	LacI	PF00356.14
contig00047-orf00007	Peripla_BP_1	PF00532.14
contig00047-orf00008	PGI	PF00342.12
contig00047-orf00011	DUF1669	PF07894.5
contig00047-orf00011	DUF2719	PF10891.1
contig00047-orf00012	PilN	PF05137.6
contig00047-orf00012	Voltage_CLC	PF00654.13
contig00047-orf00015	PEPcase	PF00311.10
contig00047-orf00019	MoaC	PF01967.14
contig00047-orf00021	PepSY_TM	PF03929.9
contig00047-orf00021	Pfam-B_496	PB000496
contig00047-orf00021	PepSY_TM	PF03929.9
contig00047-orf00021	PepSY_TM	PF03929.9
contig00047-orf00023	CTP_transf_2	PF01467.19
contig00047-orf00027	BPL_LplA_LipB	PF03099.12
contig00047-orf00027	BPL_C	PF02237.10
contig00047-orf00027	Bvg_acc_factor	PF03309.7
contig00047-orf00030	DUF1510	PF07423.4
contig00047-orf00030	Ycf1	PF05758.5
contig00047-orf00030	Herpes_DNAp_acc	PF04929.5
contig00047-orf00030	Asp-B-Hydro_N	PF05279.4
contig00047-orf00034	Na_H_antiporter	PF03553.7
contig00047-orf00035	FMN_red	PF03358.8
contig00047-orf00037	NMN_transporter	PF04973.5
contig00047-orf00041	Radical_SAM	PF04055.14
contig00047-orf00041	HHH	PF00633.16
contig00047-orf00042	Pfam-B_249	PB000249
contig00048-orf00001	GTP_EFTU	PF00009.20
contig00048-orf00001	GTP_EFTU_D2	PF03144.18

Query	Pfam Subject	Pfam ID
contig00048-orf00001	EFG_IV	PF03764.11
contig00048-orf00001	EFG_C	PF00679.17
contig00048-orf00003	Ribosomal_S7	PF00177.14
contig00048-orf00004	Ribosomal_S12	PF00164.18
contig00048-orf00007	RNA_pol_Rpb1_1	PF04997.5
contig00048-orf00007	RNA_pol_Rpb1_2	PF00623.13
contig00048-orf00007	RNA_pol_Rpb1_3	PF04983.11
contig00048-orf00007	RNA_pol_Rpb1_4	PF05000.10
contig00048-orf00007	RNA_pol_Rpb1_5	PF04998.10
contig00048-orf00007	Apocytochr_F_C	PF01333.12
contig00048-orf00007	Peptidase_M23	PF01551.15
contig00048-orf00007	ApbA_C	PF08546.4
contig00048-orf00010	RNA_pol_Rpb2_1	PF04563.8
contig00048-orf00010	RNA_pol_Rpb2_2	PF04561.7
contig00048-orf00010	SopD	PF11047.1
contig00048-orf00010	RNA_pol_Rpb2_2	PF04561.7
contig00048-orf00010	RNA_pol_Rpb2_2	PF04561.7
contig00048-orf00010	RNA_pol_Rpb2_3	PF04565.9
contig00048-orf00010	RNA_pol_Rpb2_45	PF10385.2
contig00048-orf00010	RNA_pol_Rpb2_6	PF00562.21
contig00048-orf00010	RNA_pol_Rpb2_6	PF00562.21
contig00048-orf00010	RNA_pol_Rpb2_7	PF04560.13
contig00048-orf00011	Ribosomal_60s	PF00428.12
contig00048-orf00011	Ribosomal_L12	PF00542.12
contig00048-orf00011	Pfam-B_2440	PB002440
contig00048-orf00013	Ribosomal_L1	PF00687.14
contig00048-orf00014	Ribosomal_L11_N	PF03946.7
contig00048-orf00014	Ribosomal_L11	PF00298.12
contig00048-orf00015	NusG	PF02357.12
contig00048-orf00015	KOW	PF00467.22
contig00048-orf00016	SecE	PF00584.13
contig00049-orf00001	SNF	PF00209.11
contig00049-orf00001	SNF	PF00209.11
contig00049-orf00003	ApbE	PF02424.8
contig00049-orf00005	Pfam-B_11428	PB011428
contig00049-orf00005	PCRF	PF03462.11
contig00049-orf00005	RF-1	PF00472.13
contig00049-orf00006	BPD_transp_1	PF00528.15
contig00049-orf00006	DUF3302	PF11742.1
contig00049-orf00008	ABC_tran	PF00005.20
contig00049-orf00008	Pfam-B_2271	PB002271
contig00049-orf00008	Pfam-B_817	PB000817

Query	Pfam Subject	Pfam ID
contig00049-orf00009	DUF3605	PF12239.1
contig00049-orf00010	Radical_SAM	PF04055.14
contig00049-orf00010	GrpE	PF01025.12
contig00049-orf00010	HemN_C	PF06969.9
contig00049-orf00012	cNMP_binding	PF00027.22
contig00049-orf00012	Crp	PF00325.13
contig00049-orf00014	Pfam-B_990	PB000990
contig00049-orf00021	DNA_ligase_aden	PF01653.11
contig00049-orf00021	DNA_ligase_OB	PF03120.9
contig00049-orf00021	DNA_ligase_ZBD	PF03119.9
contig00049-orf00021	Pfam-B_181	PB000181
contig00049-orf00021	BRCT	PF00533.19
contig00049-orf00022	Pfam-B_2588	PB002588
contig00049-orf00022	Nucleos_tra2_C	PF07662.6
contig00049-orf00022	ZipA_C	PF04354.6
contig00049-orf00023	Amidase_2	PF01510.18
contig00049-orf00024	HCNGP	PF07818.6
contig00049-orf00024	YceG	PF02618.9
contig00049-orf00026	DUF2478	PF10649.2
contig00049-orf00026	DHH	PF01368.13
contig00049-orf00026	DHHA1	PF02272.12
contig00049-orf00028	DUF1289	PF06945.6
contig00049-orf00028	DUF3335	PF11814.1
contig00049-orf00035	Nramp	PF01566.11
contig00049-orf00036	Usp	PF00582.19
contig00049-orf00036	PTS_EIIA_1	PF00358.13
contig00049-orf00036	AP_endonuc_2	PF01261.17
contig00049-orf00036	Acetyltransf_1	PF00583.17
contig00049-orf00036	PCP_red	PF08369.3
contig00049-orf00039	ThiF	PF00899.14
contig00049-orf00039	FA_desaturase_2	PF03405.7
contig00049-orf00043	Pfam-B_18952	PB018952
contig00049-orf00043	ScpA_ScpB	PF02616.7
contig00049-orf00046	Branch_AA_trans	PF05525.6
contig00049-orf00049	NAPRTase	PF04095.9
contig00050-orf00001	DUF305	PF03713.6
contig00050-orf00001	Ferritin	PF00210.17
contig00050-orf00002	ResIII	PF04851.8
contig00050-orf00002	Helicase_C	PF00271.24
contig00050-orf00002	UvrB	PF12344.1
contig00050-orf00002	UVR	PF02151.12
contig00050-orf00003	Thioredoxin	PF00085.13

Query	Pfam Subject	Pfam ID
contig00050-orf00006	NACHT	PF05729.5
contig00050-orf00006	ABC_tran	PF00005.20
contig00050-orf00006	Pfam-B_817	PB000817
contig00050-orf00006	oligo_HPY	PF08352.5
contig00050-orf00006	DBI_PRT	PF02277.10
contig00050-orf00006	ABC_tran	PF00005.20
contig00050-orf00006	Pfam-B_817	PB000817
contig00050-orf00006	Pfam-B_154	PB000154
contig00050-orf00006	oligo_HPY	PF08352.5
contig00050-orf00008	AMP-binding	PF00501.21
contig00050-orf00011	Pfam-B_1473	PB001473
contig00050-orf00011	BPD_transp_1	PF00528.15
contig00050-orf00014	BPD_transp_1	PF00528.15
contig00050-orf00016	Pfam-B_6833	PB006833
contig00050-orf00019	Pfam-B_6833	PB006833
contig00050-orf00019	Regulator_TrmB	PF11495.1
contig00050-orf00022	cobW	PF02492.12
contig00050-orf00022	GRDA	PF04723.7
contig00050-orf00022	CobW_C	PF07683.7
contig00050-orf00023	FUR	PF01475.12
contig00050-orf00023	Baculo_ME53	PF06061.4
contig00050-orf00028	DUF3360	PF11840.1
contig00050-orf00031	DUF21	PF01595.13
contig00050-orf00031	Mov34	PF01398.14
contig00050-orf00031	CBS	PF00571.21
contig00050-orf00031	CBS	PF00571.21
contig00050-orf00031	CorC_HlyC	PF03471.10
contig00050-orf00035	DUF88	PF01936.11
contig00050-orf00035	PGM_PMM_II	PF02879.9
contig00050-orf00035	Mitofilin	PF09731.2
contig00050-orf00037	Exonuc_VII_L	PF02601.8
contig00050-orf00037	Peptidase_C50	PF03568.10
contig00050-orf00037	YjgP_YjgQ	PF03739.7
contig00050-orf00037	Na_Ca_ex	PF01699.17
contig00050-orf00037	DUF1129	PF06570.4
contig00050-orf00038	Ldh_1_N	PF00056.16
contig00050-orf00038	Ldh_1_C	PF02866.11
contig00050-orf00041	FAD_binding_4	PF01565.16
contig00050-orf00041	FAD-oxidase_C	PF02913.12
contig00050-orf00041	L51_S25_CI-B8	PF05047.9
contig00050-orf00045	FKBP_C	PF00254.21
contig00050-orf00045	CdCA1	PF10563.2

Query	Pfam Subject	Pfam ID
contig00050-orf00049	Pfam-B_152	PB000152
contig00050-orf00049	Glyco_hydro_77	PF02446.10
contig00050-orf00049	CBM_48	PF02922.11
contig00050-orf00049	Alpha-amylase	PF00128.17
contig00050-orf00049	Alpha-amylase_C	PF02806.11
contig00051-orf00001	PIN	PF01850.14
contig00051-orf00004	Pfam-B_1765	PB001765
contig00051-orf00005	RHH_1	PF01402.14
contig00051-orf00005	MobC	PF05713.4
contig00051-orf00008	PriCT_2	PF08707.4
contig00051-orf00008	Toprim	PF01751.15
contig00051-orf00008	Pfam-B_171	PB000171
contig00051-orf00009	SKG6	PF08693.3
contig00051-orf00009	TraG	PF02534.7
contig00051-orf00010	SSB	PF00436.18
contig00051-orf00011	Pfam-B_10489	PB010489
contig00051-orf00011	HARP	PF07443.6
contig00051-orf00011	HEPN	PF05168.7
contig00051-orf00013	Memo	PF01875.10
contig00051-orf00014	GSPII_E	PF00437.13
contig00051-orf00015	TrbI	PF03743.7
contig00051-orf00017	CagX	PF03524.8
contig00051-orf00018	VirB8	PF04335.6
contig00051-orf00018	FAD_binding_5	PF00941.14
contig00051-orf00019	MLTD_N	PF06474.5
contig00051-orf00019	Pfam-B_4359	PB004359
contig00051-orf00019	Pfam-B_9194	PB009194
contig00051-orf00019	Entericidin	PF08085.4
contig00051-orf00019	Pilus_CpaD	PF09476.3
contig00051-orf00019	Pfam-B_14284	PB014284
contig00051-orf00020	DUF2938	PF11158.1
contig00051-orf00022	TrbL	PF04610.7
contig00051-orf00022	Pfam-B_6876	PB006876
contig00051-orf00023	Lipase_bact_N	PF12262.1
contig00051-orf00023	YkyA	PF10368.2
contig00051-orf00023	SBP	PF03110.7
contig00051-orf00024	T4SS	PF07996.4
contig00051-orf00024	Phage_GP20	PF06810.4
contig00051-orf00024	DUF3050	PF11251.1
contig00051-orf00026	CagE_TrbE_VirB	PF03135.7
contig00051-orf00026	TrwB_AAD_bind	PF10412.2
contig00051-orf00028	TrbC	PF04956.6

Query	Pfam Subject	Pfam ID
contig00051-orf00028	DUF571	PF04600.5
contig00051-orf00028	Colicin	PF01024.12
contig00051-orf00028	DUF1748	PF08520.3
contig00051-orf00028	DUF2133	PF09976.2
contig00051-orf00034	GSPII_E	PF00437.13
contig00051-orf00038	PNP_UDP_1	PF01048.13
contig00051-orf00038	HisKA	PF00512.18
contig00051-orf00040	GTP_EFTU	PF00009.20
contig00051-orf00040	MazG	PF03819.10
contig00051-orf00040	GTP_EFTU_D2	PF03144.18
contig00051-orf00040	EFG_C	PF00679.17
contig00051-orf00040	LepA_C	PF06421.5
contig00051-orf00041	Pfam-B_367	PB000367
contig00051-orf00041	NfeD	PF01957.11
contig00051-orf00041	Exosortase_EpsH	PF09721.3
contig00051-orf00041	CTP_transf_1	PF01148.13
contig00051-orf00041	MpPF26	PF07666.4
contig00051-orf00041	PRA1	PF03208.12
contig00051-orf00041	DUF2154	PF09922.2
contig00051-orf00041	DUF2078	PF09851.2
contig00051-orf00041	Peptidase_S24	PF00717.16
contig00051-orf00041	Peptidase_S26	PF10502.2
contig00051-orf00044	EamA	PF00892.13
contig00051-orf00044	DUF571	PF04600.5
contig00051-orf00044	EamA	PF00892.13
contig00051-orf00045	TAT_signal	PF10518.2
contig00051-orf00045	NMT1	PF09084.4
contig00051-orf00049	BPD_transp_1	PF00528.15
contig00051-orf00051	ABC_tran	PF00005.20
contig00051-orf00053	NnrS	PF05940.5
contig00051-orf00054	4HBT	PF03061.15
contig00051-orf00056	Cu-oxidase_4	PF02578.8
contig00051-orf00058	Lung_7-TM_R	PF06814.6
contig00051-orf00060	S4	PF01479.18
contig00051-orf00060	PseudoU_synth_2	PF00849.15
contig00051-orf00061	LPAM_1	PF08139.5
contig00051-orf00061	Pfam-B_2269	PB002269
contig00051-orf00061	CarD_TRCF	PF02559.9
contig00051-orf00063	PALP	PF00291.18
contig00051-orf00063	Thr_dehydrat_C	PF00585.11
contig00051-orf00063	Thr_dehydrat_C	PF00585.11
contig00051-orf00064	PALP	PF00291.18

Query	Pfam Subject	Pfam ID
contig00051-orf00064	DUF3335	PF11814.1
contig00051-orf00067	Peptidase_S11	PF00768.13
contig00051-orf00067	PBP5_C	PF07943.6
contig00051-orf00067	7TMR-HDED	PF07697.4
contig00051-orf00068	PCNA_N	PF00705.11
contig00051-orf00068	UPF0149	PF03695.6
contig00051-orf00068	SEC-C	PF02810.8
contig00051-orf00070	DUF456	PF04306.6
contig00051-orf00070	Rick_17kDa_Anti	PF05433.8
contig00051-orf00073	ATP_bind_3	PF01171.13
contig00051-orf00073	Pfam-B_13979	PB013979
contig00051-orf00075	HMA	PF00403.19
contig00051-orf00075	E1-E2_ATPase	PF00122.13
contig00051-orf00075	Hydrolase	PF00702.19
contig00051-orf00078	HMA	PF00403.19
contig00051-orf00079	MerR	PF00376.16
contig00051-orf00079	Pfam-B_200	PB000200
contig00051-orf00079	PP28	PF10252.2
contig00051-orf00079	MerR-DNA-bind	PF09278.4
contig00051-orf00079	IncA	PF04156.7
contig00051-orf00080	OsmC	PF02566.12
contig00051-orf00081	Thioredoxin	PF00085.13
contig00051-orf00083	HTH_5	PF01022.13
contig00051-orf00084	Oxidored_FMN	PF00724.13
contig00051-orf00085	Oxidored_FMN	PF00724.13
contig00051-orf00087	malic	PF00390.12
contig00051-orf00087	Malic_M	PF03949.8
contig00051-orf00088	HTH_1	PF00126.20
contig00051-orf00088	LysR_substrate	PF03466.13
contig00051-orf00090	Aldo_ket_red	PF00248.14
contig00051-orf00091	Aldo_ket_red	PF00248.14
contig00051-orf00092	LigB	PF02900.11
contig00051-orf00093	DHO_dh	PF01180.14
contig00051-orf00096	Aminotran_3	PF00202.14
contig00051-orf00102	PS_Dcarbxylase	PF02666.8
contig00051-orf00106	Pfam-B_5069	PB005069
contig00051-orf00106	Pfam-B_6541	PB006541
contig00051-orf00106	Pfam-B_19882	PB019882
contig00051-orf00106	Pfam-B_6894	PB006894
contig00051-orf00106	Pfam-B_11670	PB011670
contig00051-orf00106	ABC_tran	PF00005.20
contig00051-orf00106	Pfam-B_5069	PB005069

Query	Pfam Subject	Pfam ID
contig00051-orf00106	Pfam-B_6541	PB006541
contig00051-orf00106	ABC_tran	PF00005.20
contig00051-orf00106	DnaJ_CXXCXGXG	PF00684.12
contig00051-orf00107	GP41	PF00517.10
contig00052-orf00001	Gp_dh_N	PF00044.17
contig00052-orf00001	Gp_dh_C	PF02800.13
contig00052-orf00005	LpxC	PF03331.6
contig00052-orf00005	RecX	PF02631.9
contig00052-orf00008	Rad9	PF04139.6
contig00052-orf00010	G_glu_transpept	PF01019.14
contig00052-orf00013	NAD_binding_2	PF03446.8
contig00052-orf00013	6PGD	PF00393.12
contig00052-orf00018	2-Hacid_dh	PF00389.23
contig00052-orf00018	2-Hacid_dh_C	PF02826.12
contig00052-orf00019	DUF2061	PF09834.2
contig00052-orf00022	Bacillus_PapR	PF05968.4
contig00052-orf00023	FKBP_C	PF00254.21
contig00052-orf00025	OEP	PF02321.11
contig00052-orf00025	OEP	PF02321.11
contig00052-orf00026	Bacteriocin_IIc	PF10439.2
contig00052-orf00026	Pfam-B_6137	PB006137
contig00052-orf00026	Tape_meas_lam_C	PF09718.3
contig00052-orf00027	Bacteriocin_IIc	PF10439.2
contig00052-orf00028	DUF1129	PF06570.4
contig00052-orf00028	DUF2207	PF09972.2
contig00052-orf00028	Exosortase_EpsH	PF09721.3
contig00052-orf00030	CobD_Cbib	PF03186.6
contig00052-orf00030	7TMR-DISM_7TM	PF07695.4
contig00052-orf00030	Arteri_Gl	PF00951.11
contig00052-orf00030	Oxidored_q5_N	PF01059.10
contig00052-orf00030	ATP_synt_I	PF03899.8
contig00052-orf00030	DUF2273	PF10031.2
contig00052-orf00033	VIT1	PF01988.12
contig00052-orf00033	Reticulon	PF02453.10
contig00052-orf00033	Exosortase_EpsH	PF09721.3
contig00052-orf00034	DUF2516	PF10724.2
contig00052-orf00034	ETRAMP	PF09716.3
contig00052-orf00034	Zip	PF02535.15
contig00052-orf00034	5TM-5TMR_LYT	PF07694.5
contig00052-orf00034	SPC12	PF06645.6
contig00052-orf00036	HlyD	PF00529.13
contig00052-orf00037	Pfam-B_1684	PB001684

Query	Pfam Subject	Pfam ID
contig00052-orf00037	Peptidase_C39	PF03412.8
contig00052-orf00039	ABC_membrane	PF00664.16
contig00052-orf00039	GlpM	PF06942.5
contig00052-orf00039	Pfam-B_6424	PB006424
contig00052-orf00039	ABC_tran	PF00005.20
contig00052-orf00041	tRNA-synt_1c	PF00749.14
contig00052-orf00043	Peripla_BP_2	PF01497.11
contig00052-orf00046	tRNA-synt_1c	PF00749.14
contig00052-orf00047	Peptidase_M16_C	PF05193.14
contig00052-orf00047	Pfam-B_464	PB000464
contig00052-orf00053	ABC_membrane	PF00664.16
contig00052-orf00053	ABC_tran	PF00005.20
contig00052-orf00053	Pfam-B_11559	PB011559
contig00052-orf00053	Pfam-B_26	PB000026
contig00052-orf00055	LPAM_1	PF08139.5
contig00052-orf00057	DUF3579	PF12112.1
contig00052-orf00057	Acetyltransf_1	PF00583.17
contig00052-orf00062	DUF2730	PF10805.1
contig00052-orf00062	RmuC	PF02646.9
contig00052-orf00062	SRP1_TIP1	PF00660.10
contig00052-orf00064	DUF2254	PF10011.2
contig00052-orf00066	DUF1328	PF07043.6
contig00052-orf00068	DUF1328	PF07043.6
contig00052-orf00070	ABC_tran	PF00005.20
contig00052-orf00074	Pfam-B_14697	PB014697
contig00052-orf00074	NUDIX	PF00293.21
contig00052-orf00076	Pro_CA	PF00484.12
contig00052-orf00078	CTP_transf_2	PF01467.19
contig00052-orf00080	DUF143	PF02410.8
contig00052-orf00082	SPOUT_MTase	PF02590.10
contig00052-orf00082	LNS2	PF08235.6
contig00052-orf00087	zf-H2C2	PF09337.3
contig00052-orf00088	Pfam-B_4369	PB004369
contig00052-orf00088	UPF0093	PF03653.6
contig00052-orf00090	Pfam-B_3509	PB003509
contig00052-orf00090	CYTH	PF01928.14
contig00052-orf00094	3D	PF06725.4
contig00052-orf00095	MltA	PF03562.10
contig00052-orf00096	FTR1	PF03239.7
contig00052-orf00096	DUF2319	PF10081.2
contig00052-orf00096	GspM	PF04612.5
contig00052-orf00096	Yip1	PF04893.10

Query	Pfam Subject	Pfam ID
contig00052-orf00097	Entericidin	PF08085.4
contig00052-orf00097	Pfam-B_11439	PB011439
contig00052-orf00097	Pfam-B_11745	PB011745
contig00052-orf00097	Peptidase_M75	PF09375.3
contig00052-orf00101	TAT_signal	PF10518.2
contig00052-orf00101	Dyp_perox	PF04261.5
contig00053-orf00002	Pfam-B_2475	PB002475
contig00053-orf00006	DUF548	PF04445.6
contig00053-orf00006	DUF834	PF05754.7
contig00053-orf00010	FTHFS	PF01268.12
contig00053-orf00011	PP_kinase	PF02503.10
contig00053-orf00011	MR_MLE	PF01188.14
contig00053-orf00011	DUF3186	PF11382.1
contig00053-orf00016	MgtE_N	PF03448.10
contig00053-orf00016	CBS	PF00571.21
contig00053-orf00016	Pfam-B_1302	PB001302
contig00053-orf00016	CBS	PF00571.21
contig00053-orf00016	MgtE	PF01769.9
contig00053-orf00021	MFS_1	PF07690.9
contig00053-orf00021	DUF1689	PF07954.4
contig00053-orf00025	Glyco_hydro_65N	PF03636.8
contig00053-orf00025	Glyco_hydro_65m	PF03632.8
contig00053-orf00025	Glyco_hydro_65C	PF03633.8
contig00053-orf00028	Hydrolase	PF00702.19
contig00053-orf00030	DUF571	PF04600.5
contig00053-orf00030	EamA	PF00892.13
contig00053-orf00030	DUF2593	PF10767.2
contig00053-orf00032	Pfam-B_4224	PB004224
contig00053-orf00034	Sua5_yciO_yrdC	PF01300.11
contig00053-orf00036	DUF3329	PF11808.1
contig00053-orf00036	PGPGW	PF09656.3
contig00053-orf00036	HlyIII	PF03006.13
contig00053-orf00036	DUF454	PF04304.6
contig00053-orf00036	UbiA	PF01040.11
contig00053-orf00038	DUF1415	PF07209.5
contig00053-orf00040	SBP_bac_1	PF01547.18
contig00055-orf00001	AHS1	PF02682.9
contig00055-orf00003	AHS2	PF02626.8
contig00055-orf00005	LamB_YcsF	PF03746.9
contig00055-orf00007	Nramp	PF01566.11
contig00055-orf00007	SHR3_chaperone	PF08229.4
contig00055-orf00008	DUF45	PF01863.10

Query	Pfam Subject	Pfam ID
contig00055-orf00010	UPF0118	PF01594.9
contig00055-orf00011	SR-25	PF10500.2
contig00055-orf00011	Nse4	PF08743.3
contig00055-orf00013	MFS_1	PF07690.9
contig00055-orf00016	Hydrolase	PF00702.19
contig00055-orf00018	Acyltransferase	PF01553.14
contig00055-orf00021	Cpn60_TCP1	PF00118.17
contig00055-orf00021	RNA_pol_Rpb4	PF03874.9
contig00055-orf00021	cwf21	PF08312.5
contig00055-orf00023	Cpn10	PF00166.14
contig00055-orf00026	Plug	PF07715.8
contig00055-orf00026	Pfam-B_17361	PB017361
contig00055-orf00026	TonB_dep_Rec	PF00593.17
contig00055-orf00028	Pfam-B_5076	PB005076
contig00055-orf00028	Peripla_BP_2	PF01497.11
contig00055-orf00029	PGAM	PF00300.15
contig00055-orf00032	Flavoprotein	PF02441.12
contig00055-orf00033	Aminotran_1_2	PF00155.14
contig00055-orf00033	Aminotran_1_2	PF00155.14
contig00055-orf00035	Catalase	PF00199.12
contig00055-orf00035	Catalase-rel	PF06628.5
contig00055-orf00037	GATase_2	PF00310.14
contig00055-orf00037	GATase_2	PF00310.14
contig00055-orf00037	SIS	PF01380.15
contig00055-orf00037	SIS	PF01380.15
contig00055-orf00039	dCMP_cyt_deam_1	PF00383.15
contig00055-orf00039	RibD_C	PF01872.10
contig00055-orf00040	LPAM_1	PF08139.5
contig00055-orf00040	DRMBL	PF07522.7
contig00055-orf00042	ATP-cone	PF03477.9
contig00055-orf00044	DAHP_synth_1	PF00793.13
contig00055-orf00044	GFO_IDH_MocA	PF01408.15
contig00055-orf00045	Asp_decarbox	PF02261.9
contig00055-orf00047	CutA1	PF03091.8
contig00055-orf00047	DEP	PF00610.14
contig00055-orf00049	DUF2782	PF11191.1
contig00055-orf00049	TonB	PF03544.7
contig00055-orf00052	Put_Phosphatase	PF06888.5
contig00055-orf00053	Pfam-B_18974	PB018974
contig00055-orf00053	Bac_DnaA	PF00308.11
contig00055-orf00053	Pfam-B_3932	PB003932
contig00055-orf00053	DUF1323	PF07037.4

Query	Pfam Subject	Pfam ID
contig00055-orf00055	SNARE_assoc	PF09335.4
contig00055-orf00058	DUF2154	PF09922.2
contig00055-orf00058	DUF3465	PF11948.1
contig00055-orf00060	DUF2294	PF10057.2
contig00055-orf00061	bZIP_2	PF07716.8
contig00055-orf00061	BID	PF06393.4
contig00055-orf00062	Lipase_bact_N	PF12262.1
contig00055-orf00062	Entericidin	PF08085.4
contig00055-orf00062	SBP_bac_3	PF00497.13
contig00055-orf00065	DUF2478	PF10649.2
contig00055-orf00065	Molydop_binding	PF01568.14
contig00055-orf00066	MoCF_biosynth	PF00994.17
contig00056-orf00005	Pfam-B_19018	PB019018
contig00056-orf00005	Pfam-B_9545	PB009545
contig00056-orf00005	Pfam-B_4382	PB004382
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Pfam-B_19505	PB019505
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Pfam-B_19018	PB019018
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	Hep_Hag	PF05658.7
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Pfam-B_19505	PB019505
contig00056-orf00005	Pfam-B_4382	PB004382
contig00056-orf00005	Phage_T7_tail	PF03906.7
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Pfam-B_19505	PB019505
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Pfam-B_9106	PB009106
contig00056-orf00005	HIM	PF05662.7

Query	Pfam Subject	Pfam ID
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Pfam-B_9106	PB009106
contig00056-orf00005	Pfam-B_9106	PB009106
contig00056-orf00005	Phage_T7_tail	PF03906.7
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00005	Phage_T7_tail	PF03906.7
contig00056-orf00005	HIM	PF05662.7
contig00056-orf00008	Cytochrom_C_2	PF01322.13
contig00056-orf00008	DUF1090	PF06476.5
contig00056-orf00008	MBF1	PF08523.3
contig00056-orf00009	GIY-YIG	PF01541.17
contig00056-orf00009	DUF169	PF02596.8
contig00056-orf00011	HTH_1	PF00126.20
contig00056-orf00011	LysR_substrate	PF03466.13
contig00056-orf00012	NmrA	PF05368.6
contig00056-orf00013	SnoaL	PF07366.5
contig00056-orf00013	Pfam-B_235	PB000235
contig00056-orf00015	UDPG_MGDP_dh_N	PF03721.7
contig00056-orf00015	UDPG_MGDP_dh	PF00984.12
contig00056-orf00015	UDPG_MGDP_dh_C	PF03720.8
contig00056-orf00018	Polysacc_synt	PF01943.10
contig00056-orf00018	Pox_A14	PF05767.5
contig00056-orf00020	Wzy_C	PF04932.8
contig00056-orf00023	Pfam-B_129	PB000129
contig00056-orf00023	Pfam-B_946	PB000946
contig00056-orf00023	Glycos_transf_1	PF00534.13
contig00056-orf00025	Glycos_transf_1	PF00534.13
contig00056-orf00026	Bac_transf	PF02397.9
contig00056-orf00028	ATP-grasp_3	PF02655.7
contig00056-orf00029	Acid_phosphat_B	PF03767.7
contig00056-orf00029	Hydrolase	PF00702.19
contig00056-orf00030	Formyl_trans_N	PF00551.12
contig00056-orf00031	DegT_DnrJ_EryC1	PF01041.10
contig00056-orf00034	Fijivirus_P9-2	PF06837.4
contig00056-orf00034	CoA_binding	PF02629.12
contig00056-orf00034	Polysacc_synt_2	PF02719.8
contig00056-orf00037	Poly_export	PF02563.9
contig00056-orf00037	SLBB	PF10531.2
contig00056-orf00037	SLBB	PF10531.2
contig00056-orf00039	LMWPc	PF01451.14
contig00056-orf00040	Wzz	PF02706.8
contig00056-orf00040	Pfam-B_15209	PB015209

Query	Pfam Subject	Pfam ID
contig00056-orf00040	CbiA	PF01656.16
contig00056-orf00041	LrgB	PF04172.9
contig00056-orf00041	SecG	PF03840.7
contig00056-orf00042	7TMR-DISM_7TM	PF07695.4
contig00056-orf00042	LrgA	PF03788.7
contig00056-orf00042	DUF1616	PF07760.4
contig00056-orf00043	HTH_1	PF00126.20
contig00056-orf00043	LysR_substrate	PF03466.13
contig00056-orf00045	GFO_IDH_MocA	PF01408.15
contig00056-orf00045	GFO_IDH_MocA_C	PF02894.10
contig00056-orf00046	Nitroreductase	PF00881.17
contig00056-orf00046	PASTA	PF03793.12
contig00056-orf00048	TLV_coat	PF00429.12
contig00056-orf00048	MraY_sig1	PF10555.2
contig00056-orf00048	Glycos_transf_4	PF00953.14
contig00056-orf00049	Colicin_V	PF02674.9
contig00056-orf00049	Pfam-B_1870	PB001870
contig00056-orf00050	Mur_ligase	PF01225.18
contig00056-orf00050	Mur_ligase_M	PF08245.5
contig00056-orf00050	Mur_ligase_C	PF02875.14
contig00056-orf00050	DUF218	PF02698.10
contig00056-orf00052	DUF1887	PF09002.4
contig00056-orf00054	Peptidase_M23	PF01551.15
contig00056-orf00057	Mur_ligase	PF01225.18
contig00056-orf00057	Mur_ligase_M	PF08245.5
contig00056-orf00057	Mur_ligase_C	PF02875.14
contig00056-orf00059	PBP_dimer	PF03717.8
contig00056-orf00059	Transpeptidase	PF00905.15
contig00056-orf00061	FtsL	PF04999.6
contig00056-orf00062	Methyltransf_5	PF01795.12
contig00056-orf00063	MraZ	PF02381.11
contig00056-orf00063	KWG	PF07656.4
contig00056-orf00063	DUF2375	PF09558.3
contig00056-orf00063	MraZ	PF02381.11
contig00056-orf00064	Pfam-B_4734	PB004734
contig00056-orf00064	DUF185	PF02636.10
contig00056-orf00067	DHO_dh	PF01180.14
contig00056-orf00068	Hydrolase	PF00702.19
contig00056-orf00070	Pfam-B_1558	PB001558
contig00056-orf00070	GSH-S_ATP	PF02955.9
contig00056-orf00071	Peripla_BP_2	PF01497.11
contig00056-orf00074	FecCD	PF01032.11

Query	Pfam Subject	Pfam ID
contig00056-orf00077	ABC_tran	PF00005.20
contig00056-orf00078	Copper-bind	PF00127.13
contig00056-orf00080	HTH_1	PF00126.20
contig00056-orf00080	LysR_substrate	PF03466.13
contig00056-orf00082	DoxX	PF07681.5
contig00056-orf00083	Nitroreductase	PF00881.17
contig00056-orf00083	Arb2	PF09757.2
contig00056-orf00085	Iron_traffic	PF04362.7
contig00056-orf00087	Pfam-B_9648	PB009648
contig00056-orf00088	TPR_2	PF07719.10
contig00056-orf00088	DUF560	PF04575.6
contig00056-orf00091	SUR7	PF06687.5
contig00056-orf00091	DUF1129	PF06570.4
contig00056-orf00091	NfeD	PF01957.11
contig00056-orf00092	Pfam-B_12067	PB012067
contig00056-orf00093	Arginosuc_synth	PF00764.12
contig00056-orf00094	TRP	PF06011.5
contig00056-orf00094	Frag1	PF10277.2
contig00056-orf00094	DUF221	PF02714.8
contig00056-orf00094	Phage_Gp23	PF10669.2
contig00056-orf00096	MoCF_biosynth	PF00994.17
contig00057-orf00008	CPSase_L_chain	PF00289.15
contig00057-orf00008	CPSase_L_D2	PF02786.10
contig00057-orf00008	CPSase_L_D3	PF02787.12
contig00057-orf00008	MerR-DNA-bind	PF09278.4
contig00057-orf00008	CPSase_L_chain	PF00289.15
contig00057-orf00008	CPSase_L_D2	PF02786.10
contig00057-orf00008	MGS	PF02142.15
contig00057-orf00010	TerC	PF03741.9
contig00057-orf00010	CBS	PF00571.21
contig00057-orf00010	CBS	PF00571.21
contig00057-orf00010	CorC_HlyC	PF03471.10
contig00057-orf00011	Glyco_hydro_3	PF00933.14
contig00057-orf00015	Na_H_antiporter	PF03553.7
contig00057-orf00015	DUF1980	PF09323.3
contig00057-orf00015	TM_helix	PF05552.5
contig00057-orf00018	Trypsin	PF00089.19
contig00057-orf00018	PDZ	PF00595.17
contig00057-orf00018	Pfam-B_3163	PB003163
contig00057-orf00018	PDZ	PF00595.17
contig00057-orf00021	HhH-GPD	PF00730.18
contig00057-orf00021	HHH	PF00633.16

Query	Pfam Subject	Pfam ID
contig00057-orf00021	EndIII_4Fe-2S	PF10576.2
contig00057-orf00026	Pacs-1	PF10254.2
contig00057-orf00026	DEAD	PF00270.22
contig00057-orf00026	DUF1407	PF07191.5
contig00057-orf00026	Helicase_C	PF00271.24
contig00057-orf00027	DsbC_N	PF10411.2
contig00057-orf00027	Glutaredoxin	PF00462.17
contig00057-orf00027	DSBA	PF01323.13
contig00057-orf00029	CBS	PF00571.21
contig00057-orf00029	CBS	PF00571.21
contig00057-orf00029	CorC_HlyC	PF03471.10
contig00057-orf00031	DUF1462	PF07315.4
contig00057-orf00031	UPF0054	PF02130.10
contig00057-orf00035	Porphobil_deam	PF01379.13
contig00057-orf00035	LysR_substrate	PF03466.13
contig00057-orf00035	Porphobil_deamC	PF03900.8
contig00057-orf00037	Cys_Met_Meta_PP	PF01053.13
contig00057-orf00037	DUF3665	PF12427.1
contig00057-orf00038	TRP	PF06011.5
contig00057-orf00038	DUF2788	PF10981.1
contig00057-orf00040	HD	PF01966.15
contig00057-orf00040	Pfam-B_5967	PB005967
contig00057-orf00040	Pfam-B_11180	PB011180
contig00057-orf00041	RnaseH	PF00075.17
contig00057-orf00044	DUF1971	PF09313.4
contig00057-orf00044	TehB	PF03848.7
contig00057-orf00045	EST1	PF10374.2
contig00057-orf00045	Transposase_9	PF01548.10
contig00057-orf00045	KLRAQ	PF10205.2
contig00057-orf00045	Prefoldin	PF02996.10
contig00057-orf00045	Transposase_20	PF02371.9
contig00057-orf00045	ETRAMP	PF09716.3
contig00057-orf00047	DUF1279	PF06916.6
contig00058-orf00002	DUF3680	PF12441.1
contig00058-orf00002	APH	PF01636.16
contig00058-orf00002	Pfam-B_506	PB000506
contig00058-orf00002	Pfam-B_11904	PB011904
contig00058-orf00003	Pfam-B_229	PB000229
contig00058-orf00003	MMR_HSR1	PF01926.16
contig00058-orf00003	tRNA_lig_kinase	PF08303.4
contig00058-orf00003	UDPG_MGDP_dh_C	PF03720.8
contig00058-orf00003	NAD_Gly3P_dh_N	PF01210.16

Query	Pfam Subject	Pfam ID
contig00058-orf00003	Pfam-B_2899	PB002899
contig00058-orf00003	KH_2	PF07650.10
contig00058-orf00005	Pfam-B_14981	PB014981
contig00058-orf00005	Ribonuclease_3	PF00636.19
contig00058-orf00005	HCaRG	PF07258.7
contig00058-orf00005	dsrm	PF00035.18
contig00058-orf00006	DUF2185	PF09951.2
contig00058-orf00008	DMRL_synthase	PF00885.12
contig00058-orf00011	NusB	PF01029.11
contig00058-orf00012	MarR	PF01047.15
contig00058-orf00012	AsnC_trans_reg	PF01037.14
contig00058-orf00013	DAO	PF01266.17
contig00058-orf00016	MMR_HSR1	PF01926.16
contig00058-orf00016	DUF3482	PF11981.1
contig00058-orf00019	Pfam-B_8407	PB008407
contig00058-orf00019	DUF2868	PF11067.1
contig00058-orf00020	NDUF_B7	PF05676.6
contig00058-orf00023	IDH	PF03971.7
contig00058-orf00023	SNURF	PF07192.4
contig00058-orf00024	IDH	PF03971.7
contig00058-orf00024	FMN_red	PF03358.8
contig00058-orf00024	CoABC_C	PF12370.1
contig00058-orf00024	DUF1018	PF06252.5
contig00058-orf00026	V4R	PF02830.11
contig00058-orf00026	Sigma54_activat	PF00158.19
contig00058-orf00026	HTH_8	PF02954.12
contig00058-orf00027	Phenol_hyd_sub	PF06099.4
contig00058-orf00028	Phenol_Hydrox	PF02332.11
contig00058-orf00029	MmoB_DmpM	PF02406.10
contig00058-orf00031	Phenol_Hydrox	PF02332.11
contig00058-orf00031	Pfam-B_14733	PB014733
contig00058-orf00031	Pfam-B_14733	PB014733
contig00058-orf00031	YHS	PF04945.6
contig00058-orf00032	Phenol_monoox	PF04663.5
contig00058-orf00033	Fer2	PF00111.20
contig00058-orf00033	DHODB_Fe-S_bind	PF10418.2
contig00058-orf00033	FAD_binding_6	PF00970.17
contig00058-orf00033	NAD_binding_1	PF00175.14
contig00058-orf00034	Semialdhyde_dh	PF01118.17
contig00058-orf00034	Pfam-B_886	PB000886
contig00058-orf00034	AcetDehyd-dimer	PF09290.4
contig00058-orf00035	HMGL-like	PF00682.12

Query	Pfam Subject	Pfam ID
contig00058-orf00035	DmpG_comm	PF07836.4
contig00058-orf00036	FAA_hydrolase	PF01557.11
contig00058-orf00038	Tautomerase	PF01361.14
contig00058-orf00039	Fer2	PF00111.20
contig00058-orf00040	Glyoxalase	PF00903.18
contig00058-orf00041	Aldedh	PF00171.15
contig00058-orf00042	FAA_hydrolase	PF01557.11
contig00058-orf00043	DUF521	PF04412.6
contig00058-orf00043	Peptidase_S46	PF10459.2
contig00058-orf00043	Bro-N	PF02498.10
contig00058-orf00043	DUF1827	PF08860.3
contig00058-orf00044	GATase_2	PF00310.14
contig00058-orf00044	GATase_2	PF00310.14
contig00058-orf00044	Pribosyltran	PF00156.20
contig00058-orf00044	PEGSRP	PF07623.4
contig00058-orf00045	Pfam-B_7134	PB007134
contig00058-orf00045	Spermine_synth	PF01564.10
contig00058-orf00045	CbiA	PF01656.16
contig00058-orf00047	NIR_SIR_ferr	PF03460.10
contig00058-orf00047	NIR_SIR	PF01077.15
contig00058-orf00047	NIR_SIR_ferr	PF03460.10
contig00058-orf00047	GcpE	PF04551.7
contig00058-orf00047	NIR_SIR	PF01077.15
contig00058-orf00050	MliC	PF09864.2
contig00058-orf00050	DUF3048	PF11258.1
contig00058-orf00051	Ribosomal_L31	PF01197.11
contig00058-orf00052	MORN_2	PF07661.6
contig00058-orf00052	MORN_2	PF07661.6
contig00058-orf00052	MORN_2	PF07661.6
contig00058-orf00052	MORN_2	PF07661.6
contig00058-orf00055	DUF3135	PF11333.1
contig00058-orf00056	Bac_DNA_binding	PF00216.14
contig00058-orf00058	tRNA_bind	PF01588.13
contig00058-orf00058	B3_4	PF03483.10
contig00058-orf00058	B5	PF03484.8
contig00058-orf00058	FDX-ACB	PF03147.7
contig00058-orf00059	RE_HpaII	PF09561.3
contig00058-orf00059	DUF772	PF05598.4
contig00058-orf00061	DNA_methylase	PF00145.10
contig00058-orf00062	DNA_methylase	PF00145.10
contig00058-orf00063	Vsr	PF03852.8
contig00058-orf00063	LTXXQ	PF07813.5

Query	Pfam Subject	Pfam ID
contig00058-orf00063	DUF559	PF04480.5
contig00058-orf00065	Phe_tRNA-synt_N	PF02912.11
contig00058-orf00065	tRNA-synt_2d	PF01409.13
contig00058-orf00067	Ribosomal_L20	PF00453.11
contig00058-orf00068	Ribosomal_L35p	PF01632.12
contig00058-orf00069	IF3_N	PF05198.9
contig00058-orf00069	Y_Y_Y	PF07495.6
contig00058-orf00069	IF3_C	PF00707.15
contig00058-orf00069	DUF461	PF04314.6
contig00058-orf00070	Pfam-B_831	PB000831
contig00058-orf00070	TGS	PF02824.14
contig00058-orf00070	Pfam-B_17978	PB017978
contig00058-orf00070	Pfam-B_7586	PB007586
contig00058-orf00070	tRNA_SAD	PF07973.7
contig00058-orf00070	DUF1542	PF07564.4
contig00058-orf00070	tRNA-synt_2b	PF00587.18
contig00058-orf00070	HGTP_anticodon	PF03129.13
contig00058-orf00073	TGT	PF01702.11
contig00058-orf00073	DUF2652	PF10851.1
contig00058-orf00074	Ferrochelatase	PF00762.12
contig00058-orf00075	Cytochrom_C	PF00034.14
contig00058-orf00078	MTS	PF05175.7
contig00058-orf00079	DUF466	PF04328.6
contig00058-orf00081	CstA	PF02554.7
contig00058-orf00085	ADH_N	PF08240.5
contig00058-orf00085	Pfam-B_7734	PB007734
contig00058-orf00085	ADH_zinc_N	PF00107.19
contig00058-orf00086	HhH-GPD	PF00730.18
contig00058-orf00086	DUF1330	PF07045.4
contig00058-orf00086	HHH	PF00633.16
contig00058-orf00086	EndIII_4Fe-2S	PF10576.2
contig00058-orf00089	UPF0061	PF02696.7
contig00058-orf00090	BPD_transp_1	PF00528.15
contig00058-orf00093	DUF2536	PF10750.2
contig00058-orf00093	Peptidase_U32	PF01136.12
contig00058-orf00093	Pfam-B_10885	PB010885
contig00058-orf00093	Tachystatin_B	PF11478.1
contig00058-orf00096	CsbD	PF05532.5
contig00058-orf00096	WGG	PF10273.2
contig00058-orf00097	DUF1328	PF07043.6
contig00058-orf00097	PqiA	PF04403.6
contig00058-orf00102	GDC-P	PF02347.9

Query	Pfam Subject	Pfam ID
contig00058-orf00102	GDC-P	PF02347.9
contig00058-orf00105	Adenine_glyco	PF03352.6
contig00058-orf00105	Not3	PF04065.8
contig00058-orf00105	Adenine_glyco	PF03352.6
contig00058-orf00107	GCV_H	PF01597.12
contig00058-orf00109	GCV_T	PF01571.14
contig00058-orf00109	POPLD	PF08170.5
contig00058-orf00109	GCV_T_C	PF08669.4
contig00058-orf00111	EAP30	PF04157.9
contig00058-orf00111	MarR	PF01047.15
contig00058-orf00111	Pfam-B_15809	PB015809
contig00058-orf00111	AsnC_trans_reg	PF01037.14
contig00058-orf00112	Pfam-B_5612	PB005612
contig00058-orf00114	DEAD	PF00270.22
contig00058-orf00114	DNA_alkylation	PF08713.4
contig00058-orf00114	Helicase_C	PF00271.24
contig00058-orf00117	Lambda_Bor	PF06291.4
contig00058-orf00117	Pfam-B_5076	PB005076
contig00058-orf00117	DUF2564	PF10819.1
contig00058-orf00117	DUF3359	PF11839.1
contig00058-orf00117	DUF1672	PF07901.4
contig00058-orf00119	GST_N	PF02798.13
contig00058-orf00119	CoatB	PF10389.2
contig00058-orf00119	Glutaredoxin2_C	PF04399.6
contig00058-orf00123	RelA_SpoT	PF04607.10
contig00058-orf00123	TGS	PF02824.14
contig00058-orf00123	ACT	PF01842.18
contig00058-orf00124	ADH_N	PF08240.5
contig00058-orf00124	ADH_zinc_N	PF00107.19
contig00058-orf00124	DUF2237	PF09996.2
contig00058-orf00127	Aldedh	PF00171.15
contig00058-orf00129	FA_desaturase	PF00487.17
contig00058-orf00133	UbiD	PF01977.9
contig00058-orf00135	PHP	PF02811.12
contig00058-orf00135	DNA_pol3_alpha	PF07733.5
contig00058-orf00135	tRNA_anti	PF01336.18
contig00058-orf00135	Pfam-B_1103	PB001103
contig00058-orf00137	PfkB	PF00294.17
contig00058-orf00138	Peptidase_S24	PF00717.16
contig00058-orf00141	Mu_I-gamma	PF09039.4
contig00058-orf00141	rve	PF00665.19
contig00058-orf00141	Mu-transpos_C	PF09299.4

Query	Pfam Subject	Pfam ID
contig00058-orf00142	DUF2411	PF10304.2
contig00058-orf00143	HTH_3	PF01381.15
contig00058-orf00143	Viral_helicase1	PF01443.11
contig00058-orf00147	FTR1	PF03239.7
contig00058-orf00147	TraS	PF10624.2
contig00058-orf00147	DUF3169	PF11368.1
contig00058-orf00154	DUF2786	PF10979.1
contig00058-orf00154	Histone_HNS	PF00816.14
contig00058-orf00154	Pfam-B_13265	PB013265
contig00058-orf00154	SPOUT_MTase	PF02590.10
contig00058-orf00154	PG_binding_3	PF09374.3
contig00058-orf00155	DUF3134	PF11332.1
contig00058-orf00155	DUF2793	PF10983.1
contig00058-orf00156	MFS_1	PF07690.9
contig00058-orf00156	AA_permease	PF00324.14
contig00058-orf00156	COPI_assoc	PF08507.3
contig00058-orf00157	Pfam-B_4259	PB004259
contig00058-orf00159	RmuC	PF02646.9
contig00058-orf00159	Phage_Mu_Gam	PF07352.5
contig00058-orf00162	DUF1018	PF06252.5
contig00058-orf00165	Mor	PF08765.4
contig00058-orf00168	Pfam-B_1285	PB001285
contig00058-orf00168	CHAP	PF05257.9
contig00058-orf00171	Pfam-B_19110	PB019110
contig00058-orf00172	DUF2514	PF10721.2
contig00058-orf00172	PhnG	PF06754.5
contig00058-orf00172	PolyA_pol	PF01743.13
contig00058-orf00172	DUF1515	PF07439.4
contig00058-orf00175	Pfam-B_3705	PB003705
contig00058-orf00176	DUF2852	PF11014.1
contig00058-orf00176	DUF1110	PF06533.5
contig00058-orf00176	EzrA	PF06160.5
contig00058-orf00176	LUC7	PF03194.8
contig00058-orf00176	DUF1664	PF07889.5
contig00058-orf00176	Pfam-B_381	PB000381
contig00058-orf00176	Allexi_40kDa	PF05549.4
contig00058-orf00176	Laminin_II	PF06009.5
contig00058-orf00176	KCNQ_channel	PF03520.7
contig00058-orf00176	HR1	PF02185.9
contig00058-orf00176	NPV_P10	PF05531.5
contig00058-orf00176	Cob_adeno_trans	PF01923.11
contig00058-orf00177	Peptidase_M66	PF10462.2

Query	Pfam Subject	Pfam ID
contig00058-orf00177	Pfam-B_14726	PB014726
contig00058-orf00177	DUF1267	PF06895.4
contig00058-orf00179	DUF1804	PF08822.4
contig00058-orf00179	DUF2605	PF10792.2
contig00058-orf00180	Pfam-B_334	PB000334
contig00058-orf00182	DUF935	PF06074.5
contig00058-orf00184	Pfam-B_3058	PB003058
contig00058-orf00184	Phage_Mu_F	PF04233.7
contig00058-orf00189	Pfam-B_711	PB000711
contig00058-orf00191	DUF1320	PF07030.5
contig00058-orf00193	Phage_tail_S	PF05069.6
contig00058-orf00194	Pfam-B_2500	PB002500
contig00058-orf00195	Pfam-B_3954	PB003954
contig00058-orf00198	DUF2648	PF10855.1
contig00058-orf00198	DUF2583	PF10762.2
contig00058-orf00200	Pfam-B_727	PB000727
contig00058-orf00200	Occludin_ELL	PF07303.6
contig00058-orf00200	PhageMin_Tail	PF10145.2
contig00058-orf00208	Viral_helicase1	PF01443.11
contig00058-orf00208	DUF1975	PF09318.3
contig00058-orf00209	Pfam-B_12431	PB012431
contig00058-orf00210	Cna_B	PF05738.6
contig00058-orf00212	Pfam-B_4576	PB004576
contig00058-orf00215	Pfam-B_13333	PB013333
contig00058-orf00222	H_lectin	PF09458.3
contig00058-orf00227	MethyltransfD12	PF02086.8
contig00058-orf00229	ABC_tran	PF00005.20
contig00058-orf00229	Pfam-B_11162	PB011162
contig00058-orf00229	Pfam-B_11182	PB011182
contig00058-orf00229	Pfam-B_13170	PB013170
contig00058-orf00229	Pfam-B_14114	PB014114
contig00058-orf00229	Pfam-B_890	PB000890
contig00058-orf00229	ABC_tran	PF00005.20
contig00058-orf00229	Pfam-B_11162	PB011162
contig00058-orf00229	Pfam-B_11182	PB011182
contig00058-orf00229	Pfam-B_13947	PB013947
contig00058-orf00231	HSDR_N	PF04313.7
contig00058-orf00231	ResIII	PF04851.8
contig00058-orf00231	Pfam-B_1584	PB001584
contig00058-orf00233	Methylase_S	PF01420.12
contig00058-orf00233	Methylase_S	PF01420.12
contig00058-orf00235	HsdM_N	PF12161.1

Query	Pfam Subject	Pfam ID
contig00058-orf00235	N6_Mtase	PF02384.9
contig00058-orf00235	VitD-bind_III	PF09164.3
contig00058-orf00235	Pfam-B_813	PB000813
contig00058-orf00237	FAD_binding_2	PF00890.17
contig00058-orf00237	Fimbrial_K88	PF02432.8
contig00058-orf00237	Succ_DH_flav_C	PF02910.13
contig00058-orf00240	NadA	PF02445.9
contig00058-orf00247	QRPTase_N	PF02749.9
contig00058-orf00247	QRPTase_C	PF01729.12
contig00058-orf00253	Transgly	PF00912.15
contig00058-orf00254	Shikimate_dh_N	PF08501.4
contig00058-orf00254	Shikimate_DH	PF01488.13
contig00058-orf00256	Gln-synt_N	PF03951.12
contig00058-orf00256	Gln-synt_C	PF00120.17
contig00058-orf00260	ADH_N	PF08240.5
contig00058-orf00260	Pfam-B_7734	PB007734
contig00058-orf00260	ADH_zinc_N	PF00107.19
contig00058-orf00261	TonB_dep_Rec	PF00593.17
contig00058-orf00264	Plug	PF07715.8
contig00058-orf00267	Radical_SAM	PF04055.14
contig00058-orf00268	DUF1304	PF06993.5
contig00058-orf00272	PTPS	PF01242.12
contig00058-orf00273	DUF1543	PF07566.5
contig00058-orf00273	DUF1543	PF07566.5
contig00058-orf00276	ExsB	PF06508.6
contig00058-orf00276	DSBA	PF01323.13
contig00058-orf00278	Aldolase	PF01081.12
contig00058-orf00281	ILVD_EDD	PF00920.14
contig00058-orf00281	BOF	PF04076.6
contig00058-orf00284	G6PD_N	PF00479.15
contig00058-orf00284	G6PD_C	PF02781.9
contig00058-orf00288	Sugar-bind	PF04198.6
contig00058-orf00288	DUF498	PF04430.7
contig00058-orf00289	Glucokinase	PF02685.9
contig00058-orf00290	HTH_6	PF01418.10
contig00058-orf00290	SIS	PF01380.15
contig00058-orf00293	PGI	PF00342.12
contig00058-orf00296	Pfam-B_1652	PB001652
contig00058-orf00297	EamA	PF00892.13
contig00058-orf00297	EamA	PF00892.13
contig00058-orf00298	PRAI	PF00697.15
contig00058-orf00299	DUF2078	PF09851.2

Query	Pfam Subject	Pfam ID
contig00058-orf00301	DUF975	PF06161.4
contig00058-orf00303	Rho_N	PF07498.5
contig00058-orf00303	Rho_RNA_bind	PF07497.5
contig00058-orf00303	ATP-synt_ab	PF00006.18
contig00058-orf00305	HIT	PF01230.16
contig00058-orf00305	DN_homeodomain	PF12184.1
contig00058-orf00307	TAT_signal	PF10518.2
contig00058-orf00307	Peptidase_S66	PF02016.8
contig00058-orf00309	GTP_EFTU	PF00009.20
contig00058-orf00309	GTP_EFTU_D2	PF03144.18
contig00058-orf00312	Chor_lyase	PF04345.6
contig00058-orf00313	CbiA	PF01656.16
contig00058-orf00315	Aminotran_3	PF00202.14
contig00058-orf00317	SLT	PF01464.13
contig00058-orf00317	LysM	PF01476.13
contig00058-orf00317	LysM	PF01476.13
contig00058-orf00317	LysM	PF01476.13
contig00058-orf00319	OEP	PF02321.11
contig00058-orf00319	ATP-synt_E	PF05680.5
contig00058-orf00319	OEP	PF02321.11
contig00058-orf00321	ACR_tran	PF00873.12
contig00058-orf00323	HlyD	PF00529.13
contig00059-orf00003	Fic	PF02661.11
contig00059-orf00004	Resolvase	PF00239.14
contig00059-orf00007	DNA_methylase	PF00145.10
contig00059-orf00007	DNA_methylase	PF00145.10
contig00059-orf00008	HATPase_c	PF02518.19
contig00059-orf00008	Pfam-B_5125	PB005125
contig00059-orf00008	HATPase_c	PF02518.19
contig00059-orf00009	Response_reg	PF00072.17
contig00059-orf00009	Pfam-B_15571	PB015571
contig00059-orf00010	Peptidase_S24	PF00717.16
contig00059-orf00011	IMS	PF00817.13
contig00059-orf00011	IMS_HHH	PF11798.1
contig00059-orf00011	Pfam-B_4913	PB004913
contig00059-orf00011	DNA_pol_lambd_f	PF10391.2
contig00059-orf00011	IMS_C	PF11799.1
contig00060-orf00001	Pfam-B_807	PB000807
contig00060-orf00004	TfoX_C	PF04994.6
contig00060-orf00004	dCMP_cyt_deam_1	PF00383.15
contig00060-orf00005	IPPT	PF01715.10
contig00060-orf00008	EPSP_synthase	PF00275.13

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contig00060-orf00009	DUF2580	PF10824.1
contig00060-orf00012	Anth_synt_I_N	PF04715.6
contig00060-orf00012	Chorismate_bind	PF00425.11
contig00060-orf00014	GIY-YIG	PF01541.17
contig00060-orf00014	DEC-1_N	PF04625.6
contig00060-orf00015	2-Hacid_dh_C	PF02826.12
contig00060-orf00015	ATP-grasp	PF02222.15
contig00060-orf00017	Acetyltransf_1	PF00583.17
contig00060-orf00019	Smr	PF01713.14
contig00060-orf00022	Transketolase_N	PF00456.14
contig00060-orf00022	Transketolase_N	PF00456.14
contig00060-orf00022	Transketolase_C	PF02780.13
contig00060-orf00024	Biotin_lipoyl	PF00364.15
contig00060-orf00024	Biotin_lipoyl	PF00364.15
contig00060-orf00024	DEC-1_N	PF04625.6
contig00060-orf00024	Pfam-B_13918	PB013918
contig00060-orf00024	E3_binding	PF02817.10
contig00060-orf00024	2-oxoacid_dh	PF00198.16
contig00060-orf00027	Biotin_lipoyl	PF00364.15
contig00060-orf00027	Pyr_redox_2	PF07992.7
contig00060-orf00027	Pyr_redox	PF00070.20
contig00060-orf00027	Pyr_redox	PF00070.20
contig00060-orf00027	Pyr_redox_dim	PF02852.15
contig00060-orf00029	Methyltransf_4	PF02390.10
contig00060-orf00029	Lact_bio_phlase	PF09508.3
contig00060-orf00031	Lum_binding	PF00677.10
contig00060-orf00031	Lum_binding	PF00677.10
contig00060-orf00032	DUF815	PF05673.6
contig00060-orf00032	Pfam-B_3932	PB003932
contig00060-orf00035	DUF2594	PF10769.2
contig00060-orf00035	Lipoprotein_3	PF00938.10
contig00060-orf00036	Ribul_P_3_epim	PF00834.12
contig00060-orf00038	Pfam-B_12716	PB012716
contig00060-orf00041	Adenylsucc_synt	PF00709.14
contig00060-orf00042	Ribonuc_L-PSP	PF01042.14
contig00060-orf00043	Orthoreo_P10	PF07204.4
contig00060-orf00044	YbaK	PF04073.8
contig00060-orf00047	DnaJ	PF00226.24
contig00060-orf00047	ISK_Channel	PF02060.8
contig00060-orf00047	Pfam-B_289	PB000289
contig00060-orf00047	YjgP_YjgQ	PF03739.7
contig00060-orf00049	EamA	PF00892.13

Query	Pfam Subject	Pfam ID
contig00060-orf00049	EamA	PF00892.13
contig00060-orf00051	Lyase_1	PF00206.13
contig00060-orf00051	FumaraseC_C	PF10415.2
contig00061-orf00001	SBP_bac_5	PF00496.15
contig00061-orf00002	Pfam-B_19025	PB019025
contig00061-orf00004	Ribonuclease_BN	PF03631.8
contig00061-orf00004	DUF624	PF04854.7
contig00061-orf00004	Pfam-B_4760	PB004760
contig00061-orf00004	Rrf2	PF02082.13
contig00061-orf00004	Pfam-B_3430	PB003430
contig00061-orf00006	FMN_red	PF03358.8
contig00061-orf00009	TauE	PF01925.12
contig00061-orf00010	TauD	PF02668.9
contig00061-orf00014	Lipase_3	PF01764.18
contig00061-orf00014	DUF3089	PF11288.1
contig00061-orf00015	MFS_1	PF07690.9
contig00061-orf00016	SNARE_assoc	PF09335.4
contig00061-orf00018	Aminotran_1_2	PF00155.14
contig00061-orf00018	CPSase_L_chain	PF00289.15
contig00062-orf00002	HTH_3	PF01381.15
contig00062-orf00004	Clp_N	PF02861.13
contig00062-orf00004	Pfam-B_4550	PB004550
contig00062-orf00004	AAA	PF00004.22
contig00062-orf00004	Pfam-B_6901	PB006901
contig00062-orf00004	AAA_2	PF07724.7
contig00062-orf00004	ClpB_D2-small	PF10431.2
contig00062-orf00005	ClpS	PF02617.10
contig00062-orf00006	CSD	PF00313.15
contig00062-orf00006	CusF_Ec	PF11604.1
contig00062-orf00009	DUF3478	PF11964.1
contig00062-orf00010	DUF754	PF05449.4
contig00062-orf00010	EamA	PF00892.13
contig00062-orf00010	EamA	PF00892.13
contig00062-orf00011	HlyIII	PF03006.13
contig00062-orf00011	DUF962	PF06127.4
contig00062-orf00011	Prenyltrans	PF00432.14
contig00062-orf00014	NTP_transf_2	PF01909.16
contig00062-orf00014	GlnD_UR_UTase	PF08335.4
contig00062-orf00014	HD	PF01966.15
contig00062-orf00014	Pfam-B_3782	PB003782
contig00062-orf00014	Pfam-B_468	PB000468
contig00062-orf00014	Pfam-B_5764	PB005764

Query	Pfam Subject	Pfam ID
contig00062-orf00014	ACT	PF01842.18
contig00062-orf00014	ACT	PF01842.18
contig00062-orf00015	HTH_3	PF01381.15
contig00062-orf00015	Pfam-B_18879	PB018879
contig00062-orf00017	Ribosomal_L25p	PF01386.12
contig00062-orf00017	DUF61	PF01886.9
contig00062-orf00018	Pribosyltran	PF00156.20
contig00062-orf00019	GHMP_kinases_N	PF00288.19
contig00062-orf00019	GHMP_kinases_C	PF08544.6
contig00062-orf00022	Lambda_Bor	PF06291.4
contig00062-orf00022	LolB	PF03550.7
contig00062-orf00023	TPR_1	PF00515.21
contig00062-orf00023	TPR_2	PF07719.10
contig00062-orf00023	TPR_2	PF07719.10
contig00062-orf00027	NUDIX	PF00293.21
contig00062-orf00028	NTP_transferase	PF00483.16
contig00062-orf00029	S4	PF01479.18
contig00062-orf00029	PK	PF00224.14
contig00062-orf00029	PseudoU_synth_2	PF00849.15
contig00062-orf00033	UbiA	PF01040.11
contig00062-orf00034	UbiA	PF01040.11
contig00062-orf00034	P2_Phage_GpR	PF06891.4
contig00062-orf00035	PTS_EIIA_2	PF00359.15
contig00062-orf00037	Hpr_kinase_N	PF02603.9
contig00062-orf00037	Hpr_kinase_C	PF07475.5
contig00062-orf00037	Pfam-B_981	PB000981
contig00062-orf00039	ATP_bind_2	PF03668.8
contig00062-orf00039	Pfam-B_308	PB000308
contig00062-orf00039	Lsr2	PF11774.1
contig00062-orf00042	CENP-B_N	PF04218.6
contig00062-orf00044	Pfam-B_229	PB000229
contig00062-orf00044	MMR_HSR1	PF01926.16
contig00062-orf00046	Peptidase_M20	PF01546.21
contig00062-orf00046	M20_dimer	PF07687.7
contig00062-orf00047	Methyltransf_1N	PF02870.8
contig00062-orf00047	DNA_binding_1	PF01035.13
contig00063-orf00002	Tex_N	PF09371.3
contig00063-orf00002	S1	PF00575.16
contig00063-orf00005	PmbA_TldD	PF01523.9
contig00063-orf00007	RHH_1	PF01402.14
contig00063-orf00007	DUF778	PF05608.5
contig00063-orf00009	PspA_IM30	PF04012.5

Query	Pfam Subject	Pfam ID
contig00063-orf00009	Filament	PF00038.14
contig00063-orf00009	Cob_adeno_trans	PF01923.11
contig00063-orf00009	YiiD_Cterm	PF09500.3
contig00063-orf00015	CytB6-F_Fe-S	PF08802.3
contig00063-orf00015	NLBH	PF05211.5
contig00063-orf00020	DUF1449	PF07290.4
contig00063-orf00029	Band_7	PF01145.18
contig00063-orf00029	Pfam-B_9432	PB009432
contig00063-orf00029	Pfam-B_1379	PB001379
contig00063-orf00029	Pfam-B_1190	PB001190
contig00063-orf00029	Pfam-B_7775	PB007775
contig00063-orf00031	SMC_N	PF02463.12
contig00063-orf00031	SMC_N	PF02463.12
contig00063-orf00033	Pfam-B_12787	PB012787
contig00063-orf00033	DUF456	PF04306.6
contig00063-orf00033	Pfam-B_6	PB000006
contig00063-orf00033	Pfam-B_15	PB000015
contig00063-orf00033	Pfam-B_84	PB000084
contig00063-orf00033	Tim17	PF02466.12
contig00063-orf00033	Pfam-B_17315	PB017315
contig00063-orf00033	AIRC	PF00731.13
contig00063-orf00033	TraT	PF05818.5
contig00063-orf00033	Pfam-B_11079	PB011079
contig00063-orf00033	Bacteriocin_IIc	PF10439.2
contig00063-orf00033	Rick_17kDa_Anti	PF05433.8
contig00063-orf00033	DUF533	PF04391.5
contig00063-orf00033	Glug	PF07581.5
contig00063-orf00036	SNF	PF00209.11
contig00063-orf00036	SNF	PF00209.11
contig00063-orf00039	AMIN	PF11741.1
contig00063-orf00039	Amidase_3	PF01520.11
contig00063-orf00039	Flavodoxin_NdrI	PF07972.4
contig00063-orf00039	Tape_meas_lam_C	PF09718.3
contig00063-orf00040	UPF0079	PF02367.10
contig00063-orf00041	Semialdhyde_dh	PF01118.17
contig00063-orf00041	Semialdhyde_dhC	PF02774.11
contig00063-orf00044	Pfam-B_233	PB000233
contig00063-orf00044	tRNA_anti	PF01336.18
contig00063-orf00044	DEAD	PF00270.22
contig00063-orf00044	Helicase_C	PF00271.24
contig00063-orf00044	Pfam-B_8434	PB008434
contig00067-orf00001	PDZ	PF00595.17

Query	Pfam Subject	Pfam ID
contig00069-orf00002	TrbM	PF07424.4
contig00069-orf00005	DUF342	PF03961.6
contig00069-orf00005	CagA	PF03507.6
contig00069-orf00005	ERp29	PF07749.5
contig00069-orf00005	RPH3A_effect_N	PF02318.9
contig00070-orf00002	BPD_transp_1	PF00528.15
contig00070-orf00002	OpuAC	PF04069.5
contig00070-orf00003	HTH_11	PF08279.5
contig00070-orf00003	Phage_pRha	PF09669.3
contig00070-orf00003	NPIP	PF06409.4
contig00070-orf00003	Sigma54_DBD	PF04552.6
contig00070-orf00003	A_thal_3526	PF09713.3
contig00070-orf00003	NblA	PF04485.5
contig00070-orf00004	HMA	PF00403.19
contig00070-orf00004	PcrB	PF01884.10
contig00070-orf00006	Pfam-B_829	PB000829
contig00070-orf00006	HD	PF01966.15
contig00070-orf00006	ResIII	PF04851.8
contig00070-orf00008	DALR_1	PF05746.8
contig00070-orf00010	Pfam-B_829	PB000829
contig00070-orf00010	HD	PF01966.15
contig00070-orf00010	DEAD	PF00270.22
contig00070-orf00011	Cas_Cas5d	PF09704.3
contig00070-orf00011	zf-C4_Topoisom	PF01396.12
contig00070-orf00013	Cas_Csd1	PF09709.3
contig00070-orf00014	DUF694	PF05107.5
contig00070-orf00015	Pfam-B_14522	PB014522
contig00070-orf00015	Cas_Cas4	PF01930.10
contig00071-orf00001	Pfam-B_2244	PB002244
contig00071-orf00001	HHH	PF00633.16
contig00071-orf00001	HRDC	PF00570.16
contig00071-orf00001	DUF3701	PF12482.1
contig00071-orf00001	DUF655	PF04919.5
contig00071-orf00001	HHH	PF00633.16
contig00072-orf00002	Acyl-CoA_dh_N	PF02771.9
contig00072-orf00002	Acyl-CoA_dh_M	PF02770.12
contig00072-orf00002	Acyl-CoA_dh_1	PF00441.17
contig00072-orf00003	VIT1	PF01988.12
contig00073-orf00002	Transposase_9	PF01548.10
contig00073-orf00002	Transposase_20	PF02371.9
contig00073-orf00004	Pfam-B_1520	PB001520
contig00073-orf00004	eIF-3_zeta	PF05091.5

Query	Pfam Subject	Pfam ID
contig00073-orf00004	Pfam-B_14401	PB014401
contig00073-orf00004	Phage_GPD	PF05954.4
contig00073-orf00004	Caldesmon	PF02029.8
contig00074-orf00001	GTP_EFTU	PF00009.20
contig00074-orf00001	GTP_EFTU_D2	PF03144.18
contig00074-orf00001	GTP_EFTU_D3	PF03143.10
contig00075-orf00002	BCCT	PF02028.10
contig00075-orf00004	Pfam-B_12250	PB012250
contig00075-orf00004	Carn_acyltransf	PF00755.13
contig00075-orf00004	Pfam-B_12250	PB012250
contig00075-orf00006	YjeF_N	PF03853.8
contig00075-orf00007	FeoA	PF04023.7
contig00075-orf00008	RdgC	PF04381.5
contig00075-orf00011	FeoB_N	PF02421.11
contig00075-orf00011	Gate	PF07670.7
contig00075-orf00011	FeoB_C	PF07664.5
contig00075-orf00011	Gate	PF07670.7
contig00075-orf00012	DUF2970	PF11174.1
contig00075-orf00012	Pfam-B_14653	PB014653
contig00075-orf00012	DUF350	PF03994.7
contig00075-orf00012	ASFV_L11L	PF05293.4
contig00075-orf00014	N6_Mtase	PF02384.9
contig00075-orf00017	Mur_ligase	PF01225.18
contig00075-orf00017	Nif11	PF07862.4
contig00075-orf00017	Mur_ligase_M	PF08245.5
contig00075-orf00017	Mur_ligase_C	PF02875.14
contig00075-orf00018	Methyltransf_3	PF01596.10
contig00075-orf00018	Myosin_N	PF02736.12
contig00075-orf00022	BPD_transp_1	PF00528.15
contig00075-orf00022	BPD_transp_1	PF00528.15
contig00075-orf00027	HSDR_N	PF04313.7
contig00075-orf00028	Carb_kinase	PF01256.10
contig00075-orf00029	Cytochrom_B_N	PF00033.12
contig00075-orf00032	Tol_Tol_Ttg2	PF05494.5
contig00075-orf00032	DUF2772	PF10970.1
contig00075-orf00033	DUF1841	PF08897.4
contig00075-orf00035	DUF2466	PF04002.8
contig00075-orf00036	ABC_tran	PF00005.20
contig00075-orf00036	Pfam-B_2045	PB002045
contig00075-orf00036	TOBE_2	PF08402.3
contig00075-orf00038	BPD_transp_1	PF00528.15
contig00075-orf00039	BPD_transp_1	PF00528.15

Query	Pfam Subject	Pfam ID
contig00075-orf00039	DUF3098	PF11297.1
contig00075-orf00041	DAO	PF01266.17
contig00075-orf00043	Sar8_2	PF03058.7
contig00075-orf00043	MCP_N	PF05581.5
contig00075-orf00043	Pfam-B_3123	PB003123
contig00075-orf00043	Cytochrom_C_2	PF01322.13
contig00075-orf00043	DUF3677	PF12432.1
contig00075-orf00045	Fer2	PF00111.20
contig00075-orf00047	Ribonuc_red_sm	PF00268.14
contig00075-orf00047	Ribonuc_red_sm	PF00268.14
contig00075-orf00048	Abi_2	PF07751.4
contig00075-orf00050	ATP-cone	PF03477.9
contig00075-orf00050	Ribonuc_red_lgN	PF00317.14
contig00075-orf00050	Ribonuc_red_lgC	PF02867.8
contig00075-orf00051	DnaJ	PF00226.24
contig00075-orf00051	HSCB_C	PF07743.6
contig00075-orf00051	DUF1771	PF08590.3
contig00075-orf00053	Fe-S_biosyn	PF01521.13
contig00075-orf00053	Pfam-B_1496	PB001496
contig00075-orf00053	DUF1447	PF07288.4
contig00075-orf00056	Cdd1	PF11731.1
contig00075-orf00056	Pfam-B_4913	PB004913
contig00075-orf00056	Nitro_FeMo-Co	PF02579.10
contig00075-orf00056	BAF	PF02961.7
contig00075-orf00058	NifU_N	PF01592.9
contig00075-orf00063	Aminotran_5	PF00266.12
contig00075-orf00063	Ribosomal_S24e	PF01282.12
contig00075-orf00063	B12-binding	PF02310.12
contig00075-orf00064	Rrf2	PF02082.13
contig00075-orf00066	FMN_dh	PF01070.11
contig00075-orf00067	SpoU_sub_bind	PF08032.5
contig00075-orf00067	SpoU_methylase	PF00588.12
contig00075-orf00068	RseA_N	PF03872.6
contig00075-orf00069	Sigma70_r2	PF04542.7
contig00075-orf00069	Sigma70_r4_2	PF08281.5
contig00075-orf00070	ATP_bind_3	PF01171.13
contig00075-orf00070	DUF2392	PF10288.2
contig00075-orf00070	TilS	PF09179.4
contig00075-orf00070	TilS_C	PF11734.1
contig00075-orf00072	ACCA	PF03255.7
contig00075-orf00075	S4	PF01479.18
contig00075-orf00078	DUF3761	PF12587.1

Query	Pfam Subject	Pfam ID
contig00076-orf00001	DUF410	PF04190.6
contig00076-orf00003	SBP_bac_1	PF01547.18
contig00076-orf00003	Ribosomal_S9	PF00380.12
contig00076-orf00003	Pfam-B_2216	PB002216
contig00076-orf00005	EamA	PF00892.13
contig00076-orf00005	7TMR-DISM_7TM	PF07695.4
contig00076-orf00005	MtN3_slv	PF03083.9
contig00076-orf00005	EamA	PF00892.13
contig00076-orf00010	Radical_SAM	PF04055.14
contig00076-orf00010	BATS	PF06968.6
contig00076-orf00011	DUF3231	PF11553.1
contig00076-orf00014	FBPase	PF00316.13
contig00076-orf00014	NdhM	PF10664.2
contig00076-orf00016	Pfam-B_17252	PB017252
contig00076-orf00019	PolyA_pol	PF01743.13
contig00076-orf00019	Pfam-B_105	PB000105
contig00076-orf00019	Pfam-B_18865	PB018865
contig00076-orf00020	TruB_N	PF01509.11
contig00076-orf00020	TruB-C_2	PF09157.4
contig00076-orf00022	RBFA	PF02033.11
contig00076-orf00023	GFO_IDH_MocA	PF01408.15
contig00076-orf00023	GFO_IDH_MocA_C	PF02894.10
contig00076-orf00024	RecA	PF00154.14
contig00076-orf00024	Pilus_PilP	PF11356.1
contig00076-orf00025	Radical_SAM	PF04055.14
contig00076-orf00026	DUF596	PF04591.5
contig00076-orf00028	PFL	PF02901.8
contig00076-orf00028	Gly_radical	PF01228.14
contig00076-orf00031	Ferritin	PF00210.17
contig00076-orf00032	Ferritin	PF00210.17
contig00076-orf00035	GTP_EFTU	PF00009.20
contig00076-orf00035	GTP_EFTU_D2	PF03144.18
contig00076-orf00035	EFG_C	PF00679.17
contig00076-orf00037	Pfam-B_293	PB000293
contig00076-orf00037	Pfam-B_3288	PB003288
contig00076-orf00037	Transposase_8	PF01527.13
contig00076-orf00037	rve	PF00665.19
contig00076-orf00037	Mu-transpos_C	PF09299.4
contig00076-orf00038	TniB	PF05621.4
contig00076-orf00039	TniQ	PF06527.4
contig00076-orf00039	Pfam-B_101	PB000101
contig00076-orf00040	DDE	PF03184.12

Query	Pfam Subject	Pfam ID
contig00076-orf00043	Radical_SAM	PF04055.14
contig00076-orf00044	BPL_LplA_LipB	PF03099.12
contig00076-orf00045	DUF493	PF04359.7
contig00076-orf00049	LON	PF02190.9
contig00076-orf00049	Pfam-B_312	PB000312
contig00076-orf00049	AAA	PF00004.22
contig00076-orf00049	Lon_C	PF05362.6
contig00076-orf00051	Bac_DNA_binding	PF00216.14
contig00076-orf00051	HTH_10	PF04967.5
contig00076-orf00054	Pept_tRNA_hydro	PF01195.12
contig00076-orf00058	UPF0125	PF03658.7
contig00076-orf00059	Polyketide_cyc	PF03364.13
contig00076-orf00059	Glyco_hydro_72	PF03198.7
contig00076-orf00060	TPR_4	PF07721.7
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00060	Sel1	PF08238.5
contig00076-orf00061	SQS_PSY	PF00494.12
contig00076-orf00061	essB	PF10140.2
contig00076-orf00061	HisKA	PF00512.18
contig00076-orf00061	DUF1091	PF06477.6
contig00076-orf00063	DUF1234	PF06821.6
contig00076-orf00064	CRCB	PF02537.8
contig00076-orf00064	DUF1393	PF07155.5
contig00076-orf00065	IspD	PF01128.12
contig00076-orf00066	Exonuc_X-T	PF00929.17
contig00076-orf00068	CopC	PF04234.5
contig00076-orf00068	Pfam-B_111	PB000111
contig00076-orf00068	PBP_sp32	PF07222.5
contig00076-orf00068	Selenoprotein_S	PF06936.4
contig00077-orf00005	N6_Mtase	PF02384.9
contig00078-orf00001	Pfam-B_6	PB000006
contig00078-orf00001	Pfam-B_9393	PB009393
contig00078-orf00001	Pfam-B_3583	PB003583
contig00078-orf00001	Rick_17kDa_Anti	PF05433.8
contig00078-orf00001	OmpA	PF00691.13
contig00078-orf00002	DUF1275	PF06912.4
contig00078-orf00004	Aminotran_4	PF01063.12
contig00078-orf00006	Pfam-B_4898	PB004898

Query	Pfam Subject	Pfam ID
contig00078-orf00006	DUF1673	PF07895.4
contig00078-orf00006	UPF0104	PF03706.6
contig00078-orf00006	DUF1049	PF06305.4
contig00078-orf00014	Thymidylat_synt	PF00303.12
contig00078-orf00016	ELFV_dehydrog_N	PF02812.11
contig00078-orf00016	ELFV_dehydrog	PF00208.14
contig00078-orf00018	Peptidase_M16	PF00675.13
contig00078-orf00018	Peptidase_M16_C	PF05193.14
contig00078-orf00019	Transglut_core	PF01841.12
contig00078-orf00019	Patatin	PF01734.15
contig00078-orf00019	Pfam-B_2625	PB002625
contig00078-orf00021	Pfam-B_15347	PB015347
contig00078-orf00021	Cytochrom_C_asm	PF01578.13
contig00078-orf00022	ResB	PF05140.7
contig00078-orf00022	Pfam-B_1086	PB001086
contig00078-orf00026	Cytochrom_C	PF00034.14
contig00078-orf00026	Cytochrom_C	PF00034.14
contig00078-orf00027	Pfam-B_229	PB000229
contig00078-orf00027	MMR_HSR1	PF01926.16
contig00078-orf00029	ExbD	PF02472.9
contig00078-orf00029	DUF2149	PF09919.2
contig00078-orf00029	DUF843	PF05814.4
contig00078-orf00029	RE_SacI	PF09566.3
contig00078-orf00030	DUF106	PF01956.9
contig00078-orf00030	UPF0139	PF03669.6
contig00078-orf00030	DUF2985	PF11204.1
contig00078-orf00030	MotA_ExbB	PF01618.9
contig00078-orf00031	Pfam-B_9902	PB009902
contig00078-orf00031	Pfam-B_2348	PB002348
contig00078-orf00031	Pfam-B_3907	PB003907
contig00078-orf00031	Pfam-B_2671	PB002671
contig00078-orf00031	Pfam-B_13256	PB013256
contig00078-orf00031	Pfam-B_5319	PB005319
contig00078-orf00031	Pfam-B_18490	PB018490
contig00078-orf00031	Pfam-B_18845	PB018845
contig00078-orf00031	Pfam-B_17360	PB017360
contig00078-orf00031	TonB	PF03544.7
contig00078-orf00031	DUF336	PF03928.7
contig00078-orf00033	Rrf2	PF02082.13
contig00078-orf00033	ATP-grasp_2	PF08442.3
contig00078-orf00034	Pfam-B_15371	PB015371
contig00078-orf00034	Hemerythrin	PF01814.16

Query	Pfam Subject	Pfam ID
contig00078-orf00037	NnrS	PF05940.5
contig00078-orf00037	FMN_red	PF03358.8
contig00078-orf00038	Pfam-B_100	PB000100
contig00078-orf00038	DUF3252	PF11623.1
contig00078-orf00038	Neisseria_PilC	PF05567.4
contig00078-orf00040	Ribosomal_L35p	PF01632.12
contig00078-orf00041	CPSase_sm_chain	PF00988.15
contig00078-orf00041	GATase	PF00117.21
contig00078-orf00044	Pfam-B_2047	PB002047
contig00078-orf00044	MtN3_slv	PF03083.9
contig00078-orf00045	DUF559	PF04480.5
contig00079-orf00003	Rz1	PF06085.4
contig00079-orf00003	YjbE	PF11106.1
contig00079-orf00003	LysM	PF01476.13
contig00079-orf00003	Peptidase_M23	PF01551.15
contig00079-orf00005	SurE	PF01975.10
contig00079-orf00006	Peptidase_M48	PF01435.11
contig00079-orf00006	BSP	PF04450.5
contig00079-orf00008	Pfam-B_3652	PB003652
contig00079-orf00008	RbsD_FucU	PF05025.6
contig00079-orf00010	Pfam-B_12828	PB012828
contig00079-orf00010	DHBP_synthase	PF00926.12
contig00079-orf00010	GTP_cyclohydro2	PF00925.13
contig00079-orf00014	HATPase_c	PF02518.19
contig00079-orf00014	DNA_mis_repair	PF01119.12
contig00079-orf00014	Pfam-B_2265	PB002265
contig00079-orf00014	MutL_C	PF08676.4
contig00079-orf00016	SIR2	PF02146.10
contig00080-orf00003	Neisseria_TspB	PF05616.6
contig00080-orf00005	Neisseria_TspB	PF05616.6
contig00080-orf00005	Pfam-B_3907	PB003907
contig00080-orf00007	DUF2523	PF10734.2
contig00080-orf00009	Zot	PF05707.5
contig00080-orf00009	EthD	PF07110.4
contig00080-orf00009	GspL	PF05134.6
contig00080-orf00009	DUF2133	PF09976.2
contig00080-orf00009	Pfam-B_14715	PB014715
contig00080-orf00011	Transposase_9	PF01548.10
contig00080-orf00011	CorA	PF01544.11
contig00080-orf00011	Prefoldin_2	PF01920.13
contig00080-orf00011	Sec20	PF03908.6
contig00080-orf00011	Transposase_20	PF02371.9

Query	Pfam Subject	Pfam ID
contig00080-orf00012	Isochorismatase	PF00857.13
contig00080-orf00016	DUF1177	PF06675.4
contig00080-orf00016	Pfam-B_5403	PB005403
contig00080-orf00016	Pfam-B_5403	PB005403
contig00080-orf00016	DUF3616	PF12275.1
contig00080-orf00017	AFG1_ATPase	PF03969.9
contig00080-orf00017	RecX	PF02631.9
contig00080-orf00018	TatC	PF00902.11
contig00080-orf00019	MttA_Hcf106	PF02416.9
contig00080-orf00019	PEP-utilisers_N	PF05524.6
contig00080-orf00019	BAR	PF03114.11
contig00080-orf00019	DUF883	PF05957.6
contig00080-orf00019	DUF683	PF05082.6
contig00080-orf00020	MttA_Hcf106	PF02416.9
contig00080-orf00020	Ni_hydr_CYTB	PF01292.13
contig00080-orf00022	DcpS_C	PF11969.1
contig00080-orf00023	PRA-PH	PF01503.10
contig00080-orf00025	PRA-CH	PF01502.11
contig00080-orf00027	His_biosynth	PF00977.14
contig00080-orf00027	SBP_bac_3	PF00497.13
contig00080-orf00030	His_biosynth	PF00977.14
contig00080-orf00031	GATase	PF00117.21
contig00080-orf00035	Lactate_perm	PF02652.7
contig00080-orf00035	DUF423	PF04241.8
contig00080-orf00037	GATase	PF00117.21
contig00080-orf00037	NAD_synthase	PF02540.10
contig00080-orf00037	NAD_synthase	PF02540.10
contig00080-orf00037	GMP_synt_C	PF00958.15
contig00080-orf00038	IspA	PF04279.8
contig00080-orf00040	SmpB	PF01668.11
contig00080-orf00042	Terminase_GpA	PF05876.5
contig00080-orf00042	KaiC	PF06745.6
contig00080-orf00042	Pfam-B_8476	PB008476
contig00080-orf00042	Hap2_elong	PF10483.2
contig00080-orf00042	DUF3280	PF11684.1
contig00080-orf00042	KaiC	PF06745.6
contig00080-orf00042	Lon_C	PF05362.6
contig00080-orf00044	PDZ	PF00595.17
contig00080-orf00044	MspA	PF09203.4
contig00080-orf00044	Peptidase_S41	PF03572.11
contig00080-orf00044	Pfam-B_9465	PB009465
contig00080-orf00048	Pfam-B_237	PB000237

Query	Pfam Subject	Pfam ID
contig00080-orf00048	Peptidase_M23	PF01551.15
contig00080-orf00049	LPAM_1	PF08139.5
contig00080-orf00049	CreA	PF05981.5
contig00080-orf00049	ERF	PF04404.5
contig00080-orf00050	DUF179	PF02622.8
contig00080-orf00051	UPF0081	PF03652.8
contig00080-orf00057	DUF937	PF06078.4
contig00080-orf00057	PhageMin_Tail	PF10145.2
contig00080-orf00057	PhageMin_Tail	PF10145.2
contig00080-orf00058	NUDIX	PF00293.21
contig00080-orf00060	FolB	PF02152.11
contig00080-orf00060	HTH_9	PF08221.4
contig00080-orf00061	Mfp-3	PF04202.6
contig00080-orf00061	DUF205	PF02660.8
contig00080-orf00061	EcsB	PF05975.5
contig00080-orf00063	Pfam-B_2419	PB002419
contig00080-orf00063	Patatin	PF01734.15
contig00080-orf00066	DUF208	PF02677.7
contig00080-orf00067	CM_2	PF01817.14
contig00080-orf00067	PDT	PF00800.11
contig00080-orf00067	ACT	PF01842.18
contig00080-orf00071	Response_reg	PF00072.17
contig00080-orf00071	Trans_reg_C	PF00486.21
contig00080-orf00072	HAMP	PF00672.18
contig00080-orf00072	HisKA	PF00512.18
contig00080-orf00072	HATPase_c	PF02518.19
contig00080-orf00074	Pfam-B_10617	PB010617
contig00080-orf00074	Acetyltransf_1	PF00583.17
contig00080-orf00075	Ribosomal_S16	PF00886.12
contig00080-orf00076	RimM	PF01782.11
contig00080-orf00076	DASH_Duo1	PF08651.3
contig00080-orf00076	PRC	PF05239.9
contig00080-orf00076	NAS	PF03059.9
contig00080-orf00077	tRNA_m1G_MT	PF01746.14
contig00080-orf00078	Ribosomal_L19	PF01245.13
contig00080-orf00079	Colicin_V	PF02674.9
contig00080-orf00081	SPOR	PF05036.6
contig00080-orf00082	LpxK	PF02606.7
contig00080-orf00082	Mur_ligase_M	PF08245.5
contig00080-orf00082	Mur_ligase_C	PF02875.14
contig00080-orf00085	Pfam-B_5069	PB005069
contig00080-orf00085	Pfam-B_19882	PB019882

Query	Pfam Subject	Pfam ID
contig00080-orf00085	ABC_tran	PF00005.20
contig00080-orf00089	RrnaAD	PF00398.13
contig00080-orf00091	Oxidored_FMN	PF00724.13
contig00080-orf00091	Cellulase	PF00150.11
contig00080-orf00093	TFIIA_gamma_C	PF02751.7
contig00080-orf00094	Autoind_synth	PF00765.10
contig00080-orf00094	Gly_acyl_tr_C	PF08444.3
contig00080-orf00095	Acyltransferase	PF01553.14
contig00080-orf00098	Sigma70_r1_1	PF03979.7
contig00080-orf00098	Sigma70_r1_2	PF00140.13
contig00080-orf00098	Sigma70_ner	PF04546.6
contig00080-orf00098	Sigma70_r2	PF04542.7
contig00080-orf00098	GTP_EFTU	PF00009.20
contig00080-orf00098	Sigma70_r3	PF04539.9
contig00080-orf00098	Sigma70_r4	PF04545.9
contig00080-orf00102	zf-CHC2	PF01807.13
contig00080-orf00102	Toprim_N	PF08275.4
contig00080-orf00102	Toprim	PF01751.15
contig00080-orf00102	DnaB_bind	PF10410.2
contig00080-orf00102	DnaG_DnaB_bind	PF08278.4
contig00080-orf00105	MFS_1	PF07690.9
contig00080-orf00105	Pfam-B_15359	PB015359
contig00080-orf00109	DUF560	PF04575.6
contig00080-orf00113	Pfam-B_9648	PB009648
contig00080-orf00114	Plug	PF07715.8
contig00080-orf00114	Pfam-B_8162	PB008162
contig00080-orf00114	TonB_dep_Rec	PF00593.17
contig00080-orf00119	DUF1212	PF06738.5
contig00080-orf00119	Pfam-B_451	PB000451
contig00080-orf00119	DUF445	PF04286.5
contig00080-orf00122	Aldedh	PF00171.15
contig00080-orf00125	Rz1	PF06085.4
contig00080-orf00125	Pfam-B_5076	PB005076
contig00080-orf00125	Pfam-B_788	PB000788
contig00080-orf00125	MLTD_N	PF06474.5
contig00080-orf00125	DUF3558	PF12079.1
contig00080-orf00128	FixH	PF05751.4
contig00080-orf00128	Sec_GG	PF07549.7
contig00080-orf00128	SecD_SecF	PF02355.9
contig00080-orf00128	GLTT	PF01744.13
contig00080-orf00130	Sec_GG	PF07549.7
contig00080-orf00130	Pfam-B_4547	PB004547

Query	Pfam Subject	Pfam ID
contig00080-orf00130	DUF1786	PF08735.3
contig00080-orf00130	SecD_SecF	PF02355.9
contig00080-orf00131	YajC	PF02699.8
contig00080-orf00131	DUF912	PF06024.5
contig00080-orf00131	GspM	PF04612.5
contig00080-orf00131	CusF_Ec	PF11604.1
contig00080-orf00131	DUF2187	PF09953.2
contig00080-orf00131	S1	PF00575.16
contig00080-orf00132	Hist_deacetyl	PF00850.12
contig00080-orf00134	Lipoprotein_5	PF01298.11
contig00080-orf00134	Pfam-B_14192	PB014192
contig00080-orf00134	Pfam-B_14315	PB014315
contig00080-orf00134	Lipoprotein_5	PF01298.11
contig00080-orf00134	Lipoprotein_5	PF01298.11
contig00080-orf00134	Pfam-B_9648	PB009648
contig00080-orf00136	Heme_oxygenase	PF01126.13
contig00080-orf00139	Pfam-B_2350	PB002350
contig00080-orf00139	Hexapep	PF00132.17
contig00080-orf00140	Maf	PF02545.7
contig00080-orf00140	vMSA	PF00695.12
contig00080-orf00141	LPAM_1	PF08139.5
contig00080-orf00142	ELFV_dehydrog_N	PF02812.11
contig00080-orf00142	ELFV_dehydrog	PF00208.14
contig00080-orf00145	Hydrolase	PF00702.19
contig00080-orf00146	essB	PF10140.2
contig00080-orf00146	RecX	PF02631.9
contig00080-orf00146	Trans_reg_C	PF00486.21
contig00080-orf00149	SpoU_methylase	PF00588.12
contig00080-orf00149	DUF2431	PF10354.2
contig00080-orf00149	DUF302	PF03625.7
contig00080-orf00150	BOFC_N	PF08977.3
contig00080-orf00150	Rhodanese	PF00581.13
contig00080-orf00150	DUF442	PF04273.6
contig00080-orf00152	Monooxygenase_B	PF04744.5
contig00080-orf00152	CMD	PF02627.13
contig00080-orf00154	Pfam-B_128	PB000128
contig00080-orf00154	Pfam-B_918	PB000918
contig00080-orf00154	Cupin_2	PF07883.4
contig00080-orf00154	HTH_AraC	PF00165.16
contig00080-orf00154	HTH_AraC	PF00165.16
contig00080-orf00156	Pyr_redox_2	PF07992.7
contig00080-orf00156	Pyr_redox	PF00070.20

Query	Pfam Subject	Pfam ID
contig00080-orf00156	Pyr_redox_dim	PF02852.15
contig00080-orf00158	Redoxin	PF08534.3
contig00080-orf00158	Ig_Tie2_1	PF10430.2
contig00080-orf00158	Glutaredoxin	PF00462.17
contig00080-orf00160	Acyltransferase	PF01553.14
contig00080-orf00161	Fapy_DNA_glyco	PF01149.17
contig00080-orf00161	H2TH	PF06831.7
contig00080-orf00161	zf-FPG_IleRS	PF06827.7
contig00080-orf00163	Methyltransf_11	PF08241.5
contig00080-orf00166	PALP	PF00291.18
contig00080-orf00169	Fumerase	PF05681.7
contig00080-orf00169	Fumerase_C	PF05683.5
contig00080-orf00172	Fer2	PF00111.20
contig00080-orf00172	Fer4	PF00037.20
contig00080-orf00172	Fer4	PF00037.20
contig00080-orf00173	FAD_binding_2	PF00890.17
contig00080-orf00175	Complex1_51K	PF01512.10
contig00080-orf00175	SLBB	PF10531.2
contig00080-orf00175	Prim-Pol	PF09250.4
contig00080-orf00180	Na_sulph_symp	PF00939.12
contig00080-orf00180	DUF2613	PF11021.1
contig00080-orf00182	DUF1188	PF06690.4
contig00080-orf00182	TrkA_N	PF02254.11
contig00080-orf00186	DUF1188	PF06690.4
contig00080-orf00186	TrkA_N	PF02254.11
contig00080-orf00186	TrkA_C	PF02080.14
contig00080-orf00186	CPSase_L_chain	PF00289.15
contig00080-orf00186	TrkA_N	PF02254.11
contig00080-orf00186	TrkA_C	PF02080.14
contig00080-orf00187	SIMPL	PF04402.7
contig00080-orf00188	Porin_1	PF00267.14
contig00080-orf00191	CTP_synth_N	PF06418.7
contig00080-orf00191	GATase	PF00117.21
contig00080-orf00195	Form-deh_trans	PF09163.4
contig00080-orf00195	TrkH	PF02386.9
contig00080-orf00197	DUF1775	PF07987.4
contig00081-orf00003	tRNA-synt_2b	PF00587.18
contig00081-orf00003	YbaK	PF04073.8
contig00081-orf00003	HGTP_anticodon	PF03129.13
contig00081-orf00006	Esterase	PF00756.13
contig00081-orf00010	Fer2	PF00111.20
contig00081-orf00010	FAD_binding_6	PF00970.17

Query	Pfam Subject	Pfam ID
contig00081-orf00010	Glycoprotein	PF03409.8
contig00081-orf00010	NAD_binding_1	PF00175.14
contig00081-orf00011	Phage_Mu_Gam	PF07352.5
contig00081-orf00011	HMGL-like	PF00682.12
contig00081-orf00011	LeuA_dimer	PF08502.3
contig00081-orf00013	EamA	PF00892.13
contig00081-orf00013	EamA	PF00892.13
contig00081-orf00017	Pfam-B_1956	PB001956
contig00081-orf00017	Lipocalin_2	PF08212.5
contig00081-orf00017	PAS_3	PF08447.4
contig00081-orf00022	ABC_tran	PF00005.20
contig00081-orf00022	Pfam-B_18713	PB018713
contig00081-orf00022	ABC_tran	PF00005.20
contig00081-orf00022	Pfam-B_817	PB000817
contig00081-orf00022	ABC2_membrane	PF01061.17
contig00081-orf00024	Glyoxalase	PF00903.18
contig00082-orf00001	DUF1557	PF07591.4
contig00082-orf00001	Pfam-B_190	PB000190
contig00085-orf00001	Pfam-B_14715	PB014715
contig00085-orf00002	DUF2523	PF10734.2
contig00085-orf00004	Neisseria_TspB	PF05616.6
contig00085-orf00004	Pfam-B_18848	PB018848
contig00085-orf00004	Pfam-B_9044	PB009044
contig00088-orf00001	SATase_N	PF06426.7
contig00088-orf00001	Hexapep	PF00132.17
contig00088-orf00001	Pfam-B_16490	PB016490
contig00088-orf00001	Hexapep	PF00132.17
contig00088-orf00003	GrpE	PF01025.12
contig00088-orf00003	HalX	PF08663.3
contig00088-orf00003	DUF1811	PF08838.3
contig00088-orf00003	DUF3086	PF11285.1
contig00088-orf00003	Sigma54_CBD	PF04963.6
contig00088-orf00007	HSP70	PF00012.13
contig00088-orf00007	Pfam-B_11880	PB011880
contig00088-orf00007	DUF2336	PF10098.2
contig00088-orf00010	Fun_ATP-synt_8	PF05933.6
contig00088-orf00011	Rick_17kDa_Anti	PF05433.8
contig00088-orf00011	Pfam-B_7145	PB007145
contig00088-orf00011	Transgly_assoc	PF04226.6
contig00088-orf00013	DUF853	PF05872.5
contig00088-orf00013	Pfam-B_3932	PB003932
contig00088-orf00016	TPP_enzyme_N	PF02776.11

Query	Pfam Subject	Pfam ID
contig00088-orf00016	TPP_enzyme_M	PF00205.15
contig00088-orf00016	DUF137	PF02006.9
contig00088-orf00016	TPP_enzyme_C	PF02775.14
contig00088-orf00018	ACT	PF01842.18
contig00088-orf00018	Gaa1	PF04114.7
contig00088-orf00018	Queuosine_synth	PF02547.8
contig00088-orf00018	ALS_ss_C	PF10369.2
contig00088-orf00021	ABM	PF03992.9
contig00088-orf00023	IlvN	PF07991.5
contig00088-orf00023	IlvC	PF01450.12
contig00088-orf00028	MS_channel	PF00924.11
contig00088-orf00028	KOW	PF00467.22
contig00088-orf00033	Peptidase_M3	PF01432.13
contig00089-orf00001	SBP_bac_3	PF00497.13
contig00089-orf00001	His_biosynth	PF00977.14
contig00089-orf00001	ADH_zinc_N	PF00107.19
contig00089-orf00003	BPD_transp_1	PF00528.15
contig00089-orf00004	Pfam-B_5069	PB005069
contig00089-orf00004	ABC_tran	PF00005.20
contig00089-orf00004	Pfam-B_154	PB000154
contig00089-orf00006	ABC_tran	PF00005.20
contig00089-orf00006	NT5C	PF06941.5
contig00089-orf00006	Pfam-B_11182	PB011182
contig00089-orf00006	Pfam-B_11162	PB011162
contig00089-orf00006	Pfam-B_13170	PB013170
contig00089-orf00006	Pfam-B_6903	PB006903
contig00089-orf00006	Pfam-B_1712	PB001712
contig00089-orf00006	Pfam-B_18493	PB018493
contig00089-orf00006	Pfam-B_16279	PB016279
contig00089-orf00006	BRICHOS	PF04089.7
contig00089-orf00006	Pfam-B_1101	PB001101
contig00089-orf00006	ABC_tran	PF00005.20
contig00089-orf00006	Pfam-B_11162	PB011162
contig00089-orf00006	Pfam-B_11182	PB011182
contig00089-orf00006	OSCP	PF00213.11
contig00089-orf00006	Pfam-B_6966	PB006966
contig00089-orf00006	Pfam-B_11476	PB011476
contig00089-orf00006	Pfam-B_12964	PB012964
contig00089-orf00006	Mnd1	PF03962.8
contig00089-orf00006	Pfam-B_439	PB000439
contig00089-orf00007	DUF2514	PF10721.2
contig00089-orf00010	DUF198	PF02649.7

Query	Pfam Subject	Pfam ID
contig00089-orf00014	Cys_Met_Meta_PP	PF01053.13
contig00089-orf00015	Rz1	PF06085.4
contig00089-orf00015	META	PF03724.9
contig00089-orf00016	Pfam-B_5612	PB005612
contig00089-orf00017	FAD_binding_6	PF00970.17
contig00089-orf00017	NAD_binding_1	PF00175.14
contig00089-orf00019	MMR_HSR1	PF01926.16
contig00089-orf00026	ATPase-cat_bd	PF12156.1
contig00089-orf00026	HMA	PF00403.19
contig00089-orf00026	E1-E2_ATPase	PF00122.13
contig00089-orf00026	Hydrolase	PF00702.19
contig00092-orf00003	PNTB	PF02233.9
contig00092-orf00005	LysE	PF01810.11
contig00092-orf00010	AlaDh_PNT_N	PF05222.8
contig00092-orf00010	AlaDh_PNT_C	PF01262.14
contig00092-orf00010	Pfam-B_10	PB000010
contig00092-orf00011	Glyoxalase	PF00903.18
contig00092-orf00013	THUMP	PF02926.10
contig00092-orf00013	UPF0020	PF01170.11
contig00092-orf00014	SAYSvFN	PF10260.2
contig00092-orf00016	Lyase_1	PF00206.13
contig00092-orf00016	FumaraseC_C	PF10415.2
contig00092-orf00018	YicC_N	PF03755.6
contig00092-orf00018	GlnE	PF03710.8
contig00092-orf00018	PRA-PH	PF01503.10
contig00092-orf00018	Herpes_UL17	PF04559.5
contig00092-orf00018	CorA	PF01544.11
contig00092-orf00018	DUF1732	PF08340.4
contig00092-orf00018	K167R	PF08065.5
contig00092-orf00019	RNase_PH	PF01138.14
contig00092-orf00019	RNase_PH_C	PF03725.8
contig00092-orf00020	TOBE	PF03459.10
contig00092-orf00020	TOBE	PF03459.10
contig00092-orf00022	AA_kinase	PF00696.21
contig00092-orf00022	ACT	PF01842.18
contig00092-orf00022	ACT	PF01842.18
contig00092-orf00028	IBR	PF01485.14
contig00092-orf00028	DUF1407	PF07191.5
contig00092-orf00028	DNA_ligase_ZBD	PF03119.9
contig00092-orf00028	PqiA	PF04403.6
contig00092-orf00028	DUF983	PF06170.5
contig00092-orf00028	PqiA	PF04403.6

Query	Pfam Subject	Pfam ID
contig00092-orf00030	CcmH	PF03918.7
contig00092-orf00030	MCE	PF02470.13
contig00092-orf00030	MCE	PF02470.13
contig00092-orf00030	MCE	PF02470.13
contig00092-orf00030	Baculo_PEP_C	PF04513.5
contig00092-orf00030	DUF2730	PF10805.1
contig00092-orf00030	Fib_alpha	PF08702.3
contig00092-orf00030	Pfam-B_14956	PB014956
contig00092-orf00030	Tweety	PF04906.6
contig00092-orf00032	DUF330	PF03886.6
contig00092-orf00034	GST_N	PF02798.13
contig00092-orf00034	GST_C	PF00043.18
contig00092-orf00035	His_kinase	PF06580.6
contig00092-orf00035	HATPase_c	PF02518.19
contig00092-orf00036	Lyase_1	PF00206.13
contig00092-orf00037	ADK	PF00406.15
contig00092-orf00037	Cytidylate_kin	PF02224.11
contig00092-orf00041	S1	PF00575.16
contig00092-orf00041	S1	PF00575.16
contig00092-orf00041	S1	PF00575.16
contig00092-orf00041	S1	PF00575.16
contig00092-orf00041	S1	PF00575.16
contig00092-orf00041	S1	PF00575.16
contig00092-orf00042	Bac_DNA_binding	PF00216.14
contig00092-orf00046	AFG1_ATPase	PF03969.9
contig00092-orf00048	NDK	PF00334.12
contig00092-orf00049	Pfam-B_16137	PB016137
contig00092-orf00049	Radical_SAM	PF04055.14
contig00092-orf00050	TPR_1	PF00515.21
contig00092-orf00050	Pfam-B_3120	PB003120
contig00092-orf00050	Pfam-B_2967	PB002967
contig00092-orf00050	TPR_1	PF00515.21
contig00092-orf00050	DUF1267	PF06895.4
contig00092-orf00050	TPR_1	PF00515.21
contig00092-orf00051	HTH_3	PF01381.15
contig00092-orf00051	Pfam-B_7895	PB007895
contig00092-orf00053	GcpE	PF04551.7
contig00092-orf00056	FGE-sulfatase	PF03781.9
contig00092-orf00060	Cu-oxidase_3	PF07732.8
contig00092-orf00060	PPC	PF04151.8
contig00092-orf00060	Cu-oxidase	PF00394.15
contig00092-orf00062	Pfam-B_796	PB000796

Query	Pfam Subject	Pfam ID
contig00092-orf00062	DUF3185	PF11381.1
contig00092-orf00062	COX1	PF00115.13
contig00092-orf00064	DUF955	PF06114.6
contig00092-orf00067	TonB_dep_Rec	PF00593.17
contig00092-orf00068	Plug	PF07715.8
contig00092-orf00068	Pfam-B_1163	PB001163
contig00092-orf00068	Pfam-B_1163	PB001163
contig00092-orf00070	Lipoprotein_5	PF01298.11
contig00092-orf00070	Pfam-B_9648	PB009648
contig00092-orf00070	Lipoprotein_5	PF01298.11
contig00092-orf00071	Androgen_recep	PF02166.9
contig00092-orf00072	DUF560	PF04575.6
contig00092-orf00073	GreA_GreB_N	PF03449.8
contig00092-orf00073	GreA_GreB	PF01272.12
contig00092-orf00074	LTXXQ	PF07813.5
contig00092-orf00074	Ribosomal_S15	PF00312.15
contig00092-orf00076	LPAM_1	PF08139.5
contig00092-orf00076	DsbB	PF02600.9
contig00092-orf00076	YbhQ	PF11076.1
contig00092-orf00076	DUF2517	PF10725.2
contig00092-orf00077	Na_Ala_symp	PF01235.10
contig00094-orf00003	Fic	PF02661.11
contig00094-orf00003	TrmB	PF01978.12
contig00094-orf00004	7kD_coat	PF02495.10
contig00094-orf00004	DUF3568	PF12092.1
contig00094-orf00004	Hormone_6	PF00236.11
contig00094-orf00007	GATase_2	PF00310.14
contig00094-orf00009	Pfam-B_8110	PB008110
contig00094-orf00009	RecR	PF02132.8
contig00094-orf00009	Spt4	PF06093.6
contig00094-orf00010	Fe-S_biosyn	PF01521.13
contig00094-orf00011	Peptidase_S24	PF00717.16
contig00094-orf00012	DUF2946	PF11162.1
contig00094-orf00013	DNA_topoisoIV	PF00521.13
contig00094-orf00013	CDC37_N	PF03234.7
contig00094-orf00013	DNA_gyraseA_C	PF03989.6
contig00094-orf00016	Pfam-B_5800	PB005800
contig00094-orf00016	Pfam-B_1360	PB001360
contig00094-orf00016	Pfam-B_1889	PB001889
contig00094-orf00016	HisKA	PF00512.18
contig00094-orf00016	HATPase_c	PF02518.19
contig00094-orf00017	Response_reg	PF00072.17

Query	Pfam Subject	Pfam ID
contig00094-orf00017	Sigma54_activat	PF00158.19
contig00094-orf00017	HTH_8	PF02954.12
contig00094-orf00020	Epimerase	PF01370.14
contig00094-orf00021	NTP_transferase	PF00483.16
contig00095-orf00001	RuvA_C	PF07499.6
contig00095-orf00001	SeqA	PF03925.6
contig00095-orf00001	DUF3613	PF12266.1
contig00095-orf00003	PIN	PF01850.14
contig00095-orf00004	YukD	PF08817.3
contig00095-orf00004	SpoVT_AbrB	PF04014.11
contig00095-orf00004	Pfam-B_9787	PB009787
contig00095-orf00007	Crystallin	PF00525.11
contig00095-orf00013	Vps23_core	PF09454.3
contig00095-orf00013	GvpG	PF05120.5
contig00096-orf00001	Pfam-B_6680	PB006680
contig00096-orf00001	HTH_3	PF01381.15
contig00096-orf00002	HVSL	PF09749.2
contig00096-orf00003	Pfam-B_9471	PB009471
contig00096-orf00003	Rep_trans	PF02486.12
contig00096-orf00005	C1_2	PF03107.9
contig00096-orf00006	Pfam-B_4866	PB004866
contig00096-orf00007	LrgB	PF04172.9
contig00096-orf00008	Pfam-B_7376	PB007376
contig00096-orf00010	SinI	PF08671.3
contig00097-orf00001	rve	PF00665.19
contig00099-orf00002	Thioredoxin	PF00085.13
contig00099-orf00003	LMWPc	PF01451.14
contig00099-orf00003	PTS_IIB	PF02302.10
contig00099-orf00007	GTP_cyclohydro2	PF00925.13
contig00099-orf00007	Glyco_hydro_17	PF00332.11
contig00099-orf00009	Phage_integrase	PF00589.15
contig00099-orf00010	DUF1542	PF07564.4
contig00099-orf00010	Pfam-B_2640	PB002640
contig00099-orf00011	Phage_AlpA	PF05930.5
contig00099-orf00011	Pfam-B_8571	PB008571
contig00099-orf00013	Pfam-B_5588	PB005588
contig00099-orf00014	PLU-1	PF08429.4
contig00099-orf00014	Mnd1	PF03962.8
contig00099-orf00014	Phasin	PF05597.4
contig00099-orf00014	DUF3552	PF12072.1
contig00099-orf00015	Terminase_2	PF03592.9
contig00099-orf00015	PCI_Csn8	PF10075.2

Query	Pfam Subject	Pfam ID
contig00099-orf00016	DUF3486	PF11985.1
contig00099-orf00019	Prim_Zn_Ribbon	PF08273.5
contig00099-orf00023	DUF927	PF06048.4
contig00099-orf00023	Pfam-B_1495	PB001495
contig00099-orf00028	OEP	PF02321.11
contig00099-orf00028	Pox_L3_FP4	PF03339.7
contig00099-orf00029	OEP	PF02321.11
contig00099-orf00030	Cdd1	PF11731.1
contig00099-orf00030	Pfam-B_4913	PB004913
contig00099-orf00033	DUF1877	PF08974.3
contig00099-orf00033	Cytochrom_C_2	PF01322.13
contig00099-orf00033	ParD	PF09386.3
contig00101-orf00002	NTP_transferase	PF00483.16
contig00101-orf00002	Pfam-B_5771	PB005771
contig00101-orf00002	Hexapep	PF00132.17
contig00101-orf00002	Hexapep	PF00132.17
contig00101-orf00002	Hexapep	PF00132.17
contig00101-orf00003	LPAM_1	PF08139.5
contig00101-orf00007	Hydrolase	PF00702.19
contig00101-orf00008	2-Hacid_dh	PF00389.23
contig00101-orf00008	SBP_bac_1	PF01547.18
contig00101-orf00012	Pfam-B_11238	PB011238
contig00101-orf00014	DUF1020	PF06255.6
contig00101-orf00014	Pfam-B_569	PB000569
contig00101-orf00016	DUF1557	PF07591.4
contig00101-orf00016	Pfam-B_190	PB000190
contig00102-orf00003	Cpn10	PF00166.14
contig00102-orf00003	HIM	PF05662.7
contig00102-orf00003	HIM	PF05662.7
contig00102-orf00003	HIM	PF05662.7
contig00102-orf00003	Hep_Hag	PF05658.7
contig00102-orf00003	Hep_Hag	PF05658.7
contig00102-orf00003	Pfam-B_8974	PB008974
contig00102-orf00003	Hep_Hag	PF05658.7
contig00102-orf00003	Hep_Hag	PF05658.7
contig00102-orf00003	Hep_Hag	PF05658.7
contig00104-orf00001	Transposase_14	PF01710.9
contig00105-orf00001	Phage_T4_Ndd	PF06591.4
contig00106-orf00001	Transposase_17	PF01797.9
contig00106-orf00002	Pilin	PF00114.12
contig00106-orf00005	tRNA-synt_1b	PF00579.18
contig00106-orf00006	DWNN	PF08783.4

Query	Pfam Subject	Pfam ID
contig00106-orf00007	MMR_HSR1	PF01926.16
contig00106-orf00007	YchF-GTPase_C	PF06071.6
contig00106-orf00008	Asp_Glu_race	PF01177.15
contig00106-orf00008	SepQ	PF06622.4
contig00106-orf00012	V_cholerae_RfbT	PF05575.4
contig00106-orf00014	Pfam-B_8596	PB008596
contig00106-orf00014	Selenoprotein_S	PF06936.4
contig00106-orf00014	60KD_IMP	PF02096.13
contig00106-orf00016	DUF37	PF01809.11
contig00106-orf00017	Ribosomal_L34	PF00468.10
contig00106-orf00017	DUF3049	PF11250.1
contig00106-orf00018	Ribonuclease_P	PF00825.11
contig00106-orf00018	Synaphin	PF05835.5
contig00106-orf00022	Bac_DnaA	PF00308.11
contig00106-orf00022	Bac_DnaA_C	PF08299.4
contig00106-orf00023	DNA_pol3_beta	PF00712.12
contig00106-orf00023	DNA_pol3_beta_2	PF02767.9
contig00106-orf00023	DNA_pol3_beta_3	PF02768.8
contig00106-orf00025	DUF615	PF04751.7
contig00106-orf00025	POPLD	PF08170.5
contig00106-orf00025	TipAS	PF07739.6
contig00106-orf00027	Pfam-B_5612	PB005612
contig00106-orf00028	PmbA_TldD	PF01523.9
contig00106-orf00030	Pfam-B_9705	PB009705
contig00106-orf00030	Glyco_transf_5	PF08323.4
contig00106-orf00030	DUF3492	PF11997.1
contig00106-orf00030	Glycos_transf_1	PF00534.13
contig00106-orf00030	2-Hacid_dh	PF00389.23
contig00106-orf00032	Dus	PF01207.10
contig00106-orf00034	DSPc	PF00782.13
contig00107-orf00001	Transposase_11	PF01609.14
contig00107-orf00002	Cas_Cas1	PF01867.9
contig00107-orf00004	CRISPR_Cas2	PF09827.2
contig00107-orf00007	DUF465	PF04325.6
contig00107-orf00008	Shikimate_DH	PF01488.13
contig00107-orf00008	CysG_dimeriser	PF10414.2
contig00107-orf00008	TP_methylase	PF00590.13
contig00107-orf00010	PAPS_reduct	PF01507.12
contig00107-orf00012	Carb_anhydrase	PF00194.14
contig00107-orf00013	DJ-1_PfpI	PF01965.17
contig00107-orf00015	AraC_N	PF06719.6
contig00107-orf00015	HTH_AraC	PF00165.16

Query	Pfam Subject	Pfam ID
contig00107-orf00015	HTH_AraC	PF00165.16
contig00107-orf00018	PAPS_reduct	PF01507.12
contig00107-orf00019	IMS	PF00817.13
contig00107-orf00019	Cas_TM1812	PF09530.3
contig00107-orf00019	IMS_HHH	PF11798.1
contig00107-orf00019	IMS_C	PF11799.1
contig00107-orf00021	DUF519	PF04378.6
contig00107-orf00023	Pfam-B_5944	PB005944
contig00107-orf00023	Pfam-B_284	PB000284
contig00107-orf00023	Pfam-B_12454	PB012454
contig00107-orf00023	Pfam-B_601	PB000601
contig00107-orf00023	DUF699	PF05127.7
contig00107-orf00023	Pfam-B_6279	PB006279
contig00107-orf00023	Pfam-B_12411	PB012411
contig00107-orf00023	Viral_helicase1	PF01443.11
contig00107-orf00023	Pfam-B_6611	PB006611
contig00108-orf00001	ABC_tran	PF00005.20
contig00108-orf00001	Phage_tail_T	PF06223.5
contig00108-orf00001	Pfam-B_817	PB000817
contig00108-orf00002	Pfam-B_759	PB000759
contig00108-orf00002	Pfam-B_11556	PB011556
contig00108-orf00002	FtsX	PF02687.14
contig00108-orf00004	RecR	PF02132.8
contig00108-orf00004	DUF3761	PF12587.1
contig00108-orf00004	Toprim	PF01751.15
contig00108-orf00006	ArsC	PF03960.8
contig00108-orf00006	Cyt-b5	PF00173.21
contig00108-orf00007	GCV_T	PF01571.14
contig00108-orf00007	GCV_T_C	PF08669.4
contig00108-orf00009	UvrD-helicase	PF00580.14
contig00108-orf00009	Pfam-B_536	PB000536
contig00108-orf00009	Viral_helicase1	PF01443.11
contig00108-orf00009	Pfam-B_6611	PB006611
contig00108-orf00009	Pfam-B_9137	PB009137
contig00108-orf00009	Pfam-B_11590	PB011590
contig00108-orf00010	Phage_integrase	PF00589.15
contig00108-orf00012	DUF202	PF02656.8
contig00108-orf00012	DUF606	PF04657.6
contig00108-orf00014	Abhydrolase_1	PF00561.13
contig00108-orf00016	MetW	PF07021.5
contig00108-orf00016	F-actin_cap_A	PF01267.10
contig00108-orf00019	Aminotran_1_2	PF00155.14

Query	Pfam Subject	Pfam ID
contig00108-orf00021	Ubie_methyltran	PF01209.11
contig00108-orf00024	DUF971	PF06155.5
contig00108-orf00024	DUF2442	PF10387.2
contig00108-orf00027	Pfam-B_893	PB000893
contig00108-orf00027	CAP	PF00188.19
contig00108-orf00028	DcuA_DcuB	PF03605.7
contig00108-orf00029	DUF3460	PF11943.1
contig00108-orf00030	Methyltransf_3	PF01596.10
contig00108-orf00032	DUF3251	PF11622.1
contig00108-orf00032	TPR_2	PF07719.10
contig00108-orf00032	Pfam-B_6418	PB006418
contig00108-orf00032	TPR_2	PF07719.10
contig00108-orf00033	AIRC	PF00731.13
contig00108-orf00033	Glutaredoxin	PF00462.17
contig00108-orf00033	DUF166	PF02593.7
contig00108-orf00035	ABC_tran	PF00005.20
contig00108-orf00035	Pfam-B_11162	PB011162
contig00108-orf00035	Pfam-B_11182	PB011182
contig00108-orf00035	Pfam-B_13170	PB013170
contig00108-orf00035	Pfam-B_14114	PB014114
contig00108-orf00035	Pfam-B_17943	PB017943
contig00108-orf00035	Pfam-B_890	PB000890
contig00108-orf00035	ABC_tran	PF00005.20
contig00108-orf00035	Pfam-B_11162	PB011162
contig00108-orf00035	Pfam-B_11182	PB011182
contig00108-orf00035	Pfam-B_13947	PB013947
contig00108-orf00035	Pfam-B_5104	PB005104
contig00108-orf00035	Pfam-B_3779	PB003779
contig00108-orf00035	Pfam-B_9027	PB009027
contig00108-orf00035	Pfam-B_538	PB000538
contig00108-orf00035	Pfam-B_13879	PB013879
contig00108-orf00035	Pfam-B_14095	PB014095
contig00108-orf00035	Pfam-B_11595	PB011595
contig00108-orf00035	Pfam-B_10072	PB010072
contig00108-orf00035	Pfam-B_10120	PB010120
contig00108-orf00035	Pfam-B_18200	PB018200
contig00108-orf00036	IMPDH	PF00478.18
contig00108-orf00036	CBS	PF00571.21
contig00108-orf00036	CBS	PF00571.21
contig00108-orf00036	B12-binding	PF02310.12
contig00108-orf00039	Enolase_N	PF03952.9
contig00108-orf00039	Enolase_C	PF00113.15

Query	Pfam Subject	Pfam ID
contig00108-orf00039	Ribosomal_L37e	PF01907.12
contig00108-orf00040	Trs120	PF08626.4
contig00108-orf00040	DivIC	PF04977.8
contig00108-orf00040	HpaB_N	PF11794.1
contig00108-orf00040	CENP-H	PF05837.5
contig00108-orf00047	DEAD	PF00270.22
contig00108-orf00047	Helicase_C	PF00271.24
contig00108-orf00049	Methyltrans_SAM	PF10672.2
contig00108-orf00053	DUF2331	PF10093.2
contig00108-orf00053	Herpes_UL1	PF05259.4
contig00108-orf00054	EFP_N	PF08207.5
contig00108-orf00054	EFP	PF01132.13
contig00108-orf00054	Elong-fact-P_C	PF09285.4
contig00108-orf00058	DNA_topoisoIV	PF00521.13
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00058	DNA_gyraseA_C	PF03989.6
contig00108-orf00059	Cys_Met_Meta_PP	PF01053.13
contig00108-orf00061	UvrD-helicase	PF00580.14
contig00108-orf00061	Pfam-B_6611	PB006611
contig00108-orf00061	Pfam-B_9137	PB009137
contig00108-orf00061	Pfam-B_11590	PB011590
contig00108-orf00065	RdgC	PF04381.5
contig00108-orf00067	Toxin_20	PF08089.4
contig00108-orf00067	MORN	PF02493.13
contig00108-orf00067	MORN	PF02493.13
contig00108-orf00067	Reeler	PF02014.9
contig00108-orf00069	DUF3766	PF12611.1
contig00108-orf00069	dUTPase	PF00692.12
contig00108-orf00075	Competence	PF03772.9
contig00108-orf00075	Lactamase_B	PF00753.20
contig00108-orf00079	GshA	PF08886.4
contig00108-orf00079	RimK	PF08443.4
contig00108-orf00081	Aconitase	PF00330.13
contig00108-orf00082	Entericidin	PF08085.4
contig00108-orf00082	Pfam-B_823	PB000823
contig00108-orf00083	Entericidin	PF08085.4
contig00108-orf00084	Aconitase_C	PF00694.12
contig00108-orf00086	DUF386	PF04074.5

Query	Pfam Subject	Pfam ID
contig00108-orf00090	Iso_dh	PF00180.13
contig00108-orf00093	DUF350	PF03994.7
contig00108-orf00093	DUF350	PF03994.7
contig00108-orf00095	Pfam-B_4394	PB004394
contig00108-orf00095	Band_7	PF01145.18
contig00108-orf00095	GvpG	PF05120.5
contig00108-orf00095	DMAP_binding	PF06464.4
contig00108-orf00100	Ribosomal_S27e	PF01667.10
contig00108-orf00100	Pfam-B_989	PB000989
contig00108-orf00100	Transposase_35	PF07282.4
contig00108-orf00100	IBR	PF01485.14
contig00108-orf00100	Pfam-B_989	PB000989
contig00108-orf00100	DNA_ligase_ZBD	PF03119.9
contig00108-orf00100	Pfam-B_989	PB000989
contig00108-orf00102	AdoMet_dc	PF02675.8
contig00108-orf00104	TAT_signal	PF10518.2
contig00108-orf00104	DAO	PF01266.17
contig00108-orf00104	Pfam-B_9104	PB009104
contig00108-orf00104	Pfam-B_3461	PB003461
contig00108-orf00107	DNA_pol3_chi	PF04364.6
contig00108-orf00109	Entericidin	PF08085.4
contig00108-orf00109	FKBP_N	PF01346.11
contig00108-orf00109	FKBP_C	PF00254.21
contig00108-orf00114	Formyl_trans_N	PF00551.12
contig00108-orf00115	DUF3108	PF11306.1
contig00108-orf00117	SNase	PF00565.10
contig00108-orf00117	DUF3752	PF12572.1
contig00108-orf00118	DeoR	PF00455.15
contig00108-orf00118	Rib_5-P_isom_A	PF06026.7
contig00108-orf00118	RelA_SpoT	PF04607.10
contig00108-orf00121	YgbB	PF02542.9
contig00108-orf00122	ILVD_EDD	PF00920.14
contig00108-orf00124	DUF162	PF02589.8
contig00108-orf00124	Fer4	PF00037.20
contig00108-orf00124	Fer4	PF00037.20
contig00108-orf00124	DUF3390	PF11870.1
contig00108-orf00126	DUF162	PF02589.8
contig00108-orf00128	CCG	PF02754.9
contig00108-orf00128	CCG	PF02754.9
contig00108-orf00129	MFS_1	PF07690.9
contig00108-orf00129	MFS_1	PF07690.9
contig00109-orf00002	Phage_integrase	PF00589.15

Query	Pfam Subject	Pfam ID
contig00109-orf00002	Peptidase_C71	PF12386.1
contig00113-orf00001	Pfam-B_14192	PB014192
contig00113-orf00001	Lipoprotein_5	PF01298.11
contig00113-orf00001	Lipoprot_C	PF08794.3
contig00113-orf00001	Pfam-B_9648	PB009648
contig00113-orf00002	ApoLp-III	PF07464.4
contig00113-orf00002	DUF560	PF04575.6
contig00113-orf00006	ABC-3	PF00950.10
contig00113-orf00008	Pfam-B_601	PB000601
contig00113-orf00008	ABC_tran	PF00005.20
contig00113-orf00008	DUF2326	PF10088.2
contig00113-orf00011	Porin_1	PF00267.14
contig00113-orf00012	SBP_bac_5	PF00496.15
contig00113-orf00015	Creatinase_N	PF01321.11
contig00113-orf00015	Creatinase_N	PF01321.11
contig00113-orf00015	Peptidase_M24	PF00557.17
contig00113-orf00019	BPD_transp_1	PF00528.15
contig00113-orf00022	Pfam-B_1473	PB001473
contig00113-orf00022	BPD_transp_1	PF00528.15
contig00113-orf00024	Mg_chelatase	PF01078.14
contig00113-orf00024	Runt	PF00853.12
contig00113-orf00024	ABC_tran	PF00005.20
contig00113-orf00024	Pfam-B_817	PB000817
contig00113-orf00024	oligo_HPY	PF08352.5
contig00113-orf00024	ABC_tran	PF00005.20
contig00113-orf00024	Pfam-B_11559	PB011559
contig00113-orf00024	oligo_HPY	PF08352.5
contig00113-orf00027	DUF1469	PF07332.4
contig00113-orf00027	Arif-1	PF06770.4
contig00113-orf00027	DUF2207	PF09972.2
contig00113-orf00027	DUF2561	PF10812.1
contig00113-orf00027	NfeD	PF01957.11
contig00113-orf00027	Bac_rhodopsin	PF01036.11
contig00113-orf00028	Apolipoprotein	PF01442.11
contig00113-orf00028	Phasin	PF05597.4
contig00113-orf00028	Pfam-B_2886	PB002886
contig00113-orf00028	LEA_4	PF02987.9
contig00113-orf00028	DUF883	PF05957.6
contig00113-orf00028	CcmD	PF04995.7
contig00113-orf00029	CoA_binding	PF02629.12
contig00113-orf00029	Amidase02_C	PF12123.1
contig00113-orf00029	Ligase_CoA	PF00549.12

Query	Pfam Subject	Pfam ID
contig00113-orf00032	ATP-grasp_2	PF08442.3
contig00113-orf00032	Ligase_CoA	PF00549.12
contig00113-orf00034	Cyto_ox_2	PF02322.8
contig00113-orf00036	Pyr_redox_2	PF07992.7
contig00113-orf00036	Pyr_redox	PF00070.20
contig00113-orf00036	Pyr_redox_dim	PF02852.15
contig00113-orf00044	Biotin_lipoyl	PF00364.15
contig00113-orf00044	Pfam-B_5160	PB005160
contig00113-orf00044	E3_binding	PF02817.10
contig00113-orf00044	2-oxoacid_dh	PF00198.16
contig00113-orf00049	E1_dh	PF00676.13
contig00113-orf00049	Transket_pyr	PF02779.17
contig00113-orf00050	Citrate_synt	PF00285.14
contig00113-orf00050	ERbeta_N	PF12497.1
contig00113-orf00051	Sdh5	PF03937.9
contig00113-orf00052	Pfam-B_8147	PB008147
contig00113-orf00052	Fer4	PF00037.20
contig00113-orf00053	FAD_binding_2	PF00890.17
contig00113-orf00053	Succ_DH_flav_C	PF02910.13
contig00113-orf00054	Sdh_cyt	PF01127.15
contig00113-orf00054	Ferric_reduct	PF01794.12
contig00113-orf00054	DUF1290	PF06947.5
contig00113-orf00055	Sdh_cyt	PF01127.15
contig00113-orf00057	Sod_Cu	PF00080.13
contig00113-orf00058	DUF1232	PF06803.5
contig00113-orf00060	Entericidin	PF08085.4
contig00113-orf00060	Endonuc_Holl	PF10107.2
contig00113-orf00062	PALP	PF00291.18
contig00113-orf00062	ADH_zinc_N	PF00107.19
contig00113-orf00062	Pribosyltran	PF00156.20
contig00113-orf00062	FlaG	PF03646.8
contig00113-orf00066	DAP_epimerase	PF01678.12
contig00113-orf00066	DAP_epimerase	PF01678.12
contig00113-orf00067	TetR_N	PF00440.16
contig00113-orf00067	Pfam-B_17408	PB017408
contig00113-orf00068	FAD_binding_4	PF01565.16
contig00113-orf00068	MurB_C	PF02873.9
contig00113-orf00070	Pfam-B_2112	PB002112
contig00113-orf00073	MatE	PF01554.11
contig00113-orf00073	MatE	PF01554.11
contig00113-orf00075	P-II	PF00543.15
contig00113-orf00075	Nit_Regul_Hom	PF10126.2

Query	Pfam Subject	Pfam ID
contig00113-orf00079	AIRS	PF00586.17
contig00113-orf00079	AIRS_C	PF02769.15
contig00113-orf00079	MuDR	PF03108.8
contig00113-orf00079	AIRS_C	PF02769.15
contig00113-orf00083	Amidohydro_1	PF01979.13
contig00113-orf00083	ComA	PF02679.8
contig00113-orf00086	SirA	PF01206.10
contig00113-orf00087	CMV_US	PF08001.4
contig00113-orf00087	CNP1	PF08750.4
contig00113-orf00088	CNP1	PF08750.4
contig00113-orf00088	PFEMP	PF03011.8
contig00113-orf00089	TatD_DNase	PF01026.14
contig00113-orf00090	PilZ	PF07238.7
contig00113-orf00092	AAA	PF00004.22
contig00113-orf00092	Pfam-B_12262	PB012262
contig00113-orf00094	DUF485	PF04341.5
contig00113-orf00094	PMP22_Claudin	PF00822.13
contig00113-orf00094	DUF805	PF05656.7
contig00113-orf00094	DUF3687	PF12459.1
contig00113-orf00094	DUF2721	PF11026.1
contig00113-orf00094	DUF2154	PF09922.2
contig00113-orf00095	Pfam-B_15765	PB015765
contig00113-orf00095	Pfam-B_7145	PB007145
contig00113-orf00095	Bacteriocin_IIc	PF10439.2
contig00113-orf00095	DUF456	PF04306.6
contig00113-orf00095	DUF1269	PF06897.5
contig00113-orf00095	Rick_17kDa_Anti	PF05433.8
contig00113-orf00095	Aldedh	PF00171.15
contig00113-orf00095	DUF2693	PF10902.1
contig00113-orf00098	DUF805	PF05656.7
contig00113-orf00098	DUF443	PF04276.5
contig00113-orf00098	DUF485	PF04341.5
contig00113-orf00098	PilN	PF05137.6
contig00113-orf00098	Tetraspannin	PF00335.13
contig00113-orf00098	PMP22_Claudin	PF00822.13
contig00113-orf00098	DUF1049	PF06305.4
contig00113-orf00098	DUF2721	PF11026.1
contig00113-orf00098	IncA	PF04156.7
contig00113-orf00098	MFS_1	PF07690.9
contig00113-orf00098	DUF2154	PF09922.2
contig00113-orf00100	Ham1p_like	PF01725.9
contig00113-orf00103	Radical_SAM	PF04055.14

Query	Pfam Subject	Pfam ID
contig00113-orf00103	HemN_C	PF06969.9
contig00113-orf00104	Pfam-B_376	PB000376
contig00113-orf00104	Pfam-B_581	PB000581
contig00113-orf00104	Opacity	PF02462.8
contig00113-orf00104	DUF2490	PF10677.2
contig00113-orf00105	Ribonuc_L-PSP	PF01042.14
contig00113-orf00107	Metallophos	PF00149.21
contig00113-orf00108	Transaldolase	PF00923.12
contig00113-orf00112	SIS	PF01380.15
contig00113-orf00112	CBS	PF00571.21
contig00113-orf00112	Pfam-B_1302	PB001302
contig00113-orf00112	Corona_NS1	PF06145.4
contig00113-orf00112	CBS	PF00571.21
contig00113-orf00115	Pfam-B_10165	PB010165
contig00113-orf00115	Nol1_Nop2_Fmu	PF01189.10
contig00113-orf00124	DUF387	PF04079.9
contig00113-orf00128	G6PD_bact	PF10786.2
contig00113-orf00130	Hemerythrin	PF01814.16
contig00113-orf00133	DUF2613	PF11021.1
contig00113-orf00133	HpaP	PF09483.3
contig00113-orf00133	Copper-bind	PF00127.13
contig00113-orf00134	DUF721	PF05258.5
contig00113-orf00138	SecA_DEAD	PF07517.7
contig00113-orf00138	SecA_PP_bind	PF01043.13
contig00113-orf00138	DUF1542	PF07564.4
contig00113-orf00138	SecA_SW	PF07516.6
contig00113-orf00138	SEC-C	PF02810.8
contig00113-orf00141	tRNA-synt_1c	PF00749.14
contig00113-orf00141	tRNA-synt_1c_C	PF03950.11
contig00113-orf00144	Pfam-B_3118	PB003118
contig00113-orf00144	HTH_DeoR	PF08220.5
contig00113-orf00144	EAP30	PF04157.9
contig00113-orf00144	DeoR	PF00455.15
contig00113-orf00146	Nitroreductase	PF00881.17
contig00113-orf00148	Aminotran_5	PF00266.12
contig00113-orf00149	DUF150	PF02576.10
contig00113-orf00153	NusA_N	PF08529.4
contig00113-orf00153	S1	PF00575.16
contig00113-orf00153	KH_2	PF07650.10
contig00113-orf00153	Pfam-B_4913	PB004913
contig00113-orf00155	IF2_N	PF04760.8
contig00113-orf00155	PAT1	PF09770.2

Query	Pfam Subject	Pfam ID
contig00113-orf00155	IF2_N	PF04760.8
contig00113-orf00155	GTP_EFTU	PF00009.20
contig00113-orf00155	GTP_EFTU_D2	PF03144.18
contig00113-orf00155	IF-2	PF11987.1
contig00113-orf00155	GTP_EFTU_D2	PF03144.18
contig00113-orf00157	Lpp-LpqN	PF10738.2
contig00113-orf00157	SCO1-SenC	PF02630.7
contig00113-orf00159	HisG	PF01634.11
contig00113-orf00160	Pfam-B_2112	PB002112
contig00113-orf00160	GIY-YIG	PF01541.17
contig00113-orf00160	Pfam-B_12134	PB012134
contig00113-orf00160	WhiA_N	PF10298.2
contig00113-orf00162	Histidinol_dh	PF00815.13
contig00113-orf00163	Pfam-B_5069	PB005069
contig00113-orf00163	Pfam-B_6541	PB006541
contig00113-orf00163	ABC_tran	PF00005.20
contig00113-orf00163	ABC_ATPase	PF09818.2
contig00113-orf00163	Pfam-B_1384	PB001384
contig00113-orf00163	ImmE5	PF11480.1
contig00113-orf00163	TOBE	PF03459.10
contig00113-orf00163	MobB	PF03205.7
contig00113-orf00166	BPD_transp_1	PF00528.15
contig00113-orf00170	BPD_transp_1	PF00528.15
contig00113-orf00171	Hemerythrin	PF01814.16
contig00113-orf00171	Pfam-B_756	PB000756
contig00113-orf00171	Hemerythrin	PF01814.16
contig00113-orf00174	Nitroreductase	PF00881.17
contig00113-orf00176	DUF2079	PF09852.2
contig00113-orf00176	DUF2069	PF09842.2
contig00113-orf00179	Wzy_C	PF04932.8
contig00113-orf00179	DUF3366	PF11846.1
contig00113-orf00182	Exonuc_V_gamma	PF04257.7
contig00113-orf00182	Pfam-B_536	PB000536
contig00113-orf00184	Plug	PF07715.8
contig00113-orf00185	TonB_dep_Rec	PF00593.17
contig00113-orf00186	DUF333	PF03891.8
contig00115-orf00001	TetR_N	PF00440.16
contig00115-orf00001	TetR_C_2	PF08361.4
contig00115-orf00002	Plug	PF07715.8
contig00115-orf00002	TonB_dep_Rec	PF00593.17
contig00115-orf00006	Hydrolase	PF00702.19
contig00115-orf00008	PHP	PF02811.12

Query	Pfam Subject	Pfam ID
contig00115-orf00011	Pfam-B_16914	PB016914
contig00115-orf00011	Oxidored-like	PF09791.2
contig00115-orf00013	S4	PF01479.18
contig00115-orf00015	Plug	PF07715.8
contig00115-orf00015	TonB_dep_Rec	PF00593.17
contig00115-orf00017	Phage_Mu_Gam	PF07352.5
contig00115-orf00017	DUF2200	PF09966.2
contig00115-orf00017	Syntaxin-6_N	PF09177.4
contig00115-orf00017	DegS	PF05384.4
contig00115-orf00017	Fmp27_WPPW	PF10359.2
contig00115-orf00017	Phage_pRha	PF09669.3
contig00115-orf00017	USP8_interact	PF08941.3
contig00115-orf00017	APG6	PF04111.5
contig00115-orf00017	Ax_dynein_light	PF10211.2
contig00115-orf00017	DUF342	PF03961.6
contig00115-orf00017	DivIVA	PF05103.6
contig00115-orf00017	Fib_alpha	PF08702.3
contig00115-orf00017	Myosin_tail_1	PF01576.12
contig00115-orf00017	COG2	PF06148.4
contig00115-orf00017	DUF948	PF06103.4
contig00115-orf00017	DUF3450	PF11932.1
contig00115-orf00017	Spc24	PF08286.4
contig00115-orf00017	OmpH	PF03938.7
contig00115-orf00017	Prefoldin	PF02996.10
contig00115-orf00017	Osmo_CC	PF08946.3
contig00115-orf00017	TMF_DNA_bd	PF12329.1
contig00115-orf00017	V_ATPase_I	PF01496.12
contig00115-orf00017	DUF3373	PF11853.1
contig00115-orf00017	Mnd1	PF03962.8
contig00115-orf00017	ADIP	PF11559.1
contig00115-orf00017	HOOK	PF05622.5
contig00115-orf00017	MAP7	PF05672.4
contig00115-orf00017	SlyX	PF04102.5
contig00115-orf00017	DASH_Hsk3	PF08227.4
contig00115-orf00017	HALZ	PF02183.11
contig00115-orf00019	ABC_membrane_2	PF06472.8
contig00115-orf00019	ABC_tran	PF00005.20
contig00115-orf00022	Pfam-B_5612	PB005612
contig00115-orf00024	GntR	PF00392.14
contig00115-orf00024	FCD	PF07729.5
contig00115-orf00027	Lactate_perm	PF02652.7
contig00115-orf00033	Peptidase_M1	PF01433.13

Query	Pfam Subject	Pfam ID
contig00115-orf00033	DUF3458	PF11940.1
contig00116-orf00001	DNA_methylase	PF00145.10
contig00116-orf00001	DNA_methylase	PF00145.10
contig00116-orf00005	tRNA-synt_2c	PF01411.12
contig00116-orf00005	Halogen_Hydrol	PF10112.2
contig00116-orf00005	Pfam-B_3510	PB003510
contig00116-orf00005	tRNA_SAD	PF07973.7
contig00116-orf00005	Pfam-B_13169	PB013169
contig00116-orf00005	DHHA1	PF02272.12
contig00116-orf00006	SBP_bac_1	PF01547.18
contig00116-orf00006	BCS1_N	PF08740.4
contig00116-orf00008	PLDc	PF00614.15
contig00116-orf00010	A_deaminase	PF00962.15
contig00116-orf00013	tRNA-synt_1b	PF00579.18
contig00116-orf00016	Clp_N	PF02861.13
contig00116-orf00016	Clp_N	PF02861.13
contig00116-orf00016	AAA	PF00004.22
contig00116-orf00016	Pfam-B_1028	PB001028
contig00116-orf00016	Pfam-B_8817	PB008817
contig00116-orf00016	Pfam-B_3562	PB003562
contig00116-orf00016	Pfam-B_3538	PB003538
contig00116-orf00016	Pfam-B_16498	PB016498
contig00116-orf00016	Pfam-B_8945	PB008945
contig00116-orf00016	Pfam-B_9855	PB009855
contig00116-orf00016	Pfam-B_3561	PB003561
contig00116-orf00016	AAA_2	PF07724.7
contig00116-orf00016	ClpB_D2-small	PF10431.2
contig00116-orf00018	Dyp_perox	PF04261.5
contig00116-orf00021	Metallophos	PF00149.21
contig00116-orf00024	LemA	PF04011.5
contig00116-orf00024	IncA	PF04156.7
contig00116-orf00027	LGT	PF01790.11
contig00116-orf00029	Peptidase_M14	PF00246.17
contig00116-orf00029	TraK	PF06586.4
contig00116-orf00032	AA_kinase	PF00696.21
contig00116-orf00033	Ppx-GppA	PF02541.9
contig00116-orf00033	HemS	PF05171.5
contig00116-orf00035	TAT_signal	PF10518.2
contig00116-orf00035	Pfam-B_3751	PB003751
contig00116-orf00035	SLT	PF01464.13
contig00116-orf00036	MFS_1	PF07690.9
contig00116-orf00037	SSB	PF00436.18

Query	Pfam Subject	Pfam ID
contig00116-orf00038	Phage_integrase	PF00589.15
contig00116-orf00038	DUF1231	PF06802.4
contig00116-orf00039	DUF404	PF04169.6
contig00116-orf00039	Phage_integrase	PF00589.15
contig00116-orf00041	Pfam-B_5847	PB005847
contig00116-orf00041	Pfam-B_1470	PB001470
contig00116-orf00043	Pfam-B_11971	PB011971
contig00116-orf00043	Pfam-B_665	PB000665
contig00116-orf00043	Pfam-B_313	PB000313
contig00116-orf00043	Pfam-B_2823	PB002823
contig00116-orf00045	Haemagg_act	PF05860.6
contig00116-orf00045	Fil_haemagg	PF05594.7
contig00116-orf00045	Pfam-B_6070	PB006070
contig00116-orf00045	Pfam-B_5549	PB005549
contig00116-orf00045	Pfam-B_6070	PB006070
contig00116-orf00045	Fil_haemagg	PF05594.7
contig00116-orf00045	Pfam-B_5549	PB005549
contig00116-orf00045	Fil_haemagg	PF05594.7
contig00116-orf00045	Pfam-B_5549	PB005549
contig00116-orf00045	Pfam-B_11830	PB011830
contig00116-orf00045	Pfam-B_313	PB000313
contig00116-orf00045	Fil_haemagg	PF05594.7
contig00116-orf00045	Pfam-B_19347	PB019347
contig00116-orf00045	Pfam-B_665	PB000665
contig00116-orf00046	POTRA_2	PF08479.4
contig00116-orf00046	ShlB	PF03865.6
contig00116-orf00049	DUF2892	PF11127.1
contig00116-orf00049	Imp-YgjV	PF10688.2
contig00116-orf00052	Rhodanese	PF00581.13
contig00116-orf00052	Pfam-B_19059	PB019059
contig00116-orf00052	DUF2892	PF11127.1
contig00116-orf00054	DUF772	PF05598.4
contig00117-orf00001	TAFII28	PF04719.7
contig00117-orf00003	OB_RNB	PF08206.4
contig00117-orf00003	RNB	PF00773.12
contig00117-orf00003	S1	PF00575.16
contig00117-orf00006	Pfam-B_683	PB000683
contig00117-orf00006	HAMP	PF00672.18
contig00117-orf00006	Pfam-B_348	PB000348
contig00117-orf00006	Pfam-B_9034	PB009034
contig00117-orf00006	HisKA_3	PF07730.6
contig00117-orf00006	HATPase_c	PF02518.19

Query	Pfam Subject	Pfam ID
contig00117-orf00007	CHASE2	PF05226.4
contig00117-orf00007	Response_reg	PF00072.17
contig00117-orf00007	GerE	PF00196.12
contig00117-orf00009	DsbC	PF11412.1
contig00117-orf00009	DsbD	PF02683.8
contig00117-orf00009	DUF2933	PF11666.1
contig00117-orf00009	Thioredoxin	PF00085.13
contig00117-orf00012	UDG	PF03167.12
contig00117-orf00013	PBP	PF01161.13
contig00117-orf00014	HemolysinCabind	PF00353.12
contig00117-orf00014	Pfam-B_639	PB000639
contig00117-orf00014	Pfam-B_9305	PB009305
contig00117-orf00014	Pfam-B_7705	PB007705
contig00117-orf00014	Pfam-B_12469	PB012469
contig00117-orf00014	HemolysinCabind	PF00353.12
contig00117-orf00014	HemolysinCabind	PF00353.12
contig00117-orf00014	Pfam-B_7705	PB007705
contig00117-orf00014	HemolysinCabind	PF00353.12
contig00117-orf00015	Peptidase_C25	PF01364.11
contig00117-orf00015	Pfam-B_7705	PB007705
contig00117-orf00016	DUF3546	PF12066.1
contig00117-orf00017	ADH_zinc_N	PF00107.19
contig00117-orf00018	Esterase	PF00756.13
contig00117-orf00020	Pro_isomerase	PF00160.14
contig00117-orf00022	Na_sulph_symp	PF00939.12
contig00117-orf00022	MttA_Hcf106	PF02416.9
contig00117-orf00023	DHquinase_I	PF01487.8
contig00117-orf00025	YjgP_YjgQ	PF03739.7
contig00117-orf00027	YjgP_YjgQ	PF03739.7
contig00117-orf00028	Peptidase_M17_N	PF02789.10
contig00117-orf00028	Peptidase_M17	PF00883.14
contig00117-orf00030	SnoaL	PF07366.5
contig00117-orf00030	CHRD	PF07452.5
contig00117-orf00031	Cupin_2	PF07883.4
contig00117-orf00035	Plug	PF07715.8
contig00117-orf00035	Pfam-B_2552	PB002552
contig00117-orf00035	Pfam-B_2552	PB002552
contig00117-orf00035	Seadorna_Vp10	PF07322.4
contig00117-orf00035	TonB_dep_Rec	PF00593.17
contig00117-orf00037	Alpha-amylase	PF00128.17
contig00117-orf00037	Cyc-maltodext_C	PF10438.2
contig00119-orf00002	FLO_LFY	PF01698.9

Query	Pfam Subject	Pfam ID
contig00119-orf00002	Pfam-B_12261	PB012261
contig00119-orf00002	Pex14_N	PF04695.6
contig00119-orf00004	Plasmid_Txe	PF06769.6
contig00119-orf00004	TFIID-18kDa	PF02269.9
contig00119-orf00005	PhdYeFM	PF02604.12
contig00119-orf00007	HTH_CodY	PF08222.4
contig00119-orf00008	DUF1655	PF07868.4
contig00119-orf00010	Pfam-B_4377	PB004377
contig00119-orf00010	PIN	PF01850.14
contig00119-orf00010	DUF2577	PF10844.1
contig00119-orf00011	PhdYeFM	PF02604.12
contig00119-orf00016	rve	PF00665.19
contig00120-orf00001	Pfam-B_665	PB000665
contig00120-orf00001	Pfam-B_11049	PB011049
contig00120-orf00001	DUF3502	PF12010.1
contig00120-orf00001	DUF2078	PF09851.2
contig00120-orf00001	DUF637	PF04830.6
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_7705	PB007705
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_12469	PB012469
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_12469	PB012469
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_12469	PB012469
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_12469	PB012469
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_956	PB000956
contig00122-orf00004	He_PIG	PF05345.5
contig00122-orf00004	He_PIG	PF05345.5

Query	Pfam Subject	Pfam ID
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	Pfam-B_7705	PB007705
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	Pfam-B_9305	PB009305
contig00122-orf00004	HCBP_related	PF06594.4
contig00122-orf00004	Pfam-B_12469	PB012469
contig00122-orf00004	Pfam-B_639	PB000639
contig00122-orf00004	Pfam-B_7705	PB007705
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00004	HemolysinCabind	PF00353.12
contig00122-orf00005	Radical_SAM	PF04055.14
contig00122-orf00008	Cauli_DNA-bind	PF03310.6
contig00122-orf00008	DUF3503	PF12011.1
contig00122-orf00011	Pirin	PF02678.9
contig00122-orf00011	Pirin_C	PF05726.6
contig00122-orf00012	HxlR	PF01638.10
contig00123-orf00001	tRNA-synt_1g	PF09334.4
contig00123-orf00001	Anticodon_1	PF08264.6
contig00123-orf00004	OPT	PF03169.8
contig00124-orf00001	ATP-synt_DE_N	PF02823.9
contig00124-orf00001	DUF3359	PF11839.1
contig00124-orf00001	ATP-synt_DE	PF00401.13
contig00124-orf00002	ATP-synt_ab_N	PF02874.16
contig00124-orf00002	ATP-synt_ab	PF00006.18
contig00124-orf00002	ATP-synt_ab_C	PF00306.20
contig00124-orf00004	ATP-synt	PF00231.12
contig00124-orf00006	ATP-synt_ab_N	PF02874.16
contig00124-orf00006	ATP-synt_ab	PF00006.18
contig00124-orf00006	Arginosuc_synth	PF00764.12
contig00124-orf00006	FmdE	PF02663.7
contig00124-orf00006	ATP-synt_ab_C	PF00306.20
contig00124-orf00007	OSCP	PF00213.11
contig00124-orf00007	DUF1759	PF03564.8
contig00124-orf00008	ATP-synt_B	PF00430.11
contig00124-orf00008	DUF2774	PF11242.1
contig00124-orf00008	DUF883	PF05957.6
contig00124-orf00008	Pfam-B_2268	PB002268
contig00124-orf00008	Pex19	PF04614.5
contig00124-orf00008	DUF3294	PF07957.4
contig00124-orf00009	ATP-synt_C	PF00137.14

Query	Pfam Subject	Pfam ID
contig00124-orf00010	Glycophorin_A	PF01102.11
contig00124-orf00010	ATP-synt_A	PF00119.13
contig00124-orf00010	DUF3278	PF11683.1
contig00124-orf00013	ParBc	PF02195.11
contig00124-orf00013	RepB	PF07506.4
contig00124-orf00013	KorB	PF08535.3
contig00124-orf00013	Pfam-B_3753	PB003753
contig00124-orf00015	PHO4	PF01384.13
contig00124-orf00015	VPS11_C	PF12451.1
contig00124-orf00016	UPF0075	PF03702.7
contig00124-orf00017	Cytochrom_C	PF00034.14
contig00124-orf00017	Cytochrom_C	PF00034.14
contig00124-orf00017	Med3	PF11593.1
contig00124-orf00017	Cytochrom_C	PF00034.14
contig00124-orf00018	PspC	PF04024.5
contig00124-orf00018	FixQ	PF05545.4
contig00124-orf00018	PDR_CDR	PF06422.5
contig00124-orf00018	DUF443	PF04276.5
contig00124-orf00018	SAYSvFN	PF10260.2
contig00124-orf00019	FixO	PF02433.8
contig00124-orf00021	COX1	PF00115.13
contig00124-orf00021	Pfam-B_1188	PB001188
contig00124-orf00023	Peptidase_M61	PF05299.5
contig00124-orf00023	PDZ	PF00595.17
contig00124-orf00024	DUF442	PF04273.6
contig00124-orf00024	CbiJ	PF02571.7
contig00124-orf00025	CN_hydrolase	PF00795.15
contig00124-orf00027	E1_dh	PF00676.13
contig00124-orf00027	Transket_pyr	PF02779.17
contig00124-orf00027	Transketolase_C	PF02780.13
contig00124-orf00029	PDH	PF02153.10
contig00124-orf00031	Glyco_transf_9	PF01075.10
contig00124-orf00031	HEM4	PF02602.8
contig00124-orf00033	DUF460	PF04312.6
contig00124-orf00033	RuvC	PF02075.10
contig00124-orf00034	Lip_A_acyltrans	PF03279.6
contig00125-orf00002	Pfam-B_7376	PB007376
contig00125-orf00003	Phage_Coat_B	PF05356.4
contig00125-orf00003	SQS_PSY	PF00494.12
contig00127-orf00002	DUF3609	PF12259.1
contig00127-orf00003	Sec66	PF09802.2
contig00131-orf00001	GIY-YIG	PF01541.17

Query	Pfam Subject	Pfam ID
contig00131-orf00001	UVR	PF02151.12
contig00131-orf00001	UvrC_HhH_N	PF08459.4
contig00131-orf00001	HHH	PF00633.16
contig00131-orf00002	adh_short	PF00106.18
contig00131-orf00004	Cytochrom_C_2	PF01322.13
contig00131-orf00004	Cytochrom_B562	PF07361.4
contig00131-orf00008	Tautomerase	PF01361.14
contig00131-orf00009	Dus	PF01207.10
contig00131-orf00011	IU_nuc_hydro	PF01156.12
contig00131-orf00013	Glycos_transf_2	PF00535.19
contig00131-orf00013	Pfam-B_3567	PB003567
contig00131-orf00013	Glycos_transf_2	PF00535.19
contig00131-orf00013	Galactosyl_T_2	PF02709.7
contig00131-orf00015	Exo_endo_phos	PF03372.16
contig00131-orf00015	Pfam-B_7063	PB007063
contig00131-orf00015	HNH	PF01844.16
contig00131-orf00016	FeS	PF04060.6
contig00131-orf00016	Fer4	PF00037.20
contig00131-orf00016	Fer4	PF00037.20
contig00131-orf00019	Aldedh	PF00171.15
contig00131-orf00021	Xan_ur_permease	PF00860.13
contig00131-orf00024	OEP	PF02321.11
contig00131-orf00026	OEP	PF02321.11
contig00131-orf00026	OEP	PF02321.11
contig00131-orf00027	ABC2_membrane	PF01061.17
contig00131-orf00029	AraC_binding	PF02311.12
contig00132-orf00001	PsbL	PF02419.10
contig00132-orf00004	DUF2154	PF09922.2
contig00134-orf00001	DUF2254	PF10011.2
contig00134-orf00001	Cytochrom_C	PF00034.14
contig00134-orf00001	Cytochrom_C	PF00034.14
contig00134-orf00002	Aminotran_1_2	PF00155.14
contig00134-orf00003	Pterin_bind	PF00809.15
contig00134-orf00005	PGM_PMM_I	PF02878.9
contig00134-orf00005	PGM_PMM_II	PF02879.9
contig00134-orf00005	PGM_PMM_III	PF02880.9
contig00134-orf00005	PGM_PMM_IV	PF00408.13
contig00134-orf00007	CTP_transf_1	PF01148.13
contig00134-orf00007	SNARE_assoc	PF09335.4
contig00134-orf00007	Phage_lysis	PF03245.6
contig00134-orf00007	DUF2133	PF09976.2
contig00134-orf00010	Asparaginase	PF00710.13

Query	Pfam Subject	Pfam ID
contig00134-orf00011	TatD_DNase	PF01026.14
contig00134-orf00015	AIRS	PF00586.17
contig00134-orf00015	AIRS_C	PF02769.15
contig00134-orf00016	PgpA	PF04608.6
contig00134-orf00016	Ni_hydr_CYTB	PF01292.13
contig00134-orf00017	DUF525	PF04379.7
contig00134-orf00019	Transposase_11	PF01609.14
contig00135-orf00003	UPF0004	PF00919.13
contig00135-orf00003	Radical_SAM	PF04055.14
contig00135-orf00003	TRAM	PF01938.13
contig00135-orf00005	Pfam-B_15458	PB015458
contig00135-orf00005	PDH	PF02153.10
contig00135-orf00007	Aminotran_3	PF00202.14
contig00135-orf00011	Mem_trans	PF03547.11
contig00135-orf00011	Mem_trans	PF03547.11
contig00135-orf00015	DUF812	PF05667.4
contig00135-orf00015	ATG16	PF08614.4
contig00135-orf00015	Reo_sigmaC	PF04582.5
contig00135-orf00015	Spc7	PF08317.4
contig00135-orf00015	Baculo_PEP_C	PF04513.5
contig00135-orf00015	SlyX	PF04102.5
contig00135-orf00015	Tropomyosin	PF00261.13
contig00135-orf00015	Spc7	PF08317.4
contig00135-orf00015	DUF827	PF05701.4
contig00135-orf00015	Allexi_40kDa	PF05549.4
contig00135-orf00015	Filament	PF00038.14
contig00135-orf00015	Mnd1	PF03962.8
contig00135-orf00015	Apolipoprotein	PF01442.11
contig00135-orf00015	DUF1664	PF07889.5
contig00135-orf00015	MCPsignal	PF00015.14
contig00135-orf00015	IncA	PF04156.7
contig00135-orf00015	RmuC	PF02646.9
contig00135-orf00015	Filament	PF00038.14
contig00135-orf00015	IFT57	PF10498.2
contig00135-orf00015	FlaC_arch	PF05377.4
contig00135-orf00015	Fib_alpha	PF08702.3
contig00135-orf00015	COG2	PF06148.4
contig00135-orf00015	FUSC	PF04632.5
contig00135-orf00015	Reo_sigmaC	PF04582.5
contig00135-orf00015	Mod_r	PF07200.6
contig00135-orf00015	Tropomyosin	PF00261.13
contig00136-orf00001	Pfam-B_531	PB000531

Query	Pfam Subject	Pfam ID
contig00136-orf00001	SBP_bac_1	PF01547.18
contig00136-orf00003	Ribosomal_S20p	PF01649.11
contig00136-orf00003	Paralemmin	PF03285.8
contig00136-orf00003	CysG_dimeriser	PF10414.2
contig00136-orf00003	Hc1	PF07432.6
contig00136-orf00006	Pfam-B_6364	PB006364
contig00136-orf00006	DUF3121	PF11319.1
contig00136-orf00006	PLA1	PF02253.8
contig00136-orf00008	DUF502	PF04367.6
contig00136-orf00009	tRNA_anti	PF01336.18
contig00136-orf00009	tRNA-synt_2	PF00152.13
contig00136-orf00009	GAD	PF02938.7
contig00136-orf00011	Pfam-B_10022	PB010022
contig00136-orf00011	PIG-L	PF02585.10
contig00136-orf00013	Metallophos	PF00149.21
contig00136-orf00013	DUF668	PF05003.5
contig00136-orf00015	Peptidase_S13	PF02113.8
contig00136-orf00017	Aminotran_1_2	PF00155.14
contig00136-orf00019	IGPD	PF00475.11
contig00136-orf00022	Phasin_2	PF09361.3
contig00136-orf00022	Lipoprotein_5	PF01298.11
contig00136-orf00022	Lipoprot_C	PF08794.3
contig00136-orf00022	Pfam-B_9648	PB009648
contig00136-orf00024	DUF2524	PF10732.2
contig00136-orf00024	AAA_3	PF07726.4
contig00136-orf00024	nsp8	PF08717.3
contig00136-orf00026	Plug	PF07715.8
contig00136-orf00026	TonB_dep_Rec	PF00593.17
contig00136-orf00027	Pfam-B_355	PB000355
contig00136-orf00029	NUDIX	PF00293.21
contig00138-orf00001	LpxK	PF02606.7
contig00138-orf00003	DUF2059	PF09832.2
contig00138-orf00005	DnaI_N	PF07319.4
contig00138-orf00005	DUF2059	PF09832.2
contig00138-orf00008	Pfam-B_8169	PB008169
contig00138-orf00008	Trm112p	PF03966.9
contig00138-orf00009	CTP_transf_3	PF02348.12
contig00138-orf00009	SIP	PF04954.6
contig00138-orf00012	Pfam-B_5612	PB005612
contig00138-orf00012	SMP	PF04927.5
contig00138-orf00014	ADK	PF00406.15
contig00138-orf00014	ADK_lid	PF05191.7

Query	Pfam Subject	Pfam ID
contig00138-orf00015	OMPdecase	PF00215.17
contig00138-orf00015	MutL_C	PF08676.4
contig00138-orf00016	Semialdhyde_dh	PF01118.17
contig00138-orf00017	PfkB	PF00294.17
contig00138-orf00017	FUN14	PF04930.8
contig00138-orf00017	RPAP1_C	PF08620.3
contig00138-orf00019	Epimerase	PF01370.14
contig00138-orf00020	Aminotran_1_2	PF00155.14
contig00138-orf00021	NPD	PF03060.8
contig00138-orf00021	AIRC	PF00731.13
contig00138-orf00022	Aldose_epim	PF01263.13
contig00138-orf00022	Pfam-B_189	PB000189
contig00138-orf00025	S4	PF01479.18
contig00138-orf00025	PseudoU_synth_2	PF00849.15
contig00138-orf00025	DUF1281	PF06924.4
contig00138-orf00027	Pyridox_oxidase	PF01243.13
contig00138-orf00027	PNPOx_C	PF10590.2
contig00138-orf00029	dUTPase	PF00692.12
contig00138-orf00029	Cupin_2	PF07883.4
contig00138-orf00031	Xan_ur_permease	PF00860.13
contig00139-orf00003	Xan_ur_permease	PF00860.13
contig00139-orf00006	Reo_sigmaC	PF04582.5
contig00139-orf00006	Spc7	PF08317.4
contig00139-orf00006	Guanylate_cyc	PF00211.13
contig00139-orf00006	Fib_alpha	PF08702.3
contig00139-orf00006	IncA	PF04156.7
contig00139-orf00006	YadA	PF03895.8
contig00141-orf00002	Peptidase_M22	PF00814.18
contig00141-orf00004	DAHP_synth_1	PF00793.13
contig00141-orf00006	Entericidin	PF08085.4
contig00141-orf00006	Pfam-B_12787	PB012787
contig00141-orf00006	Pfam-B_6	PB000006
contig00141-orf00006	Peptidase_A8	PF01252.11
contig00141-orf00006	Pfam-B_16822	PB016822
contig00141-orf00006	HCV_NS4b	PF01001.12
contig00141-orf00006	DUF937	PF06078.4
contig00141-orf00006	Pfam-B_19490	PB019490
contig00141-orf00006	TraT	PF05818.5
contig00141-orf00006	Rick_17kDa_Anti	PF05433.8
contig00141-orf00008	Glycos_transf_N	PF04413.9
contig00141-orf00008	Glycos_transf_1	PF00534.13
contig00141-orf00010	Hep_Hag	PF05658.7

Query	Pfam Subject	Pfam ID
contig00141-orf00010	Hep_Hag	PF05658.7
contig00141-orf00010	Hep_Hag	PF05658.7
contig00141-orf00010	Pfam-B_19018	PB019018
contig00141-orf00010	Hep_Hag	PF05658.7
contig00141-orf00010	Hep_Hag	PF05658.7
contig00141-orf00010	Hep_Hag	PF05658.7
contig00141-orf00012	LPAM_1	PF08139.5
contig00141-orf00012	SmpA_OmlA	PF04355.6
contig00141-orf00014	GSPII_E_N	PF05157.8
contig00141-orf00014	GSPII_E	PF00437.13
contig00141-orf00015	GSPII_F	PF00482.16
contig00141-orf00015	Selenoprotein_S	PF06936.4
contig00141-orf00015	GSPII_F	PF00482.16
contig00141-orf00016	DiS_P_DiS	PF06750.6
contig00141-orf00016	Peptidase_A24	PF01478.11
contig00141-orf00017	CoaE	PF01121.13
contig00141-orf00017	DUF2015	PF09435.3
contig00141-orf00017	TM2	PF05154.9
contig00141-orf00019	FAD_syn	PF06574.5
contig00141-orf00019	Flavokinase	PF01687.10
contig00141-orf00021	TelA	PF05816.4
contig00141-orf00021	DUF1492	PF07374.4
contig00141-orf00022	LYTB	PF02401.11
contig00141-orf00022	DUF1234	PF06821.6
contig00141-orf00023	Peptidase_A8	PF01252.11
contig00141-orf00023	EamA	PF00892.13
contig00141-orf00028	TPR_2	PF07719.10
contig00141-orf00028	DUF560	PF04575.6
contig00141-orf00032	CitMHS	PF03600.9
contig00141-orf00032	DUF2078	PF09851.2
contig00141-orf00032	CitMHS	PF03600.9
contig00141-orf00035	NQRA	PF05896.4
contig00141-orf00035	NQRA_SLBB	PF11973.1
contig00141-orf00037	NQR2_RnfD_RnfE	PF03116.8
contig00141-orf00040	FMN_bind	PF04205.7
contig00141-orf00040	DUF2963	PF11178.1
contig00141-orf00041	Rnf-Nqr	PF02508.7
contig00141-orf00043	Rnf-Nqr	PF02508.7
contig00141-orf00043	DUF3353	PF11833.1
contig00141-orf00045	Fer2	PF00111.20
contig00141-orf00045	FAD_binding_6	PF00970.17
contig00141-orf00045	NAD_binding_1	PF00175.14

Query	Pfam Subject	Pfam ID
contig00141-orf00047	Flavoprotein	PF02441.12
contig00141-orf00047	DFP	PF04127.8
contig00141-orf00047	PALP	PF00291.18
contig00142-orf00001	Transposase_11	PF01609.14
contig00142-orf00004	NERD	PF08378.4
contig00142-orf00004	Gb3_synth	PF04572.5
contig00142-orf00006	PrmA	PF06325.6
contig00142-orf00006	Pfam-B_608	PB000608
contig00142-orf00009	CPSase_L_chain	PF00289.15
contig00142-orf00009	CPSase_L_D2	PF02786.10
contig00142-orf00009	Biotin_carb_C	PF02785.12
contig00142-orf00010	UPF0057	PF01679.10
contig00142-orf00010	Pfam-B_1679	PB001679
contig00142-orf00011	Biotin_lipoyl	PF00364.15
contig00142-orf00011	Orthopox_B11R	PF07033.4
contig00143-orf00001	DUF484	PF04340.5
contig00143-orf00001	NblA	PF04485.5
contig00143-orf00001	rve	PF00665.19
contig00145-orf00001	ADAM_spacer1	PF05986.7
contig00145-orf00004	DUF770	PF05591.5
contig00148-orf00002	Pfam-B_12716	PB012716
contig00148-orf00003	Pfam-B_12044	PB012044
contig00148-orf00005	S4	PF01479.18
contig00148-orf00005	PseudoU_synth_2	PF00849.15
contig00148-orf00007	Pfam-B_888	PB000888
contig00148-orf00007	MTS	PF05175.7
contig00148-orf00009	GatB_N	PF02934.8
contig00148-orf00009	GatB_Yqey	PF02637.11
contig00148-orf00010	DUF535	PF04393.6
contig00148-orf00012	Amidase	PF01425.14
contig00148-orf00012	Chorion_1	PF01723.9
contig00148-orf00012	DUF2081	PF09854.2
contig00148-orf00012	DUF881	PF05949.5
contig00148-orf00012	Pfam-B_10320	PB010320
contig00148-orf00014	Glu-tRNAGln	PF02686.8
contig00148-orf00016	MreB_Mbl	PF06723.6
contig00148-orf00017	DUF2392	PF10288.2
contig00148-orf00017	MreC	PF04085.7
contig00148-orf00017	YajC	PF02699.8
contig00148-orf00018	Pfam-B_1043	PB001043
contig00148-orf00018	MreD	PF04093.5
contig00148-orf00019	PBP_dimer	PF03717.8

Query	Pfam Subject	Pfam ID
contig00148-orf00019	CAMSAP_CKK	PF08683.4
contig00148-orf00019	Transpeptidase	PF00905.15
contig00148-orf00022	FTSW_RODA_SPOVE	PF01098.12
contig00148-orf00023	MarC	PF01914.10
contig00148-orf00023	DUF1772	PF08592.4
contig00148-orf00023	FA_desaturase	PF00487.17
contig00148-orf00023	Herpes_US9	PF06072.4
contig00148-orf00023	DUF2149	PF09919.2
contig00148-orf00026	Pfam-B_246	PB000246
contig00148-orf00026	Flavodoxin_1	PF00258.18
contig00148-orf00026	FAD_binding_1	PF00667.13
contig00148-orf00026	NAD_binding_1	PF00175.14
contig00148-orf00028	PGM_PMM_I	PF02878.9
contig00148-orf00028	Ribosomal_L18p	PF00861.15
contig00148-orf00028	PGM_PMM_II	PF02879.9
contig00148-orf00028	PGM_PMM_III	PF02880.9
contig00148-orf00028	PGM_PMM_IV	PF00408.13
contig00148-orf00030	Zn_peptidase	PF04228.6
contig00148-orf00030	Pfam-B_7730	PB007730
contig00148-orf00030	Zn_peptidase_2	PF04298.5
contig00148-orf00031	DUF2077	PF09850.2
contig00148-orf00031	RskA	PF10099.2
contig00148-orf00031	DUF2015	PF09435.3
contig00148-orf00034	NAD_binding_3	PF03447.9
contig00148-orf00034	Homoserine_dh	PF00742.12
contig00148-orf00034	ACT	PF01842.18
contig00148-orf00037	DUF498	PF04430.7
contig00148-orf00041	Redoxin	PF08534.3
contig00148-orf00044	Coprogen_oxidas	PF01218.11
contig00148-orf00046	SHMT	PF00464.12
contig00148-orf00050	MFS_1	PF07690.9
contig00148-orf00050	Herpes_pp38	PF04846.6
contig00148-orf00052	RuvB_N	PF05496.5
contig00148-orf00052	MgsA_C	PF12002.1
contig00148-orf00056	BCL_N	PF04714.6
contig00148-orf00060	Pfam-B_9290	PB009290
contig00148-orf00062	PALP	PF00291.18
contig00148-orf00062	Bcl-2	PF00452.12
contig00148-orf00064	CRS1_YhbY	PF01985.14
contig00148-orf00065	FtsJ	PF01728.12
contig00148-orf00067	FtsH_ext	PF06480.8
contig00148-orf00067	Pfam-B_512	PB000512

Query	Pfam Subject	Pfam ID
contig00148-orf00067	Pfam-B_14748	PB014748
contig00148-orf00067	Pfam-B_17200	PB017200
contig00148-orf00067	Pfam-B_8662	PB008662
contig00148-orf00067	AAA	PF00004.22
contig00148-orf00067	Peptidase_M41	PF01434.11
contig00148-orf00068	Pyr_redox_2	PF07992.7
contig00148-orf00068	Pyr_redox	PF00070.20
contig00148-orf00072	ALAD	PF00490.14
contig00148-orf00075	MLTD_N	PF06474.5
contig00148-orf00075	Pfam-B_6093	PB006093
contig00148-orf00077	MFS_1	PF07690.9
contig00148-orf00077	Peptidase_C30	PF05409.6
contig00148-orf00077	Pfam-B_9321	PB009321
contig00148-orf00079	DUF945	PF06097.4
contig00149-orf00001	Fer4	PF00037.20
contig00149-orf00001	Fer4	PF00037.20
contig00149-orf00002	Cons_hypoth95	PF03602.8
contig00149-orf00009	Toprim	PF01751.15
contig00149-orf00009	Topoisom_bac	PF01131.13
contig00149-orf00009	zf-C4_Topoisom	PF01396.12
contig00149-orf00009	zf-C4_Topoisom	PF01396.12
contig00149-orf00009	zf-C4_Topoisom	PF01396.12
contig00149-orf00010	DUF494	PF04361.6
contig00149-orf00010	TerB	PF05099.6
contig00149-orf00011	Pfam-B_5486	PB005486
contig00149-orf00013	DNA_processg_A	PF02481.8
contig00149-orf00013	Pfam-B_8526	PB008526
contig00149-orf00016	Response_reg	PF00072.17
contig00149-orf00016	Sigma54_activat	PF00158.19
contig00149-orf00016	HTH_8	PF02954.12
contig00149-orf00017	Pfam-B_197	PB000197
contig00149-orf00017	Pfam-B_9178	PB009178
contig00149-orf00017	Pfam-B_8352	PB008352
contig00149-orf00017	TatC	PF00902.11
contig00149-orf00017	HAMP	PF00672.18
contig00149-orf00017	DUF3149	PF11346.1
contig00149-orf00017	Pfam-B_1360	PB001360
contig00149-orf00017	Pfam-B_5968	PB005968
contig00149-orf00017	Pfam-B_4592	PB004592
contig00149-orf00017	PAS_4	PF08448.3
contig00149-orf00017	HisKA	PF00512.18
contig00149-orf00017	HATPase_c	PF02518.19

Query	Pfam Subject	Pfam ID
contig00149-orf00018	Pfam-B_687	PB000687
contig00149-orf00019	NusB	PF01029.11
contig00149-orf00019	Tenui_NS3	PF05310.5
contig00149-orf00019	Nol1_Nop2_Fmu	PF01189.10
contig00149-orf00022	PepSY	PF03413.12
contig00149-orf00023	Macro	PF01661.14
contig00149-orf00025	Formyl_trans_N	PF00551.12
contig00149-orf00025	Formyl_trans_C	PF02911.11
contig00149-orf00028	Pep_deformylase	PF01327.14
contig00149-orf00029	LysM	PF01476.13
contig00149-orf00029	Pfam-B_2096	PB002096
contig00149-orf00029	Pfam-B_2096	PB002096
contig00149-orf00033	Epimerase	PF01370.14
contig00149-orf00035	Radical_SAM	PF04055.14
contig00149-orf00035	Vps39_1	PF10366.2
contig00149-orf00035	DUF1008	PF06228.6
contig00149-orf00036	TonB_dep_Rec	PF00593.17
contig00149-orf00037	PPK2	PF03976.7
contig00149-orf00038	Chorismate_bind	PF00425.11
contig00149-orf00038	Chorismate_bind	PF00425.11
contig00149-orf00038	Aminotran_4	PF01063.12
contig00149-orf00040	DUF389	PF04087.7
contig00149-orf00040	ABC_cobalt	PF09819.2
contig00149-orf00040	DUF3460	PF11943.1
contig00149-orf00041	Ribosomal_L50	PF10501.2
contig00149-orf00041	PP-binding	PF00550.18
contig00149-orf00041	HLH	PF00010.19
contig00149-orf00042	ketoacyl-synt	PF00109.19
contig00149-orf00042	Ketoacyl-synt_C	PF02801.15
contig00149-orf00046	FtsX	PF02687.14
contig00149-orf00047	NESP55	PF06390.5
contig00149-orf00050	PK	PF00224.14
contig00149-orf00050	PK_C	PF02887.9
contig00149-orf00051	Pribosyltran	PF00156.20
contig00149-orf00052	EIIA-man	PF03610.9
contig00149-orf00054	PTS-HPr	PF00381.12
contig00149-orf00054	Med20	PF08612.4
contig00149-orf00056	PEP-utilisers_N	PF05524.6
contig00149-orf00056	PEP-utilizers	PF00391.16
contig00149-orf00056	PEP-utilizers_C	PF02896.11
contig00149-orf00061	DEAD	PF00270.22
contig00149-orf00061	Helicase_C	PF00271.24

Query	Pfam Subject	Pfam ID
contig00149-orf00061	HA2	PF04408.16
contig00149-orf00061	DUF1605	PF07717.9
contig00149-orf00061	DUF3418	PF11898.1
contig00151-orf00003	MS_channel	PF00924.11
contig00151-orf00004	NUDIX	PF00293.21
contig00151-orf00007	Pyrophosphatase	PF00719.12
contig00151-orf00009	Exonuc_X-T	PF00929.17
contig00151-orf00009	EIIA-man	PF03610.9
contig00151-orf00010	Hydrolase_3	PF08282.5
contig00151-orf00012	Phos_pyr_kin	PF08543.5
contig00151-orf00015	PfkB	PF00294.17
contig00151-orf00016	Ala_racemase_N	PF01168.13
contig00151-orf00016	Ala_racemase_C	PF00842.14
contig00151-orf00018	ACT	PF01842.18
contig00151-orf00020	DUF711	PF05167.5
contig00151-orf00020	Sigma54_activat	PF00158.19
contig00151-orf00023	OsmC	PF02566.12
contig00151-orf00023	DUF983	PF06170.5
contig00151-orf00026	GntR	PF00392.14
contig00151-orf00026	Phage_NinH	PF06322.4
contig00151-orf00026	FCD	PF07729.5
contig00151-orf00028	tRNA_U5-meth_tr	PF05958.4
contig00151-orf00030	TauE	PF01925.12
contig00151-orf00032	Chorismate_synt	PF01264.14
contig00151-orf00036	ProQ	PF04352.6
contig00151-orf00041	Pfam-B_9305	PB009305
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	Pfam-B_639	PB000639
contig00151-orf00041	Pfam-B_12469	PB012469
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_639	PB000639
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	HCBP_related	PF06594.4
contig00151-orf00041	Pfam-B_9305	PB009305
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	Pfam-B_639	PB000639
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	Pfam-B_639	PB000639

Query	Pfam Subject	Pfam ID
contig00151-orf00041	Pfam-B_9305	PB009305
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_639	PB000639
contig00151-orf00041	Pfam-B_9305	PB009305
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	Pfam-B_12469	PB012469
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_639	PB000639
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_12469	PB012469
contig00151-orf00041	Pfam-B_9305	PB009305
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	Pfam-B_7705	PB007705
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	HemolysinCabind	PF00353.12
contig00151-orf00041	HCBP_related	PF06594.4
contig00151-orf00041	HCBP_related	PF06594.4
contig00151-orf00042	LPAM_1	PF08139.5
contig00151-orf00042	NosL	PF05573.5
contig00151-orf00043	Pfam-B_130	PB000130
contig00151-orf00043	Pfam-B_52	PB000052
contig00151-orf00043	Pox_P21	PF05313.5
contig00151-orf00044	Pfam-B_3932	PB003932
contig00151-orf00044	ABC_tran	PF00005.20
contig00151-orf00044	Pfam-B_2260	PB002260
contig00151-orf00046	Pfam-B_331	PB000331
contig00151-orf00046	NosD	PF05048.6
contig00151-orf00050	Pfam-B_14125	PB014125
contig00151-orf00050	COX2	PF00116.13
contig00151-orf00053	FMN_bind	PF04205.7
contig00151-orf00054	FYDLN_acid	PF09538.3
contig00151-orf00054	UPF0547	PF10571.2
contig00151-orf00054	DUF2296	PF10058.2
contig00151-orf00054	Carboxyl_trans	PF01039.15
contig00151-orf00057	Trp_syntA	PF00290.13
contig00151-orf00059	DUF808	PF05661.5
contig00151-orf00059	TerC	PF03741.9
contig00151-orf00060	CN_hydrolase	PF00795.15
contig00151-orf00060	TruB_C	PF09142.4
contig00151-orf00061	Sigma70_r1_2	PF00140.13
contig00151-orf00061	Sigma70_r2	PF04542.7

Query	Pfam Subject	Pfam ID
contig00151-orf00061	UCR_14kD	PF02271.9
contig00151-orf00061	Ham1p_like	PF01725.9
contig00151-orf00061	Sigma70_r4	PF04545.9
contig00151-orf00063	YqeY	PF09424.3
contig00151-orf00063	DUF2009	PF09418.3
contig00151-orf00063	Glucokinase	PF02685.9
contig00151-orf00064	Ribosomal_S21	PF01165.13
contig00151-orf00065	Glutaredoxin	PF00462.17
contig00151-orf00066	Pribosyltran	PF00156.20
contig00151-orf00066	BAAT_C	PF08840.4
contig00151-orf00068	DUF2322	PF10084.2
contig00152-orf00003	CDP-OH_P_transf	PF01066.14
contig00152-orf00005	Pfam-B_1759	PB001759
contig00152-orf00006	FixH	PF05751.4
contig00152-orf00008	Fer4	PF00037.20
contig00152-orf00008	Fer4	PF00037.20
contig00152-orf00008	Bre5	PF11614.1
contig00152-orf00010	Neur_chan_memb	PF02932.9
contig00152-orf00014	Transketolase_N	PF00456.14
contig00152-orf00014	BMC	PF00936.12
contig00152-orf00014	Transket_pyr	PF02779.17
contig00152-orf00014	Transketolase_C	PF02780.13
contig00152-orf00018	Pfam-B_1978	PB001978
contig00152-orf00018	Sulfatase	PF00884.16
contig00152-orf00021	DUF328	PF03883.7
contig00152-orf00022	Transposase_14	PF01710.9
contig00154-orf00002	Pfam-B_19018	PB019018
contig00154-orf00002	Pfam-B_19505	PB019505
contig00154-orf00002	Pfam-B_4382	PB004382
contig00154-orf00002	HIM	PF05662.7
contig00154-orf00002	YadA	PF03895.8
contig00154-orf00002	lci	PF12197.1
contig00155-orf00001	N_methyl	PF07963.5
contig00155-orf00001	Pilin	PF00114.12
contig00156-orf00001	Rota_NS53	PF00981.10
contig00156-orf00001	DDE	PF03184.12
contig00157-orf00001	DUF746	PF05344.4
contig00157-orf00001	DUF2972	PF11186.1
contig00157-orf00001	HTH_11	PF08279.5
contig00157-orf00001	rve	PF00665.19
contig00158-orf00001	AhpC-TSA	PF00578.14
contig00161-orf00001	SpoU_sub_bind	PF08032.5

Query	Pfam Subject	Pfam ID
contig00161-orf00001	SpoU_methylase	PF00588.12
contig00161-orf00003	AzlD	PF05437.5
contig00161-orf00004	AzlC	PF03591.7
contig00161-orf00005	DHDPS	PF00701.15
contig00161-orf00006	Pfam-B_1260	PB001260
contig00161-orf00006	Lipoprotein_18	PF06804.4
contig00161-orf00006	Lipoprotein_18	PF06804.4
contig00161-orf00008	Pfam-B_15386	PB015386
contig00161-orf00008	NikM	PF10670.2
contig00161-orf00008	Xol-1_N	PF09108.3
contig00161-orf00010	PseudoU_synth_2	PF00849.15
contig00162-orf00001	Ldh_1_N	PF00056.16
contig00162-orf00001	Ldh_1_C	PF02866.11
contig00162-orf00004	Rz1	PF06085.4
contig00162-orf00004	Baculo_p74	PF04583.5
contig00162-orf00004	Lipoprot_C	PF08794.3
contig00162-orf00004	Pfam-B_9648	PB009648
contig00162-orf00006	DUF1853	PF08907.4
contig00162-orf00007	SpoU_methylase	PF00588.12
contig00162-orf00007	SpoU_methylase	PF00588.12
contig00162-orf00008	Inositol_P	PF00459.18
contig00162-orf00008	ATP-synt_E_2	PF08112.4
contig00162-orf00010	OEP	PF02321.11
contig00162-orf00010	OEP	PF02321.11
contig00162-orf00011	ABC_membrane	PF00664.16
contig00162-orf00011	Pex24p	PF06398.4
contig00162-orf00011	ABC_tran	PF00005.20
contig00162-orf00012	FixQ	PF05545.4
contig00162-orf00012	HlyD	PF00529.13
contig00162-orf00012	DMPK_coil	PF08826.3
contig00162-orf00012	CBP4	PF07960.4
contig00162-orf00012	HlyD	PF00529.13
contig00162-orf00014	Pfam-B_11265	PB011265
contig00162-orf00014	GTP_EFTU	PF00009.20
contig00162-orf00014	DUF2450	PF10475.2
contig00162-orf00014	GTP_EFTU_D2	PF03144.18
contig00162-orf00020	MFS_1	PF07690.9
contig00162-orf00020	Toxin_18	PF08087.4
contig00162-orf00020	YfhO	PF09586.3
contig00162-orf00021	Pfam-B_4888	PB004888
contig00162-orf00022	Plug	PF07715.8
contig00162-orf00022	TonB_dep_Rec	PF00593.17

Query	Pfam Subject	Pfam ID
contig00162-orf00024	TetR_N	PF00440.16
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	Pfam-B_9305	PB009305
contig00162-orf00029	Pfam-B_639	PB000639
contig00162-orf00029	Pfam-B_12469	PB012469
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_639	PB000639
contig00162-orf00029	Pfam-B_9305	PB009305
contig00162-orf00029	Pfam-B_12469	PB012469
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	Pfam-B_9305	PB009305
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_639	PB000639
contig00162-orf00029	Pfam-B_12469	PB012469
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	Pfam-B_9305	PB009305
contig00162-orf00029	Pfam-B_639	PB000639
contig00162-orf00029	Pfam-B_12469	PB012469
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_639	PB000639
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_9305	PB009305
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00029	Pfam-B_7705	PB007705
contig00162-orf00029	HemolysinCabind	PF00353.12
contig00162-orf00032	Aldedh	PF00171.15
contig00162-orf00032	Aldedh	PF00171.15
contig00162-orf00037	Glyco_transf_9	PF01075.10
contig00162-orf00038	CSD	PF00313.15
contig00162-orf00038	CcmH	PF03918.7
contig00162-orf00038	PAP_PilO	PF06864.5
contig00162-orf00038	DUF2133	PF09976.2
contig00162-orf00038	Excalibur	PF05901.4
contig00162-orf00040	DAO	PF01266.17
contig00162-orf00041	NAD_kinase	PF01513.14

Query	Pfam Subject	Pfam ID
contig00162-orf00041	Pfam-B_3317	PB003317
contig00162-orf00042	Pfam-B_3934	PB003934
contig00162-orf00042	SCP2	PF02036.10
contig00162-orf00042	Syntaxin	PF00804.18
contig00162-orf00042	TSC22	PF01166.11
contig00162-orf00042	Pox_A_type_inc	PF04508.5
contig00162-orf00043	Epimerase	PF01370.14
contig00162-orf00046	Lactamase_B	PF00753.20
contig00162-orf00048	Pfam-B_8457	PB008457
contig00162-orf00048	N_methyl	PF07963.5
contig00162-orf00049	DUF2133	PF09976.2
contig00162-orf00049	Pfam-B_8630	PB008630
contig00162-orf00049	HlyD	PF00529.13
contig00162-orf00049	TPR_MLP1_2	PF07926.5
contig00162-orf00049	Spc7	PF08317.4
contig00162-orf00049	Halogen_Hydrol	PF10112.2
contig00162-orf00049	SAB	PF04382.6
contig00162-orf00049	Cpn10	PF00166.14
contig00162-orf00052	Pfam-B_5069	PB005069
contig00162-orf00052	Pfam-B_6541	PB006541
contig00162-orf00052	ABC_tran	PF00005.20
contig00162-orf00052	Pfam-B_817	PB000817
contig00162-orf00052	Pfam-B_6897	PB006897
contig00162-orf00052	Pfam-B_16503	PB016503
contig00162-orf00052	Pfam-B_759	PB000759
contig00162-orf00052	Pfam-B_19199	PB019199
contig00162-orf00052	FtsX	PF02687.14
contig00162-orf00054	GST_N	PF02798.13
contig00162-orf00054	GST_C	PF00043.18
contig00167-orf00001	Pfam-B_4425	PB004425
contig00167-orf00001	dNK	PF01712.12
contig00167-orf00004	HPPK	PF01288.13
contig00167-orf00005	SirB	PF04247.5
contig00167-orf00005	DUF1516	PF07457.4
contig00167-orf00007	rRNA_methylase	PF06962.5
contig00167-orf00009	DUF3202	PF11451.1
contig00167-orf00009	LSM	PF01423.15
contig00167-orf00013	Pfam-B_229	PB000229
contig00167-orf00013	MMR_HSR1	PF01926.16
contig00167-orf00013	Pfam-B_229	PB000229
contig00167-orf00013	MMR_HSR1	PF01926.16
contig00167-orf00015	DUF2133	PF09976.2

Query	Pfam Subject	Pfam ID
contig00167-orf00015	MitoNEET_N	PF10660.2
contig00167-orf00015	YgbB	PF02542.9
contig00167-orf00015	Pfam-B_2269	PB002269
contig00167-orf00015	TPR_1	PF00515.21
contig00167-orf00015	TPR_2	PF07719.10
contig00167-orf00016	tRNA-synt_2b	PF00587.18
contig00167-orf00016	HGTP_anticodon	PF03129.13
contig00167-orf00019	PseudoU_synth_2	PF00849.15
contig00167-orf00021	PLDc	PF00614.15
contig00167-orf00021	PLDc	PF00614.15
contig00167-orf00024	URO-D	PF01208.10
contig00167-orf00026	HemY_N	PF07219.6
contig00167-orf00027	HemX	PF04375.7
contig00167-orf00027	Pfam-B_3907	PB003907
contig00167-orf00028	HEM4	PF02602.8
contig00167-orf00029	Pfam-B_200	PB000200
contig00167-orf00029	DUF1212	PF06738.5
contig00167-orf00032	DnaJ	PF00226.24
contig00167-orf00032	DnaJ_C	PF01556.11
contig00167-orf00032	DnaJ_C	PF01556.11
contig00167-orf00033	YibE_F	PF07907.4
contig00167-orf00035	CorA	PF01544.11
contig00167-orf00035	Pfam-B_380	PB000380
contig00167-orf00035	DUF1516	PF07457.4
contig00167-orf00036	CorA	PF01544.11
contig00167-orf00036	Cyt_c_ox_IV	PF12270.1
contig00167-orf00036	DUF1516	PF07457.4
contig00167-orf00036	PMP22_Claudin	PF00822.13
contig00167-orf00036	Adeno_E3B	PF03376.7
contig00167-orf00036	UPF0093	PF03653.6
contig00167-orf00036	SDF	PF00375.11
contig00167-orf00036	Tetraspannin	PF00335.13
contig00167-orf00036	Sre	PF03125.11
contig00167-orf00036	UPF0104	PF03706.6
contig00167-orf00036	DcuC	PF03606.8
contig00167-orf00038	4HBT	PF03061.15
contig00167-orf00041	Transposase_17	PF01797.9
contig00168-orf00001	DUF484	PF04340.5
contig00168-orf00001	NblA	PF04485.5
contig00168-orf00001	rve	PF00665.19
contig00169-orf00001	A_thal_3526	PF09713.3
contig00169-orf00001	DUF484	PF04340.5

Query	Pfam Subject	Pfam ID
contig00169-orf00001	NblA	PF04485.5

Appendix F

ROI Identified in bioinformatic screen.

The ROI identified in the bioinformatic screen are shown. The length of the identified ORFs is displayed as a yellow bar. Identified Pfam domains in the ORF are shown as the grey bars above the yellow ORF. The ORF was aligned with its closet BLAST match. Identical sequence is shown below the yellow bar as black bars. The top set of black bars represent the identified ORF and the lower black bars represent the BLAST match. The text alignment between the ORF and its BLAST match is shown either directly below the ROI figure or on the next page.

Contig 94-21

>Protein alignment 1636 Alignment of 2 sequences: Contig 94-21, thymidylyltrans
ferase

Identities = 260/289 (89%), Positives = 277/289 (95%), Gaps = 1/289 (0%)

```
Contig 94-21              1 MKGIILAGGSGTRLYPITRGVSKQLLPVYDKPMIYYPLSVLMLAGIREILVITTPEDNPS
                            MKGIILAGGSGTRLYPITRGVSKQLLPVYDKPMIYYPLSVLMLAGIR+ILVIT PEDN S
thymidylyltransferase     1 MKGIILAGGSGTRLYPITRGVSKQLLPVYDKPMIYYPLSVLMLAGIRDILVITAPEDNAS

Contig 94-21             61 FRRLLGDGSDFGISISYAEQPSPDGLAQAFIIGEEFIGNDNVCLVLGDNIFYGQSFTQTL
                            F+RLLGDGSDFGISISYA QPSPDGLAQAFIIGEEFIGNDNVCLVLGDNIFYGQSFTQTL
thymidylyltransferase    61 FKRLLGDGSDFGISISYAVQPSPDGLAQAFIIGEEFIGNDNVCLVLGDNIFYGQSFTQTL

Contig 94-21            121 KQAASKKHGATVFGYQVKDPERFGVVEFDEKFNALSIEEKPKQPKSDWAVTGLYFYDNRV
                            KQAA++ HGATVF YQVK+PERFGVVEF+E F A+SIEEKP++PKSDWAVTGLYFYDNR
thymidylyltransferase   121 KQAAAQTHGATVFAYQVKNPERFGVVEFNENFRAVSIEEKPQRPKSDWAVTGLYFYDNRA

Contig 94-21            181 VEFAKQVKPSARGELEISTLNQMYLDDGSLSVQLLGRGFAWLDTGTHESLHEAASFVQTV
                            VEFAKQ+KPSARGELEI+ LN+MYL+DGSLSVQ+LGRGFAWLDTGTHESLHEAASFVQTV
thymidylyltransferase   181 VEFAKQLKPSARGELEITDLNRMYLEDGSLSVQILGRGFAWLDTGTHESLHEAASFVQTV

Contig 94-21            241 QNIQDLQVACLEEIAWRNGWLSDERLEELARPMAKNQYGQYLLHLLKK* 289
                            QNIQ+L +ACLEEIAWRNGWLSDE+LEELARPMAKNQYGQYLL LLKK
thymidylyltransferase   241 QNIQNLHIACLEEIAWRNGWLSDEKLEELARPMAKNQYGQYLLRLLKK- 288
```

Contig 94-20

>Protein alignment 1637 Alignment of 2 sequences: Contig 94-20, glucose dehydra
tase

Identities = 331/356 (92%), Positives = 344/356 (96%), Gaps = 1/356 (0%)

```
Contig 94-20              1 MKKILVTGGAGFIGSAVIRHIIQNTQDSVINLDKLTYAGNLESLTDVADSPRYALEQVDI
                            M+KILVTGGAGFIGSAV+RHII+NT+D+V+N+DKLTYAGNLESLT+VAD+PRYA EQVDI
glucose dehydratase       1 MRKILVTGGAGFIGSAVVRHIIRNTRDAVVNVDKLTYAGNLESLTEVADNPRYAFEQVDI

Contig 94-20             61 CDRAELDRVFAQHRPDAVMHLAAESHVDRSIDSAGEFIQTNIVGTFNLLEAARAYWQQMS
                            CDRAELDRVFAQ+RPDAVMHLAAESHVDRSI SAGEFIQTNIVGTFNLLEAARAYWQQM
glucose dehydratase      61 CDRAELDRVFAQYRPDAVMHLAAESHVDRSIGSAGEFIQTNIVGTFNLLEAARAYWQQMP

Contig 94-20            121 SEKREAFRFHHISTDEVYGDLHGTDDLFTETTPYAPSSPYSASKASSDHLVRAWLRTYGL
                            SE+ EAFRFHHISTDEVYGDL GTDDLFTET PYAPSSPYSASKASSDHLVRAWLRTYGL
glucose dehydratase      121 SEQHEAFRFHHISTDEVYGDLGGTDDLFTETAPYAPSSPYSASKASSDHLVRAWLRTYGL

Contig 94-20            181 PTIVTNCSNNYGPYHFPEKLIPLMILNALDGKPLPVYGDGMQIRDWLFVEDHARALYQVV
                            PTIVTNCSNNYGPYHFPEKLIPLMILNALDGKPLPVYGDGMQIRDWLFVEDHARALYQVV
glucose dehydratase      181 PTIVTNCSNNYGPYHFPEKLIPLMILNALDGKPLPVYGDGMQIRDWLFVEDHARALYQVV

Contig 94-20            241 TEGVVGETYNIGGHNEKANIEVVKTICALLEELVPEKPAGVARYEDLITFVQDRPGHDVR
                            TEGVVGETYNIGGHNEKANIEVVKTICALLEEL PEKPAGVARYEDLITFVQDRPGHDVR
glucose dehydratase      241 TEGVVGETYNIGGHNEKANIEVVKTICALLEELAPEKPAGVARYEDLITFVQDRPGHDVR

Contig 94-20            301 YAIDAAKIGRGLGWKPQETFESGIRKTVQWYLDNKTWWQNVLNGSYRLERLGTGK* 356
                            YA+DAAKI R LGW P ETFESG+RKTVQWYLDNKTWWQNVLNGSYRLERLGTGK
glucose dehydratase      301 YAVDAAKIRRDLGWLPLETFESGLRKTVQWYLDNKTWWQNVLNGSYRLERLGTGK- 355
```

Contig 23-13

>Protein alignment 1638 Alignment of 2 sequences: Contig 23-13, epimerase

Identities = 167/185 (90%), Positives = 173/185 (93%), Gaps = 6/185 (3%)

```
Contig 23-13      1 -----MKIIDTTLPDVKLLEPQVFGDARGFFMETFRDEWFKANVCDRTFVQENHSKSDKG
                        M IIDT +PDVKLLEPQVFGDARGFFMETFRDEWFK  VC+RTFVQENHSKS KG
epimerase         1 MKDKKMNIIDTAIPDVKLLEPQVFGDARGFFMETFRDEWFKTQVCERTFVQENHSKSGKG

Contig 23-13     56 VLRGLHYQTKNTQGKLVRVVVGEVFDVAVDMRKDSPTFGKWAGEILSAENKRQLWVPEGP
                    VLRGLHYQT+NTQGKLVRVVVGEVFDVAVDMRKDSPTFGKW GEILSAENKRQLWVPEGP
epimerase        61 VLRGLHYQTENTQGKLVRVVVGEVFDVAVDMRKDSPTFGKWVGEILSAENKRQLWVPEGP

Contig 23-13    116 AHGFYVLSDEAEFVYKCTDYYNPKAEHSLIWNDPTVGIEWPLQGEPNLSPKDLAGKILAE
                    AHGFYVLSDEAEFVYKCTDYYNPKAEHSLIWNDPTVGI+WPLQGEPNLSPKDLAGK+L+E
epimerase       121 AHGFYVLSDEAEFVYKCTDYYNPKAEHSLIWNDPTVGIDWPLQGEPNLSPKDLAGKVLSE

Contig 23-13    176 AVTF* 180
                    AVTF
epimerase       181 AVTF- 184
```

Contig 20-7

>Protein alignment 1639 Alignment of 2 sequences: Contig 20-7, rhamnose synthas
e

Identities = 200/306 (65%), Positives = 241/306 (78%), Gaps = 18/306 (5%)

```
Contig 20-7            1 MRTLLTGSKGQLAHCFRDRLPDNWELIATDSSSLDITDADAVRNMVQNFQPDAIVNTAAY
                         MR LLTGSK QLA C RDRLP++WE IATDS+SLDITDADAV NMV++FQPDAIVNTAAY
rhamnose synthase      1 MRILLTGSKSQLARCLRDRLPEDWETIATDSASLDITDADAVCNMVKSFQPDAIVNTAAY

Contig 20-7           61 TAVDRAETNVPAAFAVNAAAVHNLADAARSVHARFIHISTDYVFDGTSKTPYREHDYTNP
                         TAVD+AE +  AAFAVNA+AV+NLA AA   HARFIHISTDYVFDG  K PY+E D+TNP
rhamnose synthase     61 TAVDKAEGDAAAAFAVNASAVYNLALAAHRAHARFIHISTDYVFDGKGKRPYQESDFTNP

Contig 20-7          121 QSVYGRTKAAGELLALAANPESTIIRTSWLFSEYGNNFVKTMLRLAKERDTLSVVNDQIG
                          +VYG++K AGELLAL+ANP+S I+RTSWLFSEYG+NF++TML LA+ER  LS V++QIG
rhamnose synthase     121 SNVYGQSKTAGELLALSANPDSLILRTSWLFSEYGDNFIRTMLNLARERSPLSAVHNQIG

Contig 20-7          181 CPTYAGDLAQAIITLLQHPSPSRGIYHFGGNKSVTWYEFSQAIFQTALKHDNNFNMPKLT
                         CPTYAGDL+  II LLQH +P RGIYH+ G+KSV+WYEF+Q IFQ A +   +F +P+LT
rhamnose synthase     181 CPTYAGDLSATIIRLLQHSNPVRGIYHYAGSKSVSWYEFAQHIFQAASQQQTSFPVPELT

Contig 20-7           241 PITTDQYPLPAPRPAYSIMDCRKIENDYGIKPSDWQKALN---------------DIIGK
                          ++  +YP  APRPAYSI+DCRKIEND+GIKPSDWQKAL+                + +
rhamnose synthase     241 AVSDKEYPTAAPRPAYSILDCRKIENDFGIKPSDWQKALHRSFPSCSDAARPSVSAVKHR

Contig 20-7           286 LD*--- 288
                          L
rhamnose synthase     301 LGGFLI 306
```

Contig 45-6

>Protein alignment 1253 Alignment of 2 sequences: Contig 45-6, Heptosyltransfer
ase I

Identities = 297/323 (91%), Positives = 309/323 (95%), Gaps = 1/323 (0%)

```
Contig 45-6                1 MKILLVRLSSMGDLIHTLPAIEDLARQCPDVELHWLCEAGFADIARLHPFVKKIHVIKWR
                             MKILLVRLSSMGDLIHTLPAIEDLARQCPDVELHWLCEAGFADIARLHPFVKKIHV+KWR
Heptosyltransferase I      1 MKILLVRLSSMGDLIHTLPAIEDLARQCPDVELHWLCEAGFADIARLHPFVKKIHVMKWR

Contig 45-6               61 QWRKHLFQAETWQEIGRLKQALRQEAFDFVLDSQGLIKSACFAKMAKSPIYGLDKHSARE
                             QWRKHLF+AETW+E+G LKQ LRQE FDFVLDSQGLIKSACFAKMAKSPI GLDK+SARE
Heptosyltransferase I     61 QWRKHLFRAETWREMGHLKQTLRQEVFDFVLDSQGLIKSACFAKMAKSPICGLDKNSARE

Contig 45-6              121 GLAALAYAKTYAVPKGKNAVWRNRELFAQVFGYAMPETQVFGMTVPEAGGLKNLEQPYYA
                             G AALAY KTYAVPKGKNAVWRNRELFAQVFGY MPETQVFG+TVPEAG LKNL QPYYA
Heptosyltransferase I    121 GWAALAYVKTYAVPKGKNAVWRNRELFAQVFGYVMPETQVFGLTVPEAGRLKNLAQPYYA

Contig 45-6              181 ALHATSRDSKLWSVENWRALLQKLNEEQQCNVYLPWGNETEKTRAEQIADGLPFAIVCDK
                             ALHATSRDSKLW VENWR+LLQKLNEEQQCN+YLPWGNE EKTRA+QIADGLPFAIVCDK
Heptosyltransferase I    181 ALHATSRDSKLWPVENWRSLLQKLNEEQQCNIYLPWGNEDEKTRAKQIADGLPFAIVCDK

Contig 45-6              241 MNLLQAAYLLKHAVGIVGVDTGLLHLANALEKPVVGIYTDTDPIKTGVQVSAVAKNLGNI
                             +NLLQAAYLLK+AVGIVGVDTGLLHLANALEKPVVGIYTDTDPIKTGVQVS +AKNLGNI
Heptosyltransferase I    241 INLLQAAYLLKYAVGIVGVDTGLLHLANALEKPVVGIYTDTDPIKTGVQVSPIAKNLGNI

Contig 45-6              301 GQIPTADLVYQTLMDCVAADKG* 323
                             GQIPTADLVYQ LMDCVAADKG
Heptosyltransferase I    301 GQIPTADLVYQALMDCVAADKG- 322
```

Contig 162-37

>Protein alignment 1251 Alignment of 2 sequences: Contig 162-37, Heptosyltransf
erase II

Identities = 261/341 (76%), Positives = 294/341 (86%), Gaps = 5/341 (1%)

```
Contig 162-37              1 MSKKILIITPSWIGDCVMTQPLYRRLHELHPGCTIDAFAPKWSMAVFERMPEISRVIENP
                             MS KILII+PSWIGDCVMTQPL+RRL ELHPGCTID FAPKWSMAVFERMPE++ ++EN
Heptosyltransferase II     1 MSIKILIISPSWIGDCVMTQPLFRRLKELHPGCTIDVFAPKWSMAVFERMPEVNEILENS

Contig 162-37             61 FGHGALELKKRWRIGRELGKQGYDQVIVLPGSLKSALIAFATGIKQRTGYVGESRYLLLN
                             FGHGALELK+RWR+GR+LG++GYDQVIVLPGSLKSA+IA ATGI +RTGYVGESRY LLN
Heptosyltransferase II     61 FGHGALELKRRWRVGRDLGRRGYDQVIVLPGSLKSAIIALATGIGKRTGYVGESRYFLLN

Contig 162-37            121 DIRKLDKAALPLMVDRYTALAHPTQADFNGHSDNPHFTISPESRAAALAKYGLDTDKPVL
                             DIR+LDK  LPLMVDRYTALAHP+Q DF+GHS  P F+I    R  ++  +GLD  KPVL
Heptosyltransferase II    121 DIRRLDKERLPLMVDRYTALAHPSQEDFDGHSGFPEFSIDERRREISVETPGLDIGKPVL

Contig 162-37             181 AFCPGAEYGPAKRWPARHFAELGRRYLAEGWQVWLFGSQKDFDIAEEINRLSDNLCTNLC
                             AFCPGAE+GPAKRWP RHFAELG+ YLA GWQVWLFGSQKD +IAEEINRLSD +C NLC
Heptosyltransferase II    181 AFCPGAEFGPAKRWPTRHFAELGKHYLAAGWQVWLFGSQKDDEIAEEINRLSDGMCVNLC

Contig 162-37             241 GKTNLSEAIDLLSCTDTVVCNDSGLMHLAAALDRKLVAAYGSSSPDHTPPLSQKAKIVSL
                             GKT+LS+A+DLLS  DTVVCNDSGLMHLAAAL RK+VA YGSSSP HTPPLS +AKIVSL
Heptosyltransferase II    241 GKTDLSQAMDLLSLADTVVCNDSGLMHLAAALGRKVVAVYGSSSPTHTPPLSDRAKIVSL

Contig 162-37             301 HLECSPCFKRECPLGHTDCLNKLTPDMVQKAAEELAETES* 341
                             HLECSPCFKRECPLGHTDCLN+L P+ + +A EE
Heptosyltransferase II    301 HLECSPCFKRECPLGHTDCLNRLYPEKIVQAVEEAV----- 336
```

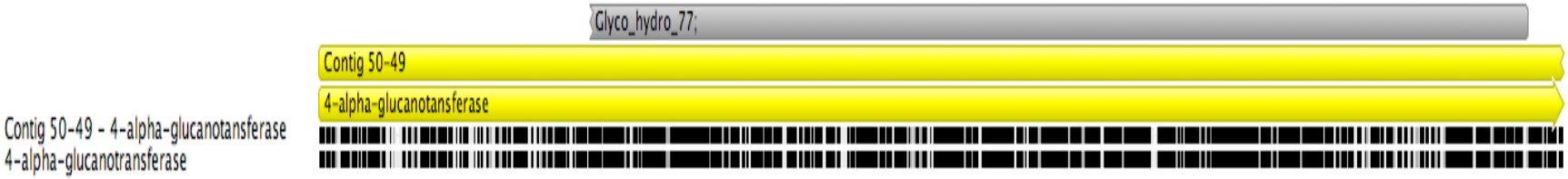
Contig 124-31

>Protein alignment 1252 Alignment of 2 sequences: Contig 124-31, Heptosyltransf
erase III

Identities = 161/372 (43%), Positives = 219/372 (58%), Gaps = 22/372 (5%)

```
Contig 124-31               1 -----MSLAQP---KRILVIKLRHHGDVLLATPVVHALKTRFPDCEIDMLVYRETADIIS
                                    +LA     +RIL++KLRHHGD+LL TPV+++L+  +P  +ID+L+Y+ET D+++
Heptosyltransferase III     1 MMNDAPALAPDTSIQRILIVKLRHHGDMLLVTPVINSLQQNYPQAQIDVLLYKETQDMLT

Contig 124-31              53 DNPEIAEIFTIDRSWKKQGLKTQLSEEKKLFSRLKKRGYDWAFNLSDQWRSAILAKFC-A
                               +P ++ +F IDR WKKQG K  L  E  L  +LK + YD   NL+DQWRSAI+A+   A
Heptosyltransferase III    61 SHPALSNVFVIDRQWKKQGTKAHLRHELNLIRQLKGQRYDLVVNLADQWRSAIIARLTGA

Contig 124-31             112 QCSVGISHIKRDHFFWRWCHDFLNPEAGRG-CHITEYHMNVLPPLIRPEETQPAKVMMPI
                              +  +G    KR  F WR CH  L P +     H  E ++++L PL  P  T   +V M
Heptosyltransferase III   121 RIRLGFDFPKRRGFLWRHCHTHLVPVSDHARLHTVEQNLSLLRPLGLP--TLSQQVTMSY

Contig 124-31             171 GEDARSNLQSKLKKQGWNGEDYVLFHPGARWEFKCWEDGKNAAIVQLLLNHGQNVVLTAA
                                      +  L++QG  G DY++  P +RW FKCW + K AA V  L   G  +V+T+
Heptosyltransferase III   179 PPQDWQTCEQLLRQQGITG-DYIVVQPTSRWFFKCWSEEKMAATVSALQADGHRLVITSG

Contig 124-31             231 PSATEQQMVDAVLERVKIPEGGKLWILSGNLNLRELAAAIDGCKLFIGVDSAPMHIAAAL
                              P   E++MV+ +L     P+G  +  L+G L LR+LAA ID  KLFIGVDS PMH+AAAL
Heptosyltransferase III   238 PDTKEREMVERILALCP-PQG--VVSLAGQLTLRQLAALIDHAKLFIGVDSVPMHMAAAL

Contig 124-31             291 DKPQIALFGPSWLDRWHPYSDNAEVIWAGDFGDLPHPDSINTSDNTRLLKAIPLEAVWNK
                                P IALFGPS L  W P+  N  VIWAGDFG LP PD+INT  + R L  IP +AV
Heptosyltransferase III   295 QTPCIALFGPSKLVFWRPWQVNGCVIWAGDFGTLPDPDAINTGTDERYLDLIPTDAVIAA

Contig 124-31             351 IAEKLGLNKEA* 362
                                +L
Heptosyltransferase III   355 ARSRLA------ 360
```

Contig 50-49A



Contig 50-49A

>Protein alignment 1260 Alignment of 2 sequences: Contig 50-49 - 4-alpha-glucan
otansferase, 4-alpha-glucanotransferase

Identities = 522/692 (75%), Positives = 597/692 (86%), Gaps = 2/692 (0%)

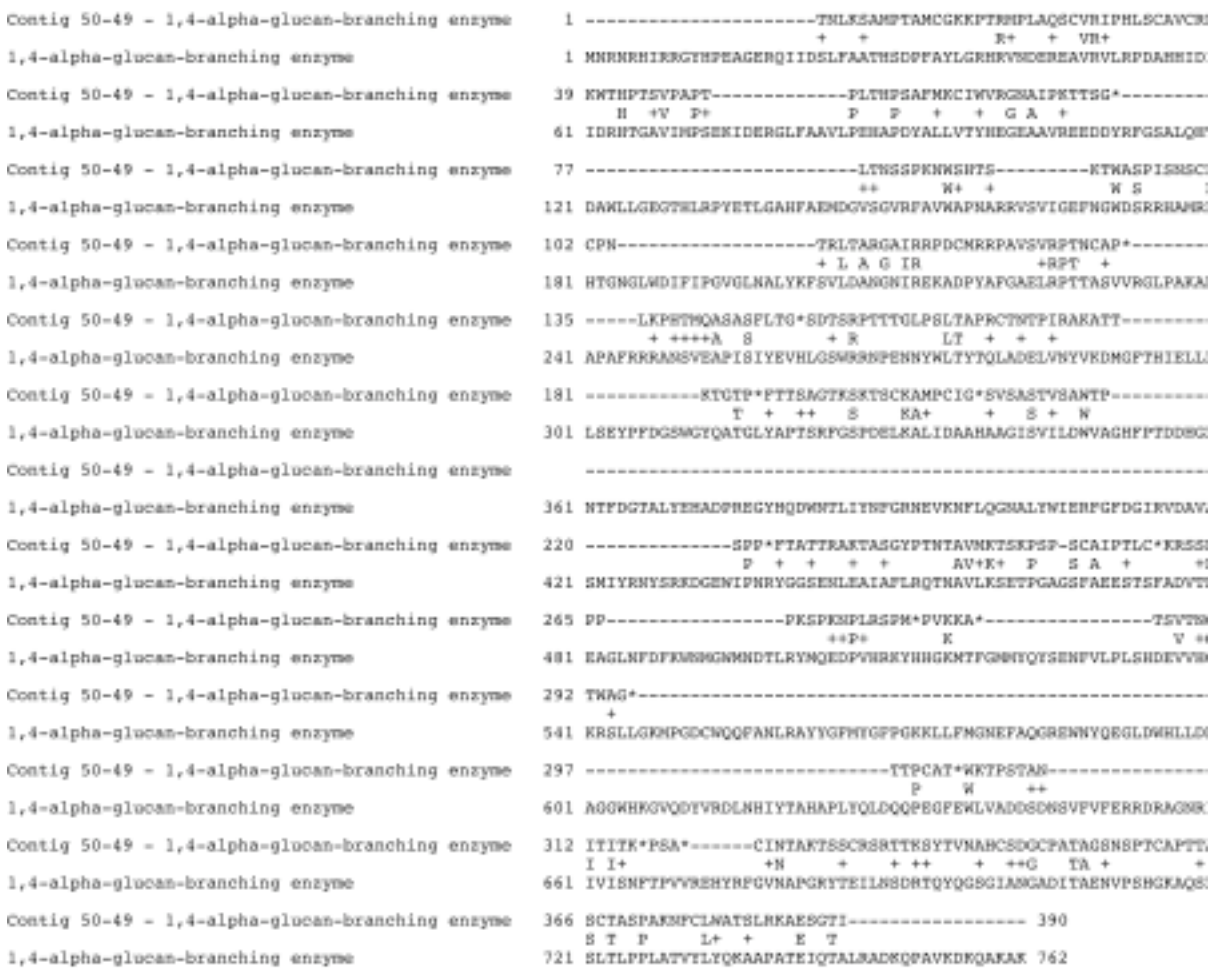
```
Contig 50-49 - 4-alpha-glucanotansferase     1 MSEHLEEQALGLGIDLGFHDIGGIYHETKPEVLEAIVGALQQD-GFSDDLYADTLAAHEH
                                               MSE LE+QA+  GIDLG+HDI G YH TKPEVLE+IV  L +    SD LY +T+ AHEH
4-alpha-glucanotransferase                   1 MSETLEQQAVEAGIDLGYHDINGTYHATKPEVLESIVAVLDKSKADSDGLYLNTMVAHEH

Contig 50-49 - 4-alpha-glucanotansferase    60 GQESLRMPSEFRGAAEVCLEDEMGGRQILALNHGEDGVLWVALPALAYGYYTLSAEIEGI
                                               G+ESL+MPSEF GA  V L DEA   Q L L  G++  LM+ LP LA GYYTLSAE  G
4-alpha-glucanotransferase                  61 GEESLQMPSEFHGAEAVVLIDEADECQSLTLYPGDNDTLWIKLPRLACGYYTLSAETGGF

Contig 50-49 - 4-alpha-glucanotansferase   120 VRKVRLVVAPQSVYQPKMLERGLRMNGLTTHLYSLRSQRNWGIGDFTDLLDLMAFAADKQ
                                                R +RL+VAP+SVYQPK+L  G RMNGLT HLYSLRS+RNWGIGDFTDLL+LM +AA+K+
4-alpha-glucanotransferase                  121 CRLIRLIVAPESVYQPKLLANGGRMNGLTMHLYSLRSERNWGIGDFTDLLNLMKYAAEKP

Contig 50-49 - 4-alpha-glucanotansferase   180 LDFVGINPLHALFSAKPAFASPYSPSSRENLNPIYLDVEKVGAFSYNEKLKNWLKQPNIC
                                               LDFVGINPLHALF++KPAFASPYSPSSRENLNPIYLD+EKVGAF+YNE+LKNWL QP I
4-alpha-glucanotransferase                  181 LDFVGINPLHALFTSKPAFASPYSPSSRENLNPIYLDIEKVGAFTYNEQLKNWLAQPKIP

Contig 50-49 - 4-alpha-glucanotansferase   240 QRIAALRITETVAYTAVWAFKRDALQKAFDAFENDECEAAEQERAAFDAFAETMGEALEC
                                               QRIAALR+TETV YTAVW  KRDALQ AF+AFE D CEAA  ERAAF+AF    G+AL+C
4-alpha-glucanotransferase                  241 QRIAALRVTETVTYTAVWTCKRDALQMAFNAFEQDTCEAAANERAAFEAFVLEKGKALQC

Contig 50-49 - 4-alpha-glucanotansferase   300 FGLFEALDQYYNRSGEVGWLSMPSEFHEPNGEAVQRFAQGHRREIRFYMWLQNLCAEQLR
                                               FGLFEALDQYY+RSG+VGW SMPSEFH+P+ +AV++FA+ H REIRFYMWLQNLCAEQL+
4-alpha-glucanotransferase                  301 FGLFEALDQYYSRSGQVGWQSMPSEFHQPDGKAVEKFARSHEREIRFYMWLQNLCAEQLQ

Contig 50-49 - 4-alpha-glucanotansferase   360 EVNEAAAARGVKLGIYGDLAVGVARGSADTWLNRADYCMDMAVGAPPDPFSPTGQNWNLR
                                               EVN+AAA  GVKLGIYGDLAVGVARGS DTWL+R DYCMD++VGAPPDPFSPTGQNW+LR
4-alpha-glucanotransferase                  361 EVNQAAAEYGVKLGIYGDLAVGVARGSVDTWLHRQDYCMDVSVGAPPDPFSPTGQNWDLR

Contig 50-49 - 4-alpha-glucanotansferase   420 PLNPTVLKHTGYEKFVRLLRENMRLYGILRIDHVMALCRLWWVAG-ETADFGAYVHYNAI
                                               PLNP++LKHTGYEKF  LLRENMRLYG+LRIDHVMALCRLWWV   +TADFGAYVHY+A+
4-alpha-glucanotransferase                  421 PLNPSMLKHTGYEKFAHLLRENMRLYGVLRIDHVMALCRLWWVLNDKTADFGAYVHYDAE

Contig 50-49 - 4-alpha-glucanotansferase   479 VMFAILALESRRNQCVVIGEDLGTVPDQARYLLNRYQVPSYKVVYFSKGWHGPELPEEYE
                                               V FAILALES+RN+CV+IGEDLGTVPDQARYLLNRYQVPSYKV+YFSKGW+GP+LPEEYE
4-alpha-glucanotransferase                  481 VTFAILALESQRNRCVIIGEDLGTVPDQARYLLNRYQVPSYKVMYFSKGWNGPQLPEEYI

Contig 50-49 - 4-alpha-glucanotansferase   539 EQAITVVSTHDVAPLAGYWTGKDLDLMFRLGTIPDAETPQTTLEAREHDKSDLFDKLKHR
                                               EQAITV+STHDVAPLAGYW GKDLD MF+LGT+PDA  PQ  L+ REHDK+DL DKLK+
4-alpha-glucanotransferase                  541 EQAITVISTHDVAPLAGYWMGKDLDTMFKLGTLPDAAAPQMALDEREHDKADLLDKLKYT

Contig 50-49 - 4-alpha-glucanotansferase   599 GCLPADAEMSSEIDEALLTALERYAVMSRSKLYAVQLENLLGMSDNLNVPGVAEGYPNWR
                                               GCL AD +M ++ DE LL AL++Y  +SRSKLYAVQLENLLG+ DNLNVPGV +GYPNWR
4-alpha-glucanotransferase                  601 GCLGADVQMPAKADETLLAALYKYGALSRSKLYAVQLENLLGVIDNLNVPGVPDGYPNWR

Contig 50-49 - 4-alpha-glucanotansferase   659 RKMPVALEDFPHNRLMGGQLAHIGEVRMKKNS 690
                                               +KMPV+LEDF  +RLMGGQLA+I EVRMK NS
4-alpha-glucanotransferase                  661 QKMPVSLEDFLQHRLMGGQLAIIDEVRMKTNS 692
```

Contig 50-49B

Contig 50-49B

>Protein alignment 1261 Alignment of 2 sequences: Contig 50-49 - 1,4-alpha-glucan-branching enzyme, 1,4-alpha-glucan-branching enzyme

Identities = 59/762 (7%), Positives = 119/762 (15%), Gaps = 372/762 (48%)



Contig 56-25

>Protein alignment 1267 Alignment of 2 sequences: Contig 56-25, Glycosyltransfe
rase group 1

Identities = 362/397 (91%), Positives = 377/397 (94%), Gaps = 7/397 (1%)

```
Contig 56-25                    1 VRSSENMNITIVAPYCSLPSEPHFNRFWYLAELLSQSHDVLLITSNFKHYDKSFRRPEDA
                                  MNITIVAPYCSLPSEPHFNRFWYLAELLSQSHDVLLITSNFKHYDKSFRRPEDA
Glycosyltransferase group 1     1 ------MNITIVAPYCSLPSEPHFNRFWYLAELLSQSHDVLLITSNFKHYDKSFRRPEDA

Contig 56-25                   61 ESASQGRLKVMLLEESGYGKNVSLDRVKSHHVFVKHFEQWLNNCRPGEQDVVFSAYPLIA
                                  E+ASQGRLKVMLLEESGY KNVSL RV SHH FVKHFE+WL NCRPGEQDVVFSAYPLIA
Glycosyltransferase group 1    55 EAASQGRLKVMLLEESGYSKNVSLGRVTSHHRFVKHFEKWLENCRPGEQDVVFSAYPLIA

Contig 56-25                  121 TNLLLGEHKARLGYKLIIDVQDVWPESFSSVVPFLKKIPHNLLPFSSRANRAYRYADALV
                                  TNLLLG+HKARLGYKLI+DVQDVWPESFSSVVPFLKK+PH LLPF+SRANRAYRYADALV
Glycosyltransferase group 1   115 TNLLLGKHKARLGYKLIVDVQDVWPESFSSVVPFLKKVPHKLLPFASRANRAYRYADALV

Contig 56-25                  181 AVSQTYLDRAKEANPNVPGEVVYIGADFPKLDAAPAKDFGDSKTRFFYLGTLSYSYDVET
                                  AVSQTYLDRAKE NPNVPGEV+YIGADFPKLDAAPAKDFGD KTRFFYLGTLSYSYDVET
Glycosyltransferase group 1   175 AVSQTYLDRAKETNPNVPGEVIYIGADFPKLDAAPAKDFGDDKTRFFYLGTLSYSYDVET

Contig 56-25                  241 VCKGIRKLLDDGENVELHIMGGGPDLDRLKQYACDGIRFYGYIPYTEMMSVAKGCDISVN
                                  VCKG+RKLLDDGENVELHIMGGGPDLDRLKQYACDGI+FYGYIPY EMMSVAKGCDI++N
Glycosyltransferase group 1   235 VCKGVRKLLDDGENVELHIMGGGPDLDRLKQYACDGIKFYGYIPYAEMMSVAKGCDIAIN

Contig 56-25                  301 AIHSYAMQSITNKLSDYMALQKPILNSQVNDEVAEVLTLLPHADYRSGDVDSFVRAAKDI
                                  AI SY+M SITNKLSDYMALQKPILNSQVNDEVAEVLTLLPHA+YRSGDVD FV+AAKDI
Glycosyltransferase group 1   295 AIQSYSMASITNKLSDYMALQKPILNSQVNDEVAEVLTLLPHANYRSGDVDGFVQAAKDI

Contig 56-25                  361 LARKNDPVQSDEIVRRFKRDVAYQKIVNLIERLAHE* 397
                                  L RK+DPVQSDEIVRRFKRDVAYQKIVNLIERLAHE
Glycosyltransferase group 1   355 LKRKSDPVQSDEIVRRFKRDVAYQKIVNLIERLAHE- 390
```

Contig 28-18

>Protein alignment 1266 Alignment of 2 sequences: Contig 28-18, glycosyl transf
erase

Identities = 83/293 (28%), Positives = 131/293 (44%), Gaps = 27/293 (9%)

```
Contig 28-18              1 -------MKPFISIGILTYNNPMSEIERCLESIFS--QTYGFESIEVIIR-NQGNKKLVE
                              + +G++ Y N   E+ER   ++    +  G      +   N  +  L
glycosyl transferase      1 MTAGGPGRSATLWVGVVLYENTPRELERLCAALQLNREMPGAPLFRTVWWDNSPSDGLRA

Contig 28-18             51 QIKSLAEGKGWEIKVYHGENIGFGAGHNQIFSEISNQ--STAYLCMNPDGFLHDEGLEKL
                            ++  LA     +   + GEN+GFGA HN++  E      + +Y+C+NPDG  H   L +L
glycosyl transferase     61 ELARLAPE---DDYHFQGENLGFGAAHNRLMREAFAAPSTRSYVCLNPDGIPHPRCLAEL

Contig 28-18            109 VSFSQKNDWHGIVEAIQEPIMHPKTFNPKTGLTDWCSGACVLIPNAIYRQINGFDDDFFL
                             + + +    G+VEA   P  HPK + P T  T WCSG  +L+   +Y+++ GFD+ FF+
glycosyl transferase    118 EAEAARPGKTGLVEARLFPDEHPKPYGPVTHETPWCSGCMLLVTRPLYQEVGGFDERFFM

Contig 28-18            169 YCEDVDLSWRVKAAGYQCYTCADAFFFHYAMDR---QSRESEIWRAATFLAYKWRSEKFQ
                            YCEDVDLSWR +AAG+       A   HY +DR     RE  + R+A  L  K+    F
glycosyl transferase    178 YCEDVDLSWRARAAGFSIRVAPRALIHHYTVDRPLTPGRERSVRRSAALLGAKYGDAAFT

Contig 28-18            226 ETAMQMWLQHVDMKKNDLLEQLEHLSQHSVTEVLKANPNFNNGLYFAQPMWG* 278
                               +  ++           E     +       L    +F +   FA+  W
glycosyl transferase    238 RDRVAEYVALGG-------EPFAWPTVARPEAPLARISDFRHLYTFAESRW-- 281
```

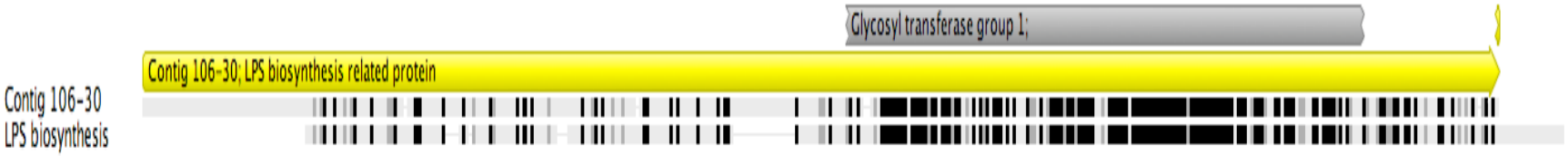
Contig 28-17

>Protein alignment 1265 Alignment of 2 sequences: Contig 28-17, glucosyltransfe
rase

Identities = 87/359 (24%), Positives = 139/359 (38%), Gaps = 58/359 (16%)

```
Contig 28-17            1 --MNQTVSIVIRTMPGREHFLDKCLFILSGQQYQDLEPIVVAQCKTDSESVEKIDVLIAK
                            +   SI+I T   R  F+   L  +  QQY D E IVV  C TD+ ++E +  LI +
glucosyltransferase     1 MTPSPYFSIIIPTYN-RVDFILNTLDTVFNQQYTDYEVIVVDNCSTDN-TLEVLQPLIDE

Contig 28-17           59 WKKHFPKISFLHHTSDTDARAKSLNMGMKYASGRYLAFLDDDDKVYPHHYQQMVQALQKS
                           K     I F+ H  +   RAKS N GM+ A G YL FLD DD +YP +        Q+
glucosyltransferase    59 GK-----IRFIQHDKN-YERAKSRNTGMQNAQGEYLTFLDSDDFMYPDNLLDAYNYAQQH

Contig 28-17           119 KFSWVYCEIVRADFNKDGQLVSRSYPFRRGDYSFHDHIRGNFIPIHAFVVDRERAKDIGF
                           V+  +   +   + + V   Y F+           GNF+      V R+  ++I +
glucosyltransferase    113 PDKKVFHNLY--ELVDEDKKVLSKYDFQPLTDPVRQISEGNFLSCIGVFVHRDIYQNISW

Contig 28-17           179 IN-ETLCKNEDYDFLLRLAFKYEPLHIPNYSAEYCIRSDGTNTVLSHGTLTHTEAVQKRQ
                               L  +EDYDF LRL   +               + G     ++G L H
glucosyltransferase    171 DETPVLTGSEDYDFALRLVAAFP--------------AIGRINKFNNGVLDHPARTINTA

Contig 28-17           238 EWAEADRQLYQLKTEQFGWWIKEIDTASISNPSSNDVGGHASAKVYLLKIYHSYTWKILR
                           +  +A+         E+F ++IK+++               +A    YL KI  +    +
glucosyltransferase    217 QLHKAE--------ERFEYFIKKLNED----------EDYAFFGKYLNKIKATLYIFLAG

Contig 28-17           298 LGKKINWLFRRRPKKKNIIPETESLARAELLKIVFSPAMLILSPLYCVEQFLKKILKK* 3
                           + K+      + PK K  I     + +    +  F      L+  Y  ++ LK
glucosyltransferase    259 MAKEA----HKLPKMKTYIRMAYKVDKGVWKRRNFQS----LNYHYIKKKLLKN----- 3
```

Contig 106-30



Contig 106-30

>Protein alignment 1264 Alignment of 2 sequences: Contig 106-30, LPS biosynthes
is

Identities = 137/418 (32%), Positives = 178/418 (42%), Gaps = 98/418 (23%)

```
Contig 106-30         1 MHVAVIPSWYPKTETDVDGIFFRLQAQALQRKGLKVGVIAPMFRYLRVHTKSIFTGPYGI
                                                                + +F  P  +
LPS biosynthesis      1 ----------------------------------------------MARHVFLPPLSV

Contig 106-30        61 RKHNQGGLNTYAYDSMY-FFPRFPVVDLDRIRWVRAGMKAFARYVRENGRPDIVHAHSMN
                         +H    L    ++S     PR      D     R  +    R+      P I H    +
LPS biosynthesis     13 HRHRPHPLGVCGFESFQTLHPRKRAARPD----SRP-LYELCRHTCLQDFPKIRHPLCRH

Contig 106-30       120 YAGILAYEIYKTYGIPYVITEHSST-ITRNLIRSHQWPIMRLAAEHSAARFAVSRDFSRL
                              Y  +G P  +  +     TR      Q P     A     R AV
LPS biosynthesis     68 GT---QQHHYARFGAPAPMAAYEKCGGTRRRTSRRQPPFRTRPATQIRLRMAVP------

Contig 106-30       179 LKEKYGLEWEYLPNVLGDNFARDFTFPDKGNQ--DYTFCTVSHLRHLKGHDLLLPAFAKA
                            P      ++ D    +K N    + FCTVSHLR LKGHD+LL AFA+A
LPS biosynthesis    119 ------------PPTYWAEYSTDRLNKEKKNNKPHFVFCTVSHLRRLKGHDVLLTAFARA

Contig 106-30       237 LEKYPFLKLKIGGDGVEAANLRRLAQELGITNAVSFLGALTTDEVLDLMRESDAFVLASR
                        L + P L+L IGG G E   L++ A +LGIT+AV+FLGAL  + VLDLMR SDAFVLASR
LPS biosynthesis    167 LAQCPQLRLNIGGSGQEEQRLKQQAADLGITHAVTFLGALQPEAVLDLMRNSDAFVLASR

Contig 106-30       297 TETFGVVFIEALSQGLPVIATMCGGPQSIVTPENGILVPTENIPALTDALIEMYENRERF
                        TETFGVV+IEALSQGLPVIAT CGG +SIV+  NG LVP ++  AL DALI+M E+   F
LPS biosynthesis    227 TETFGVVYIEALSQGLPVIATRCGGAESIVSDGNGYLVPVDDDDALADALIKMCEHHSDF

Contig 106-30       357 DHEKLRQDCLAEPSEEVIASSLIRTFEKIVGEK-QKQP*------------------- 39
                        +  +LR++CL EF E  +   LI  F + + E  +K P
LPS biosynthesis    287 EPARLRENCLNEPGENAVIGRLIGIFRQAIAEYGKKIPVKYSGLTKIRTRRRSRRQYK 34
```

Contig 131-13

Contig 131-13

>Protein alignment 1262 Alignment of 2 sequences: Contig 131-13, LOS glycosyltr
ansferase

Identities = 233/529 (44%), Positives = 334/529 (63%), Gaps = 25/529 (4%)

```
Contig 131-13              1 MNPKIPATAAMLVKNSERYLTEVLTALQDFDEVLLLDNGSTDRTFEIA----ERFTNVSY
                               MN K   +A ++VKN+++ L E L +L+DFDE++LL+N S+D T  IA    + F N+
LOS glycosyltransferase    1 MNLKQ-ISAIIIVKNAKQTLLECLNSLKDFDEIILLNNESSDNTLNIANEFKKDFANLHI

Contig 131-13             57 YKYDFIGFGPMKNLAARLAQNNWIFSIDSDEVADGELIAAIRKAVAENKEQNIFSLSRLN
                              Y   PIGPG +KNLA   A+N+WI SID+DEV + E I  ++    E +E NI +LSR N
LOS glycosyltransferase    60 YHSAPIGPGALKNLALSYAKNDWILSIDADEVLENECIKELKN--LELQEDNIIALSRKN

Contig 131-13             117 HYNGRLIKACGWYPDIIPRLYHRRFTRFSDRQVHESLILPPDANIRPLEGRLKHYSFENA
                               Y G  IKACGW+PD + R++++ FTRF+D  VHESL+LP +A    L+  L+HY+F +
LOS glycosyltransferase   118 LYKGEWIKACGWWPDYVWRIFNKNFTRFNDNLVHESLVLPSNAKKIYLKNGLRHYAFRDI

Contig 131-13             177 EGLIQKMQQYSSLYAEENRYKKDSSPFKALLHGSVSFVKNYLLKRGFAYGADGLTISIAN
                                 LI KMQ YSSL+A++N +KK S   KA L    +F +NY LK GF YG  G  IS+ N
LOS glycosyltransferase   178 SHLIDKMQYYSSLWAKQNIHKK-SGVLKANLRAFWTFFRNYFLKNGFLYGYKGFIISVCN

Contig 131-13             237 AQGSYYKYVKLYERNRN--ISVALIVTTYNRPDALELVLKSALAQTRRPDEIIVADDGSR
                              A G+++KY+KLYE  +    + ALI+TTYN+ + L+LVL S       P+E+++ADDGS+
LOS glycosyltransferase   237 ALGTFFKYMKLYELQKQKPKTCALIITTYNQKERLKLVLDSVKNLAFLPNEVLIADDGSK

Contig 131-13             295 QDTAEVVEFIRSHTDIPVKHSWRPDDGFRAAESRNRALAQAKSDYIILIDGDMILDPSFV
                              +DTA ++E  +     P+KH W+ D+GFRAA+SRN A+  +KS+YIILIDGDMIL+  FV
LOS glycosyltransferase   297 EDTARLIEEYQKDFPCPLKHIWQEDEGFRAAKSRNNAIKASKSEYIILIDGDMILEKDFV

Contig 131-13             355 ADHLKLARKGRLVQGSRVILTQARTEEILDSGELPDLSVFSQGIEKRLSALRCR---SLS
                               +HL+ A++  ++QGSRVIL +  +EEIL +     L+   +G + + S    +     S
LOS glycosyltransferase   357 KNHLEPAKRKVILQGSRVILNKNESEEILKNNNYS-LAFNKKGFKNQRSIFLAKCVYKFS

Contig 131-13             412 ALIGR--QSSRKHKGIKTCNMGFFRSDALAVNGFDNRFVGWGREDSEFVARLFHNGMKRH
                               L  +  + S+  KG KTCNM F++SD  A+ GF+ +F+GWGREDSEFVAR   N
LOS glycosyltransferase   416 KLTKKFFKKSQLVKGSKTCNMSFYKSDFEAIEGFNEKFIGWGREDSEFVARFLFNDGVFK

Contig 131-13             470 NLKFAGIAYHLWHHEAERDALPQNDALLKATLSEQKIRCEHGMDEFIK* 518
                               LKF  +AYH++H E  ++ L  N  +   T+  +K
LOS glycosyltransferase   476 RLKFNALAYHIYHEENSKNMLEINHQIYLETIKNEKTTWR--------- 515
```

Contig 56-23


Glycosyl transferase group 1;
Contig 56-23; Glycosyltransferase Group 1
Contig 56-23
Glycosyltransferase

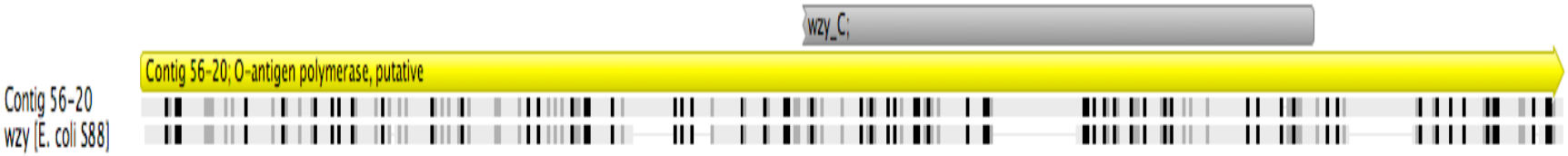
Contig 56-23

>Protein alignment 1255 Alignment of 2 sequences: Contig 56-23, Glycosyltransfe
rase

Identities = 293/361 (81%), Positives = 323/361 (89%), Gaps = 5/361 (1%)

```
Contig 56-23              1 MKKIVLTTSMSGLGGTENATFRLGRLLRQRGHEVVLASSDGPLIKETQALGIQWRPIDFY
                              KIVLTTSM+GLGGTE AT RLGRLLRQ GH+++LASSDGPL+KE QALGI+W+P+DFY
Glycosyltransferase       1 -MKIVLTTSMAGLGGTETATVRLGRLLRQHGHDIMLASSDGPLLKEAQALGIRWQPVDFY

Contig 56-23             61 QGGILGYIKGMPAYMKMLKQEKPDIVHCQMARIVPACAIAAKIASPKTKVFYHARGLDAE
                              +GG+ GY+KGM AY +ML++E+PDI+ CQMAR+VPACAIAAKI SPKTK+ YH+ GLDA
Glycosyltransferase      60 RGGLFGYLKGMIAYARMLRREQPDIIDCQMARVVPACAIAAKIVSPKTKIIYHSHGLDAA

Contig 56-23            121 TYPKIAKLFDKLGVYIIGNCRHEREKLIRHGFPANRIAYTYNALHK---ADYVPEKTAKE
                              TYPKIAKLFDKLGVYIIGNC+HEREKLIRHGFPA+RI Y YNAL      ++   KT K
Glycosyltransferase      120 TYPKIAKLFDKLGVYIIGNCKHEREKLIRHGFPADRIVYAYNALPPPPPPEFPFWKTVKG

Contig 56-23            178 YVMLGTLSRLDTVRAVHVMLDIFKKMIDRNMPVRLNVAGIGEEMDNLKAQAKRLGIDDKV
                              YVMLGTLSRLDTVRAVH+MLDIFKKM+DR+MPVRLNVAGIGEEMDNLKAQA+RLGID KV
Glycosyltransferase      180 YVMLGTLSRLDTVRAVHLMLDIFKKMVDRDMPVRLNVAGIGEEMDNLKAQAERLGIDGKV

Contig 56-23            238 NFLGGVRDLTGYFKDVDILVNTPHCIGDHGAGVGNNILEAGLYDTPVVTYNMGGISEMVI
                               FLGGVRDLT YFKDVDILVNTPHCIGDHGAGVGNNILEAGLYDTPVVTY+M GISEMV+
Glycosyltransferase      240 TFLGGVRDLTAYFKDVDILVNTPHCIGDHGAGVGNNILEAGLYDTPVVTYDMAGISEMVV

Contig 56-23            298 TGETGYCYPFGEDEAFIEAVDKLIKQPELREKMGKALHKHVETLCSDDEIYRTTMAAYDM
                               GETGYC PFGEDEAFIEAVD LIK PELR +MGKALHKHVETLCSDDEIYRTTMAAY M
Glycosyltransferase      300 NGETGYCIPFGEDEAFIEAVDTLIKHPELRGQMGKALHKHVETLCSDDEIYRTTMAAYTM

Contig 56-23            358 * 358

Glycosyltransferase         -
```

Contig 56-20


wzy_C;
Contig 56-20; O-antigen polymerase, putative
Contig 56-20
wzy [E. coli S88]

Contig 56-20

>Protein alignment 1247 Alignment of 2 sequences: Contig 56-20, wzy [E. coli S8
8]

Identities = 61/427 (14%), Positives = 128/427 (29%), Gaps = 65/427 (15%)

```
Contig 56-20          1 VKLKTQTLYITLIYTISTAYMLGPMLSYKAGIPRIDNPLTILLLPTALLLFALESKRFNG
                          L+ TL       +++   + +   I       +  L+   +   +L    F G
wzy [E. coli S88]     1 -MANIYFLPGTLFIFSPVFFIIQFCVFFLVFIQGKCKVSSQGLIFILVSFTSLIFHVFFG

Contig 56-20         61 KAGKMLAALAIMCGWGGIHLFITTLDSVRIMDTFFFLSLPSLFYLLYLVLSRHENPAAFI
                           K+     + C +  + +       V+ + +  +L +       ++     +  A  I
wzy [E. coli S88]     60 VVDKIFIFTLVCCFY-ALTVPSIYSYCVKRIKSCDWLKVIDFCIKFHIFTFLLQYLAFKI

Contig 56-20        121 RRLLLFFCAFIIIPPAVEILTGIQFVQADEVLAIDAGIIKGFFFNPNNLGTTALCFAPAV
                          + + +  F++ PP      G  +               G F  P     +
wzy [E. coli S88]    119 INVDIDYGKFLLGPPHRSSYDGFDYRAT----------GVFAEP-----SIFSIHMVT

Contig 56-20        181 LVFFNIDVSKKEYLLGWMLFLCLGVVIFASASRTATLCYIILFILNLIYRNNGLFTLMTI
                         L+     V+    LL ++  +C+ +     +     L +I+   L L +   GL +L+ +
wzy [E. coli S88]    162 LLVMRYIVANNNSLLSYIALMCMVLSGSTFSVICVMLFFILTCRLTLKWIATGLISLVLV

Contig 56-20        241 GVTGAGLSMIPKHYIADFLLSLHGNAFLENISSRLYLFLFDLESDNSVGYRQEIYNYFWE
                             M    YI+                          SD S  Y+ E+   F++
wzy [E. coli S88]    222 SPIIYQNIMWRMSYIS-----------------------SGSDGSTSYKLELMKSFFD

Contig 56-20        301 HPPFLLLGYGPKKFQEYFGGHLSDSLAFENPHSFLIELYLGFG-LISLAAFFFYAAYYFF
                         P    +G+G   + +    +            S  I      G ++S++    +  Y  F
wzy [E. coli S88]    257 SPLVFNIGHGMVGYYDNAPDYFQSLFDMTLFGSNFIVPGFWLGSILSVSWLVLFLKYSRF

Contig 56-20        360 CVAAGRNMKSKQRVIGLAAMGLFLLAGFIPSTILRMPFIWLPCFLIFLYSVLPQRDAAYN
                         +                     +L   +P   L   F     +L+FL      ++  Y
wzy [E. coli S88]    317 SLR------------------LMLLCLLPCLKLTFLFPMFWLYLVFLAGYAGIKNEKY-

Contig 56-20        420 AYRYTP* 426
                           RY+
wzy [E. coli S88]    357 TTRYSKI 363
```

Contig 56-40


Wzz, Chain length determinant;
CbiA;
Contig 56-40; Chain length determinant protein
Contig 56-40
Wzc

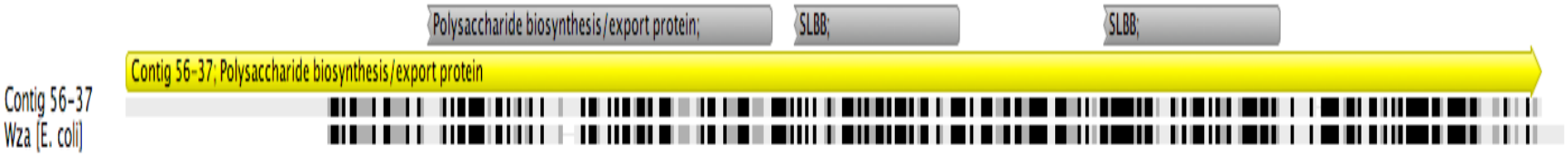
Contig 56-40

>Protein alignment 1258 Alignment of 2 sequences: Contig 56-40, Wzc

Identities = 305/734 (41%), Positives = 448/734 (61%), Gaps = 18/734 (2%)

```
Contig 56-40     1 -MYKQYPSSAPAGNDEIDFGQQMQSLWQNKNKIAAAILAGGLAGAVIGLASTPLYRADAM
                     K   S+A  G+DEID G+ + ++ + +  +         L   +    +TP+Y ADA+
Wzc              1 MTEKVKQSAAATGSDEIDIGRLVGTVIEARRWVLGTTAIFALCAVIYTFFATPIYSADAL

Contig 56-40    60 LEIETKQ-NQILTEINNMLSNEPAPSEAEVELVQSRLVLGKTVEDLQLDQEVKATYFPIF
                   ++IE    N ++ +IN+ L+N+P  S+AE++L++SRLVLGKTV+DL LD  V    FP+F
Wzc             61 VQIEQNAGNSLVQDINSALANKPPASDAEIQLIRSRLVLGKTVDDLDLDIAVTKNTFPLF

Contig 56-40   119 GNIVHNLSGSDDPMLKIGSFTVSEDWINKPFKLTVKDSKTYLLTLPDGTTKEGRVGAPLK
                   G     L G  + M+K+ +FT  E    + F L V   K Y L    G + +G VG PL
Wzc            121 GAGWERLMGRHNEMVKVTTFTRPETMSGQIFTLKVLGDKRYQLVSDGGFSAQGVVGQPLN

Contig 56-40   179 VNNETVLKVDRILAEAEQDFELTKFSKLSAIENLKNKLSVISKGKTSPIINLSYTDTDPK
                    +    ++V+ I A  + +F ++KFS L  I NL+N L+V   GK + +++L++T  D
Wzc            181 KD-GVTMRVEAIDARPDTEFTVSKFSTLGMINNLQNNLTVTETGKDTGVLSLTFTGEDRD

Contig 56-40   239 KTSTILNSIADNYVSQNRERDVQVASSGLAFISEELPRLKETLQDAENKLNAYRERSGSL
                   +   ILNSI  NY  Q+  R  + A   LAF++++LP ++  L  AENKLNA+R+   S+
Wzc            240 QIRDILNSITRNYQQQDIARKSEEAGKSLAFLAKQLPEVRSRLDVAENKLNAFRQDKDSV

Contig 56-40   299 DIPLESKGALESLTSIETQITLLKTEEAGLAELYTPEHPSYKAVLDKLAVLERAKSKINQ
                   D+PLE+K  L+S+ +I+ Q+  L  +EA +++L+T  HP+Y+ +L+K   LE  K+K+N
Wzc            300 DLPLEAKAVLDSMVNIDAQLNELTFKEAEISKLFTKAHPAYRTLLEKRKALEDEKAKLNG

Contig 56-40   359 QIAGLPNTQQEVIRLTRDVETNQATYVQLLAKQQELNIMKASAQGNVRVVDHAYTPEKPI
                   ++  +P TQQE++RLTRDVE+ Q  Y+QLL KQQEL I +AS  G+VR+VD A T    +
Wzc            360 RVTAMPKTQQEIVRLTRDVESGQQVYMQLLNKQQELKITEASTVGDVRIVDPAITQPGVL

Contig 56-40   419 APRKAVIAALGALAAGALASMWFLLQGRMRRGITSSEEIEALDLEVSALIPHSKTQQKRD
                    P+KA+I     +    L+ +  LL+    RGI S + +E   + V A IP S+ Q+ RD
Wzc            420 KPKKALIILGSIILGLMLSIVGVLLRSLFNRGIESPQALEEHGISVYASIPLSEWQKARD

Contig 56-40   479 LIKRKFKSLKGRSNYLLANEDSTDIAVEAIRALRTNIYFSMLDARNNILMITGAAPEAGK
                    +K      + + + LLA  + TD+A+EAIR+LRT+++F+M+ A+NN+LM+TG +P  GK
Wzc            480 SVKTIKGIKRYKQSQLLAVGNPTDLAIEAIRSLRTSLHFAMMQAQNNVLMLTGVSPSIGK

Contig 56-40   539 SFISANLATVMAQSGKRILLIDTDMRKGYLDQLLNVTPEFGLSDLLSGEVSPAQAVTQTN
                   +F+ ANLA V++Q+ KR+LLID DMRKGY  +LL      GLSD+L+G+   A     T
Wzc            540 TFVCANLAAVISQTHKRVLLIDCDMRKGYTHELLGTNNVDGLSDILAGKGEIASCAKPTA

Contig 56-40   599 IPNLHLISTGSYPKNPSELLMDNRFKELLSNAQKRYDYVIIDTPPVLAVTDAVVVGQHAG
                   I N  LI  G  P NPSELLM  RF EL++ A  RYD V+IDTPP+LAVTDA +VG+HAG
Wzc            600 IANFDLIPRGQVPPNPSELLMSERFGELIAWASSRYDLVLIDTPPILAVTDAAIVGRHAG

Contig 56-40   659 TVLLVSRYGNTTTKELAISAERLRQNKITIKGVILNGMKREANSTYDY-YYSYITPTEGK
                   T L+V+RY   T KE+  S  R  QN I +KGVILN + R A    DY YY Y   ++ K
Wzc            660 TTLMVARYAVNTLKEVETSLSRFDQNGIQVKGVILNSIFRRATGYQDYGYYEYEYQSDSK

Contig 56-40   718 KTAKKTTSEKPKA* 731

Wzc                --------------
```

Contig 56-37


Polysaccharide biosynthesis/export protein;
SLBB;
SLBB;
Contig 56-37; Polysaccharide biosynthesis/export protein
Contig 56-37
Wza [E. coli]

Contig 56-37

>Protein alignment 1257 Alignment of 2 sequences: Contig 56-37, Wza [E. coli]

Identities = 148/385 (38%), Positives = 221/385 (57%), Gaps = 64/385 (16%)

```
Contig 56-37      1 MKKQLALISLSLMALTACNSSTVIPGSTINTRNKTIVYENGETVADTKFDKRVAIYPITF
                                                                +YP+T
Wza [E. coli]     1 ----------------------------------------------------VYPMTP

Contig 56-37     61 GLVEKMRKPPVLSQNNGVLERSKAAYRYHIGKGDVLNIMVWAHTDLNSPVQQSNPQTNQV
                    GL++++R  PV++++N  L+    +Y Y IG GDVL + VW H +L +P  Q    +
Wza [E. coli]     7 GLIDQLRPEPVIARSNPQLDNLLKSYEYRIGVGDVLMVTVWDHPELTTPAGQYRSAS---

Contig 56-37    121 SRGAWVDEGGYITYPLVGKIQAQGKTIDELQNILTGRLKRYLKNPQVAINVTEFRSQRVS
                      G WV+  G I YP +GK+Q  GKT+ +++  +T RL  Y+++PQV +++  FRSQ+V
Wza [E. coli]    64 DTGNWVNSDGTIFYPYIGKVQVAGKTVSQVRQDITSRLTTYIESPQVDVSIAAFRSQKVY

Contig 56-37    181 VAGAVGQAGQLPITNVPMTILDAVNQAGGVAQNADTHNIKWTHNGVDRTISLQSIMQYGD
                    V G V  +G+  ITN+P+T++DA+N AGG+A +AD  N+  THNG D  ISL ++MQ GD
Wza [E. coli]   124 VTGEVANSGKQAITNIPLTVMDAINAAGGLAADADWRNVVLTHNGKDTKISLYALMQKGD

Contig 56-37    241 MSQNHLLSNGDIVYVPNNSNSKVYVMGEVGRQATLPIGNHGLNLTQALGEAGGMNQTQAD
                    ++QNHLL  GDI+++P N + KV+VMGEVG+Q+TL +   G+ L +ALG A G++Q  +D
Wza [E. coli]   184 LTQNHLLYPGDILFIPRNDDLKVFVMGEVGKQSTLKMDRSGMTLAEALGNAEGISQEMSD

Contig 56-37    301 ATGVFVIRRAPEDAIKPIH-IYQLNLKDATAYALGNDFDLRPNDIVYVTAAPVTRWNRVV
                    ATG+FV+R+   D    I  IYQLN +DA+A  LG +F L+P DIVYVT AP+ RWNRV+
Wza [E. coli]   244 ATGIFVVRQLKGDRTGKIADIYQLNAQDASAMVLGTEFQLQPYDIVYVTTAPLVRWNRVI

Contig 56-37    360 SQITSFVTNVNSIDSTFK*------ 378
                    SQ+   ++ V+ +  T +
Wza [E. coli]   304 SQLVPTISGVHDMTETVRYIKRWPN 328
```

Contig 56-18


Polysaccharide biosynthesis protein;
Contig 58-18; LPS biosynthesis translocase
Contig 56-18
LPS translocase

Contig 56-18

>Protein alignment 1256 Alignment of 2 sequences: Contig 56-18, LPS translocase

Identities = 223/476 (46%), Positives = 310/476 (65%), Gaps = 4/476 (0%)

```
Contig 56-18          1 MNIKKILGYALGPIGSAAFGILSLPLISWYYPAEDIGRIVLLQTISGLTILILGLGLDQA
                        M+ K+ILGYA G IGSA   ++ LPL+SWY+PA+DIGRIVL+QT +GLT+ +L LGLDQA
LPS translocase       1 MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA

Contig 56-18         61 YIREYYAAKDKASLFKSISLSPFVLAIVVILAVLVWNTAWPADLIFDLQDKTLGLLFLIF
                        Y+REYYAA DK +LFK++ L P +L+   I A+L+   + P++++F L D   G+  ++F
LPS translocase      61 YVREYYAAADKDTLFKTLFLPP-LLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLF

Contig 56-18        121 LLTSLFARFLSLILRMQEKAVAFSLSQLTPKFLILALVLLFVFSG---VETDTVSLVLAY
                         L+ L  RFL L+LRM+ +A+AFS +QL PK  IL L+LL +  G      +T  L   Y
LPS translocase     120 ELSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLLLLPLTVGLLHFPANTAVLTAVY

Contig 56-18        178 TVAQVLTVAVLTYQTRHELRAAARAPWSSETHHASLRYGLPLAFGNLAYWGLTSIDRFAL
                         +A +   A L +Q R  L+A   AP+S    H  LRYG+P+A  ++AYWGL S DR  L
LPS translocase     180 ALANLAAAAFLLFQNRCRLKAVRHAPFSPAVLHRGLRYGIPIALSSIAYWGLASADRLFL

Contig 56-18        238 KQWAGLDELGIYSMAVSFGAVALIFQSVFSTIWAPLVFKWVENKTHLDKIGGITLSMTEL
                        K++AGL++LG+YSM +SFG  AL+FQS+FST+W P +F+ +E      ++     S   L
LPS translocase     240 KKYAGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAAL

Contig 56-18        298 ISAMICFIGIFSPVVTWILPDKYATVQFLLLSCMLYPLFYTLTEVSGIGLNVVKRTWLIT
                        +++ +C  GIFSP+ + +LP+ YA V+F+++SCML PLF TL E+SGIGLNVV++T  I
LPS translocase     300 LASALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIA

Contig 56-18        358 AVNIVAFAINFGLLSLLVPHLGARGAAIASAISFWVFCVIKTEFSSRVWRSLPRLKIYTN
                           + A A N  LL L VP  GARGAA+A A SFW+F V KTE S R+W+ L RL +YT+
LPS translocase     360 LATLGALAANLLLLGLAVPSGGARGAAVACATSFWLFFVFKTESSCRLWQPLKRLPLYTH

Contig 56-18        418 TALSVLLCVSYTYFGTKENYPLFALLWLAGLSYLIWCRKSSLISAAAAVKSRLKR* 473
                        T L +    +YT FGT  NYPLFA +W   L+  I      L      +K +
LPS translocase     420 TLLCLTSSAAYTCFGTPANYPLFAGVWAVYLAGCILRHWKDLHKLFHYLKKQGFPL 475
```

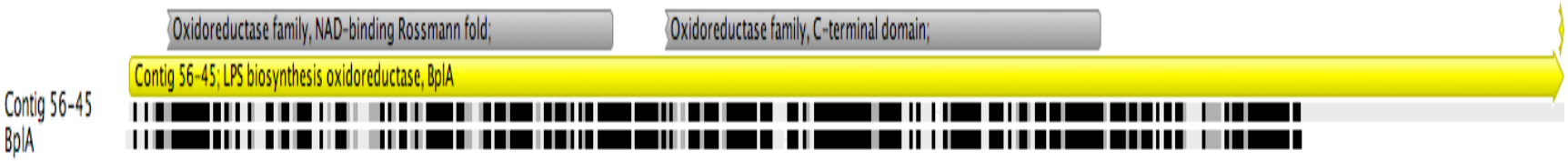
Contig 11-2

>Protein alignment 1263 Alignment of 2 sequences: Contig 11-2, capsular biosynthesis

Identities = 75/345 (21%), Positives = 121/345 (35%), Gaps = 86/345 (24%)

```
Contig 11-2                ------------------------------------------------------------

capsular biosynthesis      1 MKLSIIIPVYNVEKYISTCLDSIVNQDLKKDEYEVIIINDGSTDNSGKIVKTYSENYSNI

Contig 11-2                1 -LIDTPNGGVSRARNIGLSKVRGEYVMFMDHDDNIDPPLLTGLVEKMKHSDADMLQFN--
                             L    NGGV  ARN GLS  +G++V F+D DD +   +L  L       + D+L F+
capsular biosynthesis     61 FLYTQKNGGVGSARNKGLSYAKGDFVYFLDPDDYLAMNVLKTLTSTAVQYNLDVLTFDST

Contig 11-2               58 -----------VDARYPANEDEVIGLADYMDRYLFWSCVWSYIYKRSLLEKAGLKFIEGM
                                          AN  +VI   DY+ +  + S VW ++  RS L    LKFI+G
capsular biosynthesis    121 SFNDSSVLPENNSNNSEANLSDVITGIDYIAKTKYSSTVWLFLINRSFLIDIDLKFIKG-

Contig 11-2              107 KYLEDGVFLTEYFLQCQTVIASNTVVYDYVDNPESAMRSKRTPEQTKKYLDDIG--LAVR
                             +++ED +F  E F++ + +   N   Y Y  + ESAM S       K   D+I   L
capsular biosynthesis    180 RWMEDAIFTLELFIKVKRMAHLNINAYFYRVSSESAMNSYEPNHYLKLIDDNINAALVFN

Contig 11-2              165 EYTRLLATPGQPPKVVRRLLEIRDSFQFIHLVSMLKSGVSTDELFRRLEENG--YDFRMA
                                + L      P  ++R+   + SF F  ++ M+KS +S +E+ + + +      F +
capsular biosynthesis    240 PIIQKLENDKVNPNCIKRVKARQQSFLFFSMIRMIKSTISFNEVKQIMNKMSEQNIFPLH

Contig 11-2              223 GYPSKFNRRRDVRLLCHVFRSR-----LLLKLLAASKIMAKD*-- 260
                              +  K        +L  V  S+       L      K++ K
capsular biosynthesis    300 MFLGKDYNLLSYHILTRVLNSKRRFYFFFLLFNPFLKLVYKYSPK 344
```

Contig 56-45


Oxidoreductase family, NAD-binding Rossmann fold;
Oxidoreductase family, C-terminal domain;
Contig 56-45; LPS biosynthesis oxidoreductase, BplA
Contig 56-45
BplA

Contig 56-45

>Protein alignment 1259 Alignment of 2 sequences: Contig 56-45, BplA

Identities = 192/378 (50%), Positives = 239/378 (63%), Gaps = 72/378 (19%)

```
Contig 56-45     1 -MSETIQNRKIKFALVGCGRISNNHFGSFEVLQEDCGLVAVCDIDPAALATAVKRTGAKG
                     S  I +RK++FALVGCGRIS NH G+ E  Q+   LV +CD +PAAL  A + TGA+
BplA             1 MTSTPIGDRKVRFALVGCGRISKNHIGAIEKHQDRAELVEICDTNPAALKAAHEATGARP

Contig 56-45    60 YAHYTEMLTETDADVIVITTPSGLHPEQAVQALEAGFHVVTEKPMATCFTDGERMVQAAD
                   +   +++L E+ AD +V+ TPSGLHP QA++  +AG HVV+EKPMAT + DG+RMV+A D
BplA            61 FESLSDLLAESTADAVVLATPSGLHPWQAIEVAQAGRHVVSEKPMATRWEDGKRMVKACD

Contig 56-45   120 KAGKRLFVVKQNRLNATLQLLKRAVTEQRFGKIYMVHLNVFWTRPQSYYDQGGGWRGTWK
                   +AG RLFVVKQNR NATLQL+K+A+ + RFG+IYMV +NVFWTRPQ YYD    WRG W+
BplA            121 EAGVRLFVVKQNRRNATLQLVKKAIEQNRFGRIYMVTVNVFWTRPQEYYDAAR-WRGKWE

Contig 56-45   180 LDGGAFMNQASHYVDLMEWLIGPVAEVQAMIAT-HRKIEAEDTGVMNLRWRDGTLGSMAV
                    DGGAFMNQASHYVDL++WLIGPV  V A   T  R+IEAEDTGV  LRWR G +GS+ V
BplA            180 WDGGAFMNQASHYVDLLDWLIGPVESVYAYTGTLARRIEAEDTGVAALRWRHGAMGSINV

Contig 56-45   239 TMCTYPKNLEGSITILGKTGTVRIGGMAVNEIQEWNFADERDYDEQVKTANYETTSVYGF
                   TM TYP+NLEGSITILG+ GTVR+GG+AVN I EW FA+    D++++ A+YET+SVYGF
BplA            240 TMLTYPQNLEGSITILGEHGTVRVGGVAVNRIDEWKFAEPHPDDDKIRDASYETSSVYGF

Contig 56-45   299 GHPLYYRNVVDVLRGKAEPVVDGREGLKSLELINAAYLSAHNRQTVSLPLVLQTLQTFDH
                   GHPLYY NV
BplA            300 GHPLYYDNV-----------------------------------------------------

Contig 56-45   359 SYYSKGSPFHNQSKESS* 376

BplA               ------------------
```

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